(51) International Patent Classification[7]: C07H 21/04, C12N 1/20, 5/02, 15/00, 15/12, C12P 21/06, C12Q 1/68

(21) International Application Number: PCT/US01/10472

(22) International Filing Date: 30 March 2001 (30.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/540,217	31 March 2000 (31.03.2000)	US
09/649,267	23 August 2000 (23.08.2000)	US
09/649,167	23 August 2000 (23.08.2000)	US
60/250,583	30 November 2000 (30.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:
US	09/540,217 (CIP)
Filed on	31 March 2000 (31.03.2000)
US	09/649,167 (CIP)
Filed on	23 August 2000 (23.08.2000)
US	60/250,583 (CIP)
Filed on	30 November 2000 (30.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvalle, CA 94086 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). LIU, Chenghua [CN/US]; Apt. #14, 1125 Ranchero Way, San Jose, CA 95117 (US). DRMANAC, Radoje, T. [YU/US]; 850 Greenwich Place, Palo Alto, CA 94303 (US). FORD, John, E. [US/US]; 2763 South Norfolk #210, San Mateo, CA 94403 (US). BOYLE, Bryan, J. [US/US]; 1947 10th Avenue, San Francisco, CA 94116 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL BONE MARROW NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel bone marrow expressed nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL BONE MARROW NUCLEIC ACIDS AND POLYPEPTIDES

1. BACKGROUND OF THE INVENTION

5   **1.1 TECHNICAL FIELD**

The present invention provides novel bone marrow-expressed polynucleotides and bone marrow-expressed proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

10   **1.2 BACKGROUND**

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the

15 discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the

20 state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

The bone marrow is a well-organized tissue located within the central cavity of bone. It

25 has a complex three-dimensional structure that is richly innervated and highly vascularized. Two primary cell types make up the structure of the bone marrow. These are the stromal, and parenchymal cells. Stromal cells include reticular cells such as fibroblasts, endothelial cells, adipocytes, as well as cells of the osteochondrogenic lineage. They exert important influences on osteoclastogenesis and lymphopoiesis, and have additional effects on bone turnover.

30 Parenchymal cells are comprised of the hematopoietic cells, and are important for proliferation, maturation, and migration of cells that make up the blood.

In the adult, hematopoiesis takes place primarily in the bone marrow. Therefore, all of the cells that make up the blood, such as erythrocytes, platelets, basophils, natural killer cells, eosinophils, T- and B-lymphocytes, neutrophils, macrophages, and others, are produced in this

35 structure. Each of these cells is derived from a common, self-renewing stem cell that

proliferates, and/or differentiates depending on regulatory molecules that are produced by the stromal cells. Stromal cells are predominantly a mixture of fibroblasts, macrophage/dendritic lineage cells, epithelial cells, and endothelial cells. They influence the fate of hematopoietic cells through the secretion of soluble factors, cytokines, and the expression of membrane-

5   anchored growth factors, and cell surface recognition molecules.

Cytokines are necessary for normal hematopoiesis in the bone marrow, and provide a means of fine-tuning bone marrow function in response to stimulation. They are not only produced by stromal cells, but can also be secreted by macrophages, and antigen-stimulated T lymphocytes for the purpose of replenishing leukocytes that may be consumed during immune

10   and inflammatory reactions. Many cytokines that influence the differentiation and expansion of hematopoietic progenitor cells are termed colony-stimulating factors, because they were initially assayed by their ability to stimulate the formation of cell colonies in bone marrow cultures. Some of these colony-stimulating factors (CSFs) include, granulocyte-CSF, granulocyte/macrophage-CSF, monocyte-CSF, Kit-ligand, interleukin (IL)-6, FLK-2 ligand, and

15   leukemia inhibitory factor. Each of these stimulates the growth and development of various leukocytic or erythroid colonies. Other cytokines secreted in the bone marrow include IL-9, a T cell line and mast cell progenitor-stimulating factor, IL-11, a megakaryocytopoiesis stimulator, and IL-7, a cytokine that influences the survival and expansion of immature precursors committed to the B and T cell lineages. Many other cytokines are also secreted in the bone

20   marrow.

Cell-surface molecules that represent several adhesion molecule superfamilies including integrins, selectins, sialomucins and the immunoglobulin domain-containing proteins, are important in supporting cell-cell and cell-extracellular matrix interactions in the bone marrow. These proteins are critical to the homing of progenitor cells selectively to the marrow stroma for

25   proliferation and differentiation. They also serve to influence the fate of the progenitor cells by directing them to differentiate into a specific lineage. For example, VLA-4 directs control of late erythroid differentiation and pro-B cell maturation.

The bone marrow is also the site of B cell development. B cells begin as lymphoid stem cells that differentiate into progenitor B-cells, or pro-B cells. Pro-B cells proliferate within the

30   bone marrow, and fill the extravascular spaces between large sinusoids in the shaft of the bone. They next mature into precursor B cells, pre-B cells. The stromal cells of the bone marrow are crucial for both pro- and pre-B cell development because they provide a source of cytokines, and a substrate for direct interaction with the pro- and pre-B cells. Pro-B cells require interaction with VCAM-1 and stem-cell factor (SCF) on the stromal cells to induce expression of the IL-7

35   receptor. Secretion of IL-7 by the stromal cells then induces the pro-B cells to mature into pre-B

cells. Continued IL-7 secretion by stromal cells induces pre-B cells to begin proliferating and eventually differentiates them into immature B-cells. In addition, a selection process within the bone marrow eliminates B cells with self-reactive phenotypes, functioning to protect against autoimmune disease.

5   The bone marrow environment also influences bone turnover and bone precursor cell functions. Bone marrow stromal cells include the precursors of the osteochondrogenic lineage, and can modulate the effects of some systemic factors on bone turnover. Furthermore, hematopoietic cells may influence the differentiation of osteogenic cells, and mature lymphocytes may impact osteoclastic and osteoblastic functions. For instance, B-lymphocytes

10   have been implicated in the secretion of factors that change the immunological milieu at sites of new bone induction and influence new bone formation.

The identified bone marrow-expressed polynucleotide and polypeptide sequences may have applications in hematopoiesis, stem cell survival, and bone growth and remodeling. Identification of secreted factors that stimulate hematopoiesis may serve to produce greater

15   immune responses in immunosuppressed individuals. The identification of factors that preferentially stimulate specific hematopoietic cell types may also allow the prevention of specific disorders such as anemia in the case erythroid cell stimulating factors, or platelet deficiency in the case of megakaryocyte stimulating factors. Likewise, stem cell stimulating factors may be used to restore blood cell populations following chemotherapy treatments for

20   cancer. Therapy to stimulate bone healing and remodeling may also be identified by the discovery of novel factors in the bone marrow that influence bone resorption by osteoclasts, or new bone cell differentiation from stromal cells.

2. SUMMARY OF THE INVENTION

25   The compositions of the present invention include novel isolated polypeptides from bone marrow tissue, and novel isolated polynucleotides from bone marrow tissue encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as

30   well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid

35   sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by

hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-84, or 168-251 are provided in the Sequence Listing. In

5   the nucleic acids provided in the Sequence Listing, A is adenine; C is cytosine; G is guanosine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-84, or 168-251 under stringent hybridization

10   conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-84, or 168-251. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-84, or 168-251 or a degenerate variant or fragment thereof. The

15   identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-84, or 168-251. The sequence information can be a segment of any one of SEQ ID NO: 1-84, or 168-251 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-84, or 168-251.

20   A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information are provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection

25   can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety

30   of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-84, or 168-251, or

35   novel segments or parts of the nucleic acids of the invention are used as primers in expression

assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid

sequences of SEQ ID NO: 1-84, or 168-251 or novel segments or parts of the nucleic acids provided

herein are used in diagnostics for identifying bone marrow tissues and cells; for identifying

expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59

5   (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a

polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-84, or

168-251; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID

NO: 1-84, or 168-251; and a polynucleotide comprising any of the nucleotide sequences of the

10   mature protein coding sequences of SEQ ID NO: 1-84, or 168-251. The polynucleotides of the

present invention also include, but are not limited to, a polynucleotide that hybridizes under

stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set

forth in SEQ ID NO: 1-84, or 168-251; (b) a nucleotide sequence encoding any one of the amino

acid sequences comprising SEQ ID NO: 85-167, or 252-335; (c) a polynucleotide which is an allelic

15   variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog

(e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a

polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an

amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide

20   comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding

full length or mature protein. Polypeptides of the invention also include polypeptides with

biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence

set forth in SEQ ID NO: 1-84, or 168-251; or (b) polynucleotides that hybridize to the complement

of the polynucleotides of (a) under stringent hybridization conditions, or (c) polypeptides

25   comprising any of the polypeptide sequences set forth in SEQ ID NO: 85-167, or 252-335.

Biologically or immunologically active variants of any of the polypeptide sequences in the

Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%,

80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological

activity are also contemplated. The polypeptides of the invention may be wholly or partially

30   chemically synthesized but are preferably produced by recombinant means using the genetically

engineered cells (e.g. host cells) of the invention. The polypeptides may have the initial methionine

(Met) removed.

The invention also provides compositions comprising a polypeptide of the invention.

Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a

35   hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the

identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a

5   complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is

10   detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as

15   recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are

20   not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene

25   sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provide methods for treatment that involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

30   symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can affect such modulation either on the level of target gene/protein expression or target protein activity.

7

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Tables 1A-D); for which they have a signature region (as set forth in Table 2); or for which they have homology to a gene family (as set forth in Tables 3). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in increasing hematopoiesis, stem cell survival, and bone growth and remodeling.

3. DETAILED DESCRIPTION OF THE INVENTION

3.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide that retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly

from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that

5   comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides that modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs

10   include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs is nucleic acid fragments that induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the

15   sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention

20   may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or

25   "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

30   nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray

35   procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A

fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-84, or 168-251.

Probes may, for example, be used to determine whether specific mRNA molecules are

5   present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor

10   Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-84, or 168-251. The sequence

15   information can be a segment of any one of SEQ ID NO: 1-84, or 168-251 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-84, or 168-251. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there

20   are 300 times more twenty-mers than there are base pairs in a set of human chromosome. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than

25   approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an

30   eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic

5   elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

10   The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino

15   acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that

20   have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence that encodes for the full-length protein which may include any leader sequence or any processing sequence.

25   The term "mature protein coding sequence" means a sequence that encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell that removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be

30   removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer

35   attachment such as pegylation (derivatization with polyethylene glycol) and insertion or

substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*,

5   recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

10   Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes that produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the

15   polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino

20   acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and

25   glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using

30   recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide

35   characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover

rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

5   The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water,

10   buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 Daltons, can be present).

           The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in

15   the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

           The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian)

20   expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of glycosylation modifications; polypeptides or

25   proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

           The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements

30   having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant

35   protein is expressed without a leader or transport sequence, it may include an amino terminal

13

methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells that have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional

5   unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells that have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined

10   herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is

15   expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney,

20   P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence

25   may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO$_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65

30   °C, and washing in 0.1X SSC/0.1% SDS at 68 °C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42 °C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37 °C (for

14-base oligonucleotides), 48 °C (for 17-base oligos), 55 °C (for 20-base oligonucleotides), and 60 °C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" or "substantially similar" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a

5   reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding

10 reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further

15 variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence

20 identity, more preferably at least 90% sequence identity, more preferably at least 95% sequence identity, more preferably at least 98% sequence identity, and most preferably at least 99% sequence identity. Substantially equivalent nucleotide sequence of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, the nucleotide sequence has at least about 65% identity, more

25 preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least about 95% sequence identity, more preferably at least 98% sequence identity, and most preferably at least 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially

30 equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying

35 hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides that mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

3.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-84, or 168-251; a polynucleotide encoding any one of

5   the peptide sequences of SEQ ID NO: 85-167, or 252-335; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1-84, or 168-251. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-84, or 168-251; (b)

10 nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 85-167, or 252-335. Domains of interest may depend on the nature

15 of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

20   The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed

25 herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that

30 corresponds to any of the polynucleotides of SEQ ID NO: 1-84, or 168-251 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-84, or 168-251 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-84, or 168-251 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic

35 DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length

5   gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%,

10 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99% sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-84, or 168-251 or complements thereof, which fragment is greater than about 5

15 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to) any one of the polynucleotides of the invention are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

20 the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NO: 1-84,

25 or 168-251, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-84, or 168-251 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that

30 encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-84, or 168-251, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST, which stands for Basic Local Alignment Search Tool, is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993)

and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm could also be used.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making

5   suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the

10   polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences that encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the

15   location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by

20   substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or

25   carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine

30   sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the

35   site of being changed. In general, the techniques of site-directed mutagenesis are well known to

those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids.

5   When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this

10   gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic

15   code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those that are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used

20   to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known

25   to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-84, or 168-251, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct

30   the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful

35   nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g.,

plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a

5   selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid

10   having any of the nucleotide sequences of SEQ ID NO: 1-84, or 168-251or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-84, or 168-251or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of

15   the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBS, phagescript, PsiX174, pBluescript SK, pBS KS,

20   pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al.,

25   *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector

30   or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt,

35   lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine

kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli

5   and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and

10   preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA

15   sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species

20   within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322

25   (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by

30   appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., Nat. Biotech. 17:870-872 (1999), incorporated herein by

35   reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies

against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

3.2.1 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide . sequence of SEQ ID NO: 1-84, or 168-251, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO: 85-167, or 252-335 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-84, or 168-251are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO: 1-84, or 168-251), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified

nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid

5   include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

10   7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

15   3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

20   The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of

25   an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified

30   such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the

35   control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an

α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific

double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the

strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The

5   antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*

(1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987)

FEBS Lett 215: 327-330).

3.2.2 RIBOZYMES AND PNA MOIETIES

10   In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a

single-stranded nucleic acid, such as a mRNA, to which they have a complementary region.

Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988)

Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit

15   translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-84,

or 168-251). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in

which the nucleotide sequence of the active site is complementary to the nucleotide sequence to

be cleaved in an mRNA of SEQ ID NO: 1-84, or 168-251 (see, *e.g.*, Cech *et al.* U.S. Pat. No.

20   4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the

invention can be used to select a catalytic RNA having a specific ribonuclease activity from a

pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences

complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical

25   structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and

Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base

moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or

30   solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic

acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med*

Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid

mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a

pseudopeptide backbone and only the four natural nucleobases are retained. The neutral

35   backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under

conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

　　　　PNAs of the invention can be used in therapeutic and diagnostic applications. For

5　　example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or

10　　primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

　　　　In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug

15　　delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between

20　　the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA

25　　and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

30　　　　In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134). In addition,

35　　oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et

al., 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

5

3.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection

10   methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell that drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or

15   increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication

20   No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding

25   sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by

30   calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or

5   protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et

10   al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts; described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a

15   compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of

20   replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced

25   in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient

30   method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or

35   any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial

strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent

5   attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used

10   to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences that affect the structure or stability of

15   the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences that alter or improve the function or stability of protein or RNA molecules.

20   The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, an enhancer that

25   has broader or different cell-type specificity than the naturally occurring elements can replace a tissue-specific enhancer. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The

30   identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable

marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase

(TK) gene or the bacterial *xanthine-guanine phosphoribosyl-transferase (gpt)* gene.

The gene targeting or gene activation techniques, which can be used in accordance with

this aspect of the invention, are more particularly described in U.S. Patent No. 5,272,071 to

5   Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No.

PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No.

PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference

herein in its entirety.

10   ### 3.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide

comprising: the amino acid sequences set forth as any one of SEQ ID NO: 85-167, or 252-335 or

an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-84, or

168-251 or the corresponding full length or mature protein. Polypeptides of the invention also

15   include polypeptides preferably with biological or immunological activity that are encoded by:

(a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-84,

or 168-251or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ

ID NO: 85-167, or 252-335 or (c) polynucleotides that hybridize to the complement of the

polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also

20   provides biologically active or immunologically active variants of any of the amino acid

sequences set forth as SEQ ID NO: 85-167, or 252-335 or the corresponding full length or

mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least

about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at

least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically

25   at least about 98%, or most typically at least about 99% amino acid identity) that retain

biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or

decreased activity compared to polypeptides comprising SEQ ID NO: 85-167, or 252-335.

Fragments of the proteins of the present invention that are capable of exhibiting

biological activity are also encompassed by the present invention. Fragments of the protein may

30   be in linear form or they may be cyclized using known methods, for example, as described in H.

U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer.

Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such

fragments may be fused to carrier molecules such as immunoglobulins for many purposes,

including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length

5   polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

10   Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments that differ from a

15   nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid

20   sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for

25   example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells that have been altered to express the desired polypeptide or protein. As used herein, a cell

30   is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell that produces one of the polypeptides or

35   proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable

5   expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

10   In an alternative method, the polypeptide or protein is purified from bacterial cells that naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography,

15   and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein

20   domains.

The purified polypeptides can be used in *in vitro* binding assays that are well known in the art to identify molecules that bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist

25   activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to

30   cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 85-167, or 252-335.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein

5   sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such

10   alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the

15   importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein.

20   Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A.

25   (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under

30   culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose,

35   heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving

hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form, which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of

5 maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially

10 available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially

15 homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted.

20 Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which

25 provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties, which may be fused to the polypeptide, include therapeutic agents that are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and

30 steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

3.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group,

5   University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Mol. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMATRIX software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), PFam

10   software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference), SignalP software package (Nielsen H et al., Int. J. Neural Syst., Vol. 8, pp. 581 – 599 (1997), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol. Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for

15   Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

3.4.2 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

20   another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively

25   linked" is intended to indicate that the polypeptide(s) according to the invention and the other polypeptide(s) are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus or in the middle.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

30   In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to

35   sequences derived from a member of the immunoglobulin protein family. The immunoglobulin

fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the

5   ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.,* cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used to bind and to dimerize 2 receptors and thereby transduce an intracellular signal. The immunoglobulin fusion proteins may also be used as immunogens to produce antibodies in a

10   subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing

15   blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that

20   give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the

25   invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

3.5 GENE THERAPY

Mutations in the polynucleotides of the invention may result in loss of normal function of

30   the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo, in situ,* or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer

35   methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature,

supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be

5   accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the

10   activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA

15   sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a

20   regulatory sequence heterologous to the host cell, which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by

25   homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT

30   International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in

35   co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to

5   replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences that affect the structure or stability of the RNA or

10   protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences that alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene

15   under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally

20   occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the

25   property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial

30   xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques that can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436

35   (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

3.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or

5   inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be

10   prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and

15   PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even

20   replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express

25   polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

3.7 USES AND BIOLOGICAL ACTIVITY

30   The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The

35   mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5   polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10   indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15   or in one of the other physiological pathways described herein.

3.7.1 RESEARCH USES AND UTILITIES

The research community can use the polynucleotides provided by the present invention for various purposes. The polynucleotides can be used to express recombinant protein for

20   analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25   disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30   an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35   the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

3.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

3.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present

invention is evidenced by any one of a number of routine factor dependent cell proliferation

assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3,

MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

5   HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described

in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E.

M. Shevach, W. Strober, Pub. *Greene Publishing Associates and Wiley-Interscience (Chapter 3,*

In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in

10   Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.

145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli,

et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or

thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,

15   Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan

eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse

and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan

eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells

20   include, without limitation, those described in: Measurement of Human and Murine Interleukin 2

and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in

Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991;

deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988;

Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse

25   and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol

1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci.

U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J.,

Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.

6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin

30   9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology.

J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins

that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described in: Current Protocols in

35   Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse

Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7,

Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095,

1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol.

5   137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

3.7.4   STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and

be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem

10   cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or

germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or

ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential

state which would be useful for re-engineering damaged or diseased tissues, transplantation,

manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce

15   large quantities of human cells has important working applications for the production of human

proteins which currently must be obtained from non-human sources or donors, implantation of

cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases;

tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including

cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs

20   for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may

be administered in combination with the polypeptide of the invention to achieve the desired

effect, including any of the growth factors listed herein, other stem cell maintenance factors, and

specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-

25   3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, bone marrow

inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet

factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic

fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of

30   these cells in culture will facilitate the production of large quantities of mature cells. Techniques

for culturing stem cells are known in the art and administration of polypeptides of the invention,

optionally with other growth factors and/or cytokines, is expected to enhance the survival and

proliferation of the stem cell populations. This can be accomplished by direct administration of

the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected

35   with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

5   Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and

10   identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

        Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be

15   used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In

20   addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

        Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated

25   cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al.,

30   Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

        In vitro cultures of stem cells can be used to determine if the polypeptide of the invention

35   exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells

5   proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

3.7.5   HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis

10   and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with

15   irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/bone marrows (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or

20   treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and

25   paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

30   Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular

35   and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al.,

5 Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21,

10 Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

15

3.7.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

20 A polypeptide of the present invention that induces cartilage and/or bone growth in circumstances where bone is not normally formed has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De

25 novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of

30 bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the
present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other
tissue formation in circumstances where such tissue is not normally formed, has application in
the healing of tendon or ligament tears, deformities and other tendon or ligament defects in

5   humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing
protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as
use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing
defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by
a composition of the present invention contributes to the repair of congenital, trauma induced, or

10   other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for
attachment or repair of tendons or ligaments. The compositions of the present invention may
provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or
ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming
cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect

15   tissue repair. The compositions of the invention may also be useful in the treatment of
tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may
also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the
art.

The compositions of the present invention may also be useful for proliferation of neural

20   cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral
nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which
involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a
composition may be used in the treatment of diseases of the peripheral nervous system, such as
peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous

25   system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager syndrome. Further, conditions that may be treated in
accordance with the present invention include mechanical and traumatic disorders, such as spinal
cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies
resulting from chemotherapy or other medical therapies may also be treatable using a

30   composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of
non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular
insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or

35   regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5   A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the 10   growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. 15   WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

20

3.7.7   IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A 25   protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More 30   specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders that may be treated using a protein of the present invention
include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,
rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome,
autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host

5   disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof,
including antibodies) of the present invention may also to be useful in the treatment of allergic
reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect
venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria,
angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme,

10   Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal
keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma
(particularly allergic asthma) or other respiratory problems. Other conditions, in which immune
suppression is desired (including, for example, organ transplantation), may also be treatable
using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the

15   polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals
models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66,
1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization
test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J.
Toxicol. Environ. Health 53: 563-79).

20   Using the proteins of the invention it may also be possible to modulate immune
responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking
an immune response already in progress or may involve preventing the induction of an immune
response. The functions of activated T cells may be inhibited by suppressing T cell responses or
by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is

25   generally an active, non-antigen-specific, process that requires continuous exposure of the T cells
to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T
cells, is distinguishable from immunosuppression in that it is generally antigen-specific and
persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be
demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence

30   of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high
level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and
organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell

35   function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

49

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be

5   sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

10   The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et

15   al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

        Blocking antigen function may also be therapeutically useful for treating autoimmune

20   diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of auto-reactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of

25   autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of auto-reactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine

30   experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

        Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means

35   of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5   Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected

10   cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T

15   cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain

20   protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as

25   the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the

30   following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

35   Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J.

Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al.,

Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5   Assays for T-cell-dependent immunoglobulin responses and isotype switching (which

will identify, among others, proteins that modulate T-cell dependent antibody responses and that

affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J.

Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production,

Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1

10   pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

        Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins

that generate predominantly Th1 and CTL responses) include, without limitation, those described

in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E.

M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,

15   In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in

Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,

1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

        Dendritic cell-dependent assays (which will identify, among others, proteins expressed

by dendritic cells that activate naive T-cells) include, without limitation, those described in:

20   Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine

173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et

al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology

67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of

Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation

25   94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

        Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins

that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte

homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry

13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research

30   53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology

145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International

Journal of Oncology 1:639-648, 1992.

        Assays for proteins that influence early steps of T-cell commitment and development

include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

3.7.8   ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related

5   activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive

10   based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH

15   release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by

20   the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

25

3.7.9   CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the

30   invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5   Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent

10 chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates

15 and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

20 **3.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY**

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events

25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

Therapeutic compositions of the invention can be used in the following:

30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 **3.7.11 CANCER DIAGNOSIS AND THERAPY**

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

5   may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,

10   inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma,

15   acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including

20   bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma,

25   tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically

30   effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a

35   portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

55

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

5   Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),

10   Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15   In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20   *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30

25   (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,

30   e.g. from American Type Tissue Culture Collection catalogs.

3.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the

35   invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

5   recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10   The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28,

15   Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a

20   ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the

25   present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent

30   molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

3.7.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a

5   solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of

10   complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and

15   organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

20   The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a

25   review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein,

30   peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

5   art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding

10   molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

3.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a

15   ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to

20   isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for

25   the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) is then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known

30   in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the

35   cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a

protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in

5   the art can also be used to identify signaling molecules involved in receptor activity.

3.7.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the

10   inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute

15   conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be

20   useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary

25   disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

3.7.16 LEUKEMIAS

30   Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic

(granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

3.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i)   traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions that sever a portion of the nervous system, or compression injuries;

(ii)   ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii)   infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv)   degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v)   lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi)   neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii)   lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii)   demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human

5   immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit

10   any of the following effects may be useful according to the invention:

(i)   increased survival time of neurons in culture;

(ii)   increased sprouting of neurons in culture or in vivo;

(iii)   increased production of a neuron-associated molecule in culture or *in vivo, e.g.,* choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

15   (iv)   decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al.

20   (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.,* depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.,* weakness, motor neuron conduction velocity, or functional disability.

25   In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal

30   muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

3.7.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

3.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment

of genomic DNA, which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately

5   adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

10   nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g.,

15   by an antibody specific to the variant sequence.

3.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model

20   system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant

25   mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and

30   24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

35   ### 3.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

3.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

3.9   PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the

invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined

5   with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents that either enhance the

10   activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other

15   hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti- inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with

20   itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that

25   therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the

30   relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or

35   simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

3.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from

similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

3.9.2 COMPOSITIONS/FORMULATIONS

5   Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations that can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing,

10   dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered

15   in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil,

20   mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from

25   about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other

30   active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or

35   other vehicle as known in the art. The pharmaceutical composition of the present invention may

also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

5   to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules,

10   liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose

15   preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this

20   purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

25   Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in

30   suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present

35   invention are conveniently delivered in the form of an aerosol spray presentation from

pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

5   in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or

10   emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

        Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or

15   vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

20   Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

        The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be

25   formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

30   A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system

35   (VPD:5W) consists of VPD diluted 1:1 with 5% dextrose in water solution. This co-solvent

system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

5   be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents

10   such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the

15   compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

       The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium

20   carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases

25   such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

       The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide

30   antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T-lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide

35   antigen(s) to T lymphocytes. The antigen components could also be supplied as purified

MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5   The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides,

10   sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

      The amount of protein or other active ingredient of the present invention in the

15   pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments that the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention

20   and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about

25   0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention that are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable

30   form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention that may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or

35   sequentially with the composition in the methods of the invention. Preferably for bone and/or

cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly (ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly (vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in

question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

5   Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of

10   damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final

15   composition, may also affect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a

20   mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

25

3.9.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount

30   effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a

35   circulating concentration range that can be used to more accurately determine useful doses in

humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

5   A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose

10   ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds that exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may

15   vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety that are sufficient to maintain the

20   desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be

25   administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention

30   will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

5   ### 3.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device that may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

10   invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

3.10 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the

15   invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from

20   humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

25   An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An

30   antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 85-167, or 252-335, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least

35   15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues.

Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of the protein that is located on the surface of the protein, *e.g.*, a

5   hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

10   Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

15   A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives,

20   fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

3.10.1 POLYCLONAL ANTIBODIES

25   For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a

30   recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not

35   limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface

active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

3.10.2 MONOCLONAL ANTIBODIES

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can

be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and

5   thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

10   California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

15   The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the

20   art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting

25   dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such

30   as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using

35   oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and

light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of

5   monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

10   polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

3.10.3 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise

15   humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')$_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human

20   immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some

25   instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human

30   immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

35

3.10.4 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

5 Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using

10 human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991);

15 Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach

20 is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

25 Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins

30 are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™

35 as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B

cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

5   immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No.

10   5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells

15   contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another

20   mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication

25   WO 99/53049.

3.10.5 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778).

30   In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$

35   fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

3.10.6 BISPECIFIC ANTIBODIES

5   Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the
10   recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct
15   bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion
20   preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable
25   host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the
30   CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for
35   increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')$_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

5   wherein intact antibodies are proteolytically cleaved to generate F(ab')$_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is

10 mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe

15 the production of a fully humanized bispecific antibody F(ab')$_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

20 Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region

25 to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V$_H$) connected to a light-chain variable domain (V$_L$) by a linker

30 which is too short to allow pairing between the two domains on the same chain. Accordingly, the V$_H$ and V$_L$ domains of one fragment are forced to pair with the complementary V$_L$ and V$_H$ domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

84

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an

5   immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These

10   antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

3.10.7 HETEROCONJUGATE ANTIBODIES

15   Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic

20   protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

25   ### 3.10.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have

30   improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and

ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

3.10.9 IMMUNOCONJUGATES

5   The invention also pertains to immunoconjugates comprising an antibody conjugated to a

cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a

radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been

10   described above. Enzymatically active toxins and fragments thereof that can be used include

diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from

Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin,

Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and

PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin,

15   mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of

radionuclides are available for the production of radioconjugated antibodies. Examples include

^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional

protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP),

20   iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL),

active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido

compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as

bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate),

and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a

25   ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987).

Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-

DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See

WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such

30   streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is

administered to the patient, followed by removal of unbound conjugate from the circulation

using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn

conjugated to a cytotoxic agent.

3.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are

5   not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

10   a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a

15   computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file,

20   formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

25   By providing any of the nucleotide sequences SEQ ID NO: 1-84, or 168-251, or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-84, or 168-251 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information

30   provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein-encoding fragments and may be useful in producing commercially important proteins

such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the

5   present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

10   therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

15   As used herein, "search means" refers to one or more programs that are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available

20   software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

25   As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues.

30   However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a

35   three-dimensional configuration that is formed upon the folding of the target motif. There are a

variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

5

3.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

10   Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix-see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense-Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca

15   Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

20

3.13 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated

25   with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also

30   comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting

35   a sample with a compound that binds to and forms a complex with the polypeptide for a period

sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for

5   binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

10   amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice

15   and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or

20   extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention

25   provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate

30   containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container, which will accept the test

35   sample, a container, which contains the antibodies used in the assay, containers, which contain

90

wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers, which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of

5   reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats that are well known in the art.

3.14 MEDICAL IMAGING

10   The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. No. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a

15   pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

3.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention

20   further provides methods of obtaining and identifying agents which bind to a polypeptide set forth in SEQ ID NO: 85-167, or 252-335 encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-84, or 168-251, or which binds to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

25   (a)   contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b)   determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of

30   the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the

35   invention for a time sufficient to form a polypeptide/compound complex, and detecting the

complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time

5   sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds that modulate the

10   activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds that modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the

15   invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

20   For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can

25   readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

30   In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or

35   multiple ORFs that rely on the same EMF for expression control. One class of DNA binding

agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives that have base attachment capacity.

5   Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix-see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense-Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca

10   Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

15   Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents that bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

20   **3.16 USE OF NUCLEIC ACIDS AS PROBES**

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-84, or 168-251. Because the corresponding gene is only expressed in

25   a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-84, or 168-251 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample. Preferably a hybridization probe from any of nucleotide sequences SEQ ID NO: 1-84, or 168-251 can be used as an indicator of bone marrow tissue.

Any suitable hybridization technique can be employed, such as, for example, in situ

30   hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

93

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

5   polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well-known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers,

10   hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical

15   chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect

20   differences in gene sequences between normal, carrier or affected individuals.

3.17 PREPARATION OF SEQUENCING CHIPS AND ARRAYS

A basic example is using 6-mers attached to 50 micron surfaces to give a chip with dimensions of 3 x 3 mm which can be combined to give an array of 20 x 20 cm. Another

25   example is using 9-mer oligonucleotides attached to 10 x 10 microns surface to create a 9-mer chip, with dimensions of 5 x 5 mm. 4000 units of such chips may be used to create a 30 x 30 array. In an array in which 4,000 to 16,000 oligochips are arranged into a square array. A plate, or collection of tubes, as also depicted, may be packaged with the array as part of the sequencing kit.

30   The arrays may be separated physically from each other or by hydrophobic surfaces. One possible way to utilize the hydrophobic strip separation is to use technology such as the Iso-Grid Microbiology System produced by QA Laboratories, Toronto, Canada.

Hydrophobic grid membrane filters (HGMF) have been in use in analytical food microbiology for about a decade where they exhibit unique attractions of extended numerical

35   range and automated counting of colonies. One commercially available grid is ISO-GRID™

from QA Laboratories Ltd. (Toronto, Canada) which consists of a square (60 x 60 cm) of polysulfone polymer (Gelman Tuffryn HT-450, .45 um pore size) on which is printed a black hydrophobic ink grid consisting of 1600 (40 x 40) square cells. HGMF have previously been inoculated with bacterial suspensions by vacuum filtration and incubated on the differential or selective media of choice.

Because the microbial growth is confined to grid cells of known position and size on the membrane, the HGMF functions more like an MPN apparatus than a conventional plate or membrane filter. Peterkin et al. (1987) reported that these HGMFs can be used to propagate and store genomic libraries when used with a HGMF replicator. One such instrument replicates growth from each of the 1600 cells of the ISO-GRID and enables many copies of the master HGMF to be made (Peterkin et al., 1987).

Sharpe et al. (1989) also used ISO-GRID HGMF form QA Laboratories and an automated HGMF counter (MI-100 Interpreter) and RP-100 Replicator. They reported a technique for maintaining and screening many microbial cultures.

Peterkin and colleagues later described a method for screening DNA probes using the hydrophobic grid-membrane filter (Peterkin et al., 1989). These authors reported methods for effective colony hybridization directly on HGMFs. Previously, poor results had been obtained due to the low DNA binding capacity of the epoxysulfone polymer on which the HGMFs are printed. However, Peterkin et al. (1989) reported that the binding of the DNA to the surface of the membrane was improved by treating the replicated and incubated HGMF with polyethyleneimine, a polycation, prior to contact with DNA. Although this early work uses cellular DNA attachment, and has a different objective to the present invention, the methodology described may be readily adapted for Format 3 SBH.

In order to identify useful sequences rapidly, Peterkin et al. (1989) used radiolabeled plasmid DNA from various clones and tested its specificity against the DNA on the prepared HGMFs. In this way, DNA from recombinant plasmids was rapidly screened by colony hybridization against 100 organisms on HGMF replicates that can be easily and reproducibly prepared.

Manipulation with small (2-3 mm) chips, and parallel execution of thousands of the reactions. The solution of the invention is to keep the chips and the probes in the corresponding arrays. In one example, chips containing 250,000 9-mers are synthesized on a silicon wafer in the form of 8 x 8 mM plates (15 uM/oligonucleotide, Pease et al., 1994) arrayed in 8 x 12 format (96 chips) with a 1 mM groove in between. Probes are added either by multichannel pipette or pin array, one probe on one chip. To score all 4000 6-mers, 42 chip arrays have to be used, either using different ones, or by reusing one set of chip arrays several times.

In the above case, using the earlier nomenclature of the application, F=9; P=6; and F+P=15. Chips may have probes of formula BxNn, where x is a number of specified bases B; and n is a number of non-specified bases, so that x= 4 to 10 and n= 1 to 4. To achieve more efficient hybridization, and to avoid potential influence of any support oligonucleotides, the specified bases can be surrounded by unspecified bases, thus represented by a formula such as (N)nBx(N)m.

3.18   PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using

only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via a phosphoramidate bond, the oligonucleotide terminus must have a 5'-end
5   phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm$_7$), is then added to a final concentration of 10 mM 1-MeIm$_7$. A ss DNA solution is
10   then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm$_7$, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed
15   3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic
20   hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe
25   arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor et al. (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness et al. (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem.
30   169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness et al. (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the
35   light-generated synthesis described by Pease et al., (1994) Proc. Natl. Acad. Sci. USA 91(11) 5022-

6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and

5   versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

3.19 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA,

10   including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples

15   may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

20   Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA

25   fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and

30   sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the

randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate

5   consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

10   Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

15   **3.20   PREPARATION OF DNA ARRAYS**

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is

20   achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene

25   segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

30   Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The

5   present invention is not to be limited in scope by the exemplified embodiments that are intended as illustrations of single aspects of the invention, and compositions and methods that are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations that should be placed upon

10   the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

4.0   EXAMPLES

4.1   EXAMPLE 1

15   <u>Novel Nucleic Acid Sequences Obtained From Various Libraries</u>

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosomes using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences that

20   flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones from each cluster were selected for sequencing.

The sequence of the amplified inserts, in some cases, was then deduced using a typical

25   Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences.

4.2 EXAMPLE 2

<u>Novel Nucleic Acids</u>

30   The novel nucleic acids of the present invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids of SEQ ID NO: 1-84, inclusive, were assembled using an EST sequence as a seed. Then a recursive algorithm was used

to extend some of the seed ESTs into an extended assemblage, by pulling additional sequences from
different databases (i.e., Hyseq's database containing EST sequences, dbEST version 119, gb pri
119, and UniGene version 119, Geneseq October version, and Genscan, Genemark and Hyseq gene
predictions on human genomic sequence from the human genome project updated October 2000)

5   that belong to this assemblage. The algorithm terminated when there was no additional sequences
from the above databases that would extend the assemblage. Inclusion of component sequences
into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score
greater than 300 and percent identity greater than 95%.

10   **4.3 EXAMPLE 3**

       <u>Further Characterization</u>

              Clusters from Example 1 were identified which were expressed in bone marrow tissue
cDNA libraries, but not in other tissues. Novel nucleic acids were assembled by the method of
Example 2. A subset of the assembled nucleic acids comprising sequences from the identified

15   clusters was selected. This subset includes SEQ ID NO: 1-84. The tissue sources in which SEQ ID
NO: 1-84 were exclusively expressed were found to be in BMD001 and BMD002 bone marrow
libraries (Clontech).

              The homologies for SEQ ID NO:1-84, and the corresponding peptide sequences, SEQ ID
NO: 85-167, were obtained by performing various searches as shown in Tables 1A to 1D and as

20   discussed herein.

              The homologous sequences to the amino acid sequences corresponding to SEQ ID NO:
1-84 were obtained by a BLASTP version 2.0al 19MP-WashU search against the Geneseq
database updated November 9, 2000, update 23 for year 2000 (Derwent), using the BLAST
algorithm. The homologues for the amino acid sequences corresponding to SEQ ID NO: 1-84

25   from Geneseq are shown in Table 1A below.

              The homologous sequences to the amino acid sequences corresponding to SEQ ID NO:
1-84 were also obtained by a BLASTP version 2.0al 19MP-WashU search against the NCBI
Genbank nr database updated November 10, 2000, using the BLAST algorithm. The
homologues for the amino acid sequences corresponding to SEQ ID NO: 1-84 from Genbank are

30   shown in Table 1B below.

              The homologous sequences to SEQ ID NO: 1-84 were also obtained by a BLASTN
version 2.0al 19MP-WashU search against the Geneseq database updated November 9, 2000,
update 23 for year 2000 (Derwent), using the BLAST algorithm. The homologues for SEQ ID
NO: 1-84 from Geneseq are shown in Table 1C below.

The homologous sequences to SEQ ID NO: 1-84 were also obtained by a BLASTN version 2.0al 19MP-WashU search against the NCBI Genbank nt database updated November 10, 2000, using the BLAST algorithm. The homologues for SEQ ID NO: 1-84 from Genbank are shown in Table 1D below.

5   Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), the polypeptide sequences corresponding to SEQ ID NO: 1-84 were examined to determine whether they had identifiable signature regions. Table 2 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the

10   position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences corresponding to SEQ ID NO: 1 – 84 were examined for domains with homology to certain peptide domains. Table 3 shows the name of the domain found, the description, the e-value and

15   the PFam score for the identified domain within the sequence.

The polypeptide sequence within each of the polypeptides corresponding to SEQ ID NO: 1-84 that is the predicted signal peptide sequence and its cleavage site can be determined using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic

20   signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A mean S score, as described in the Nielson et. al. was obtained for the polypeptide sequences. Table 4 shows the position of the

25   predicted signal peptide in each of the polypeptides corresponding to SEQ ID NO: 1-84 and the mean score associated with that signal peptide.

4.4 EXAMPLE 4

Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 168-251

30   were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103 and exons from public domain genomic sequences predicted by Genscan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above

databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

      Table 6 sets forth the novel predicted polypeptides (including proteins) encoded by the

5   novel polynucleotides (SEQ ID NO: 168-251) of the present invention, and their corresponding translation start and stop nucleotide locations to each of SEQ ID NO: 168-251. Table 6 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known

10   polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997),

15   incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. These polynucleotides and polypeptides have homology to the sequences selected in Example 3.

103

Table 1A

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
1	T93038	1691 (259.8bits)	1.0e-70	93	T93038 Human monoclonal antibody light chain GM4-IgG4.lambda encoding DNA.
3	C10865	2666 (406.1bits)	9.0e-170	98	C10865 Human secreted protein 5' EST, SEQ ID NO: 14940. Length = 896
4	Q61170	1119 (173.9bits)	8.7e-45	97	Q61170 Human brain Expressed Sequence Tag EST01715. Length = 305
5	C06514	630 (100.6bits)	6.3e-45	100	C06514 Human secreted protein 5' EST, SEQ ID NO: 10589. Length = 741
7	C27831	2177 (332.7bits)	1.1e-90	99	C27831 Human secreted protein 5' EST, SEQ ID NO: 31906. Length = 442
8	Z13365	806 (127.0bits)	1.2e-30	99	Z13365 Human gene expression product cDNA sequence SEQ ID NO:834. Length = 300
10	T18679	588 (94.3bits)	2.1e-20	77	T18679 Human lastin cDNA (partial sequence). Length = 2223
11	Z65341	3392 (515.0bits)	1.3e-255	97	Z65341 Human secreted protein gene 92. Length = 1416
12	Q78896	2269 (346.5bits)	1.7e-97	99	Q78896 VHL disease gene g7. Length = 1816
13	Z97028	2999 (456.0bits)	2.5e-130	97	Z97028 Human secreted protein gene 10 cDNA clone HDPWU34, SEQ ID NO:20.
14	A46361	1943 (297.6bits)	1.0e-82	90	A46361 Nucleotide sequence of the gene insert of CINN 1. Length = 1549
15	A16623	3512 (533.0bits)	1.5e-236	73	A16623 Human secreted protein clone pt332_1 nucleotide sequence SEQ ID NO:11.
16	Z17710	3692 (560.0bits)	2.1e-161	98	Z17710 Human gene expression product cDNA sequence SEQ ID NO:5183. Length = 758
17	V84468	5332 (806.1bits)	0.0	95	V84468 Human secreted protein gene 58 clone HE9HU17. Length = 2483
18	C17456	345 (57.8bits)	1.5e-09	85	C17456 Human secreted protein 5' EST, SEQ ID NO: 21531. Length = 157
20	V57903	2178 (332.8bits)	1.0e-110	89	V57903 Hereditary haemochromatosis subregion from an HH affected individual.
21	X87150	5147	1.0e-227	98	X87150 Human protease

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
		(778.3bits)			HUPM-2 cDNA. Length = 3043
22	A45360	1189 (184.4bits)	4.9e-48	88	A45360 Mouse secreted expressed sequence tag SEQ ID NO:1935. Length = 374
23	C26801	1830 (280.6bits)	5.2e-77	96	C26801 Human secreted protein 5' EST, SEQ ID NO: 30876. Length = 393
24	Z16343	1930 (295.6bits)	7.9e-80	97	Z16343 Human gene expression product cDNA sequence SEQ ID NO:3813. Length = 465
25	X29140	6333 (956.3bits)	2.0e-281	72	X29140 Hypoxia-regulated gene sequence RTP220. Length = 4121
26	Z90631	6131 (925.9bits)	0.0	99	Z90631 Human adipose tissue protein #1 encoding DNA. Length = 3211
28	Z77502	1581 (243.3bits)	6.7e-66	84	Z77502 Human ovarian tumor cDNA library derived EST fragment 53. Length = 540
30	A58471	377 (62.6bits)	2.5e-07	55	A58471 Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
32	X98701	3063 (465.6bits)	5.2e-132	95	X98701 Human validated cancer cell derived cDNA #23. Length = 750
33	V34159	1317 (203.7bits)	3.5e-53	89	V34159 Human secreted protein gene 6 clone HBMCY91. Length = 425
34	X34656	1275 (197.4bits)	1.1e-52	66	X34656 Human ZIP-kinase (serine/threonine kinase) encoding DNA. Length = 2132
36	C08395	580 (93.1bits)	1.4e-20	79	C08395 Human secreted protein 5' EST, SEQ ID NO: 12470. Length = 406
40	X37471	400 (66.1bits)	7.4e-19	100	X37471 Human secreted protein cDNA fragment containing gene 21. Length = 990
41	T22028	487 (79.1bits)	7.3e-16	95	T22028 Human gene signature HUMGS03571. Length = 127
42	Z94751	447 (73.1bits)	2.1e-12	57	Z94751 Human ATP binding cassette ABCA8 (ABC-new) cDNA. Length = 2911
43	C31590	1353 (209.1bits)	1.7e-55	98	C31590 Human secreted protein 5' EST, SEQ ID NO: 35665. Length = 417
44	C02717	1313 (203.1bits)	1.7e-53	98	C02717 Human secreted protein 5' EST, SEQ ID NO: 2715.

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
					Length = 268
45	Z87318	385 (63.8bits)	9.9e-08	57	Z87318 S. venezuelae pik (macrolide biosynthesis) gene cluster. Length = 36,778
46	V12391	383 (63.5bits)	5.9e-09	64	V12391 Mouse osteoclast transporter protein encoding cDNA. Length = 2102
47	Z16086	318 (53.8bits)	3.2e-06	59	Z16086 Human gene expression product cDNA sequence SEQ ID NO:3556. Length = 754
48	V32401	1467 (226.2bits)	1.7e-60	99	V32401 Homo sapiens spry3 gene. Length = 300
50	C26006	996 (155.5bits)	4.6e-39	98	C26006 Human secreted protein 5' EST, SEQ ID NO: 30081. Length = 208
60	C09439	913 (143.0bits)	2.4e-35	94	C09439 Human secreted protein 5' EST, SEQ ID NO: 13514. Length = 222
71	C27703	640 (102.1bits)	2.7e-23	73	C27703 Human secreted protein 5' EST, SEQ ID NO: 31778. Length = 431
82	C32463	177 (32.6bits)	4.1e-07	94	C32463 Human secreted protein 5' EST, SEQ ID NO: 36538. Length = 100

Table 1B

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
1	L29164.1	2253 (344.1bits)	3.5E-95	96	HUMIGLZF Human immunoglobulin light chain variable region (lambda-IIIb subgroup) from IgM rheumatoid factor
2	AF305057.1	2236 (341.5bits)	1.4E-93	98	"AF305057 Homo sapiens RTS (RTS) gene, complete cds, alternatively spliced"
3	X52851.1	1092 (169.9bits)	6.9E-143	82	HSCPH70 Human cyclophilin gene for cyclophilin (EC 5.2.1.8) Length = 6711
4	L21936.1	2302 (351.4bits)	4.2E-102	96	"HUMSDHX Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds"
5	AL033529.25	681 (108.2bits)	1.6E-46	98	"HS27O5 Human DNA sequence from clone RP1-27O5 on chromosome 1p34.1-35.3, complete sequence [Homo sapiens]"
6	AL121601.13	1097 (170.6bits)	3.6E-94	98	"HSDJ315G1 Human DNA sequence from clone RP1-315G1 on chromosome Xq24-25. Contains a PDZ (DHR, GLGF) domain protein"
7	AL162331.1	33983 (5104.9bits)	0.0	98	HS118D241 Novel human gene mapping to chomosome 1 Length = 6941
8	AK023176.1	5874 (887.4bits)	1.8E-259	99	"AK023176 Homo sapiens cDNA FLJ13114 fis, clone NT2RP3002603 Length = 2730"
9	AB037855.1	5253 (794.2bits)	0.0	93	"AB037855 Homo sapiens mRNA for KIAA1434 protein, partial cds Length = 5443"
10	AC004890.2	617 (98.6bits)	2E-20	94	"AC004890 Homo sapiens PAC clone RP4-800G7 from 7q35-q36, complete sequence"
11	AB020653.1	5341 (807.4bits)	0.0	97	"AB020653 Homo sapiens mRNA for KIAA0846 protein, complete cds Length = 4204"
12	AC007999.11	1914 (293.2bits)	9.1E-144	96	AC007999 Homo sapiens 3q25-26 BAC CTB-177N7 (California Institute of Technology BAC Library) complete sequence

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
13	AB020598.1	6253 (944.3bits)	1.7E-276	98	"AB020598 Homo sapiens mRNA for peptide transporter 3, complete cds"
14	AF153607.1	1995 (305.4bits)	8.2E-84	91	"AF153607 Homo sapiens px19 mRNA, complete cds Length = 943"
15	AB032996.1	12529 (1885.9bits)	0.0	99	"AB032996 Homo sapiens mRNA for KIAA1170 protein, partial cds Length = 5073"
16	AB033007.1	12151 (1829.2bits)	0.0	99	"AB033007 Homo sapiens mRNA for KIAA1181 protein, partial cds Length = 2432"
17	AL117430.1	5341 (807.4bits)	7.7E-293	95	HSM800939 Homo sapiens mRNA; cDNA DKFZp434D156 (from clone DKFZp434D156); partial cds
18	AL357654.9	685 (108.8bits)	1.6E-23	100	"AL357654 Human DNA sequence from clone RP5-1025P18 on chromosome 20 Contains ESTs, STSs and GSSs, complete sequence [Homo"
19	AB020677.2	15274 (2297.8bits)	0.0	99	"AB020677 Homo sapiens mRNA for KIAA0870 protein, partial cds Length = 4628"
20	AC009505.3	2855 (434.4bits)	8.5E-201	89	"AC009505 Homo sapiens BAC clone RP11-526D2 from 2, complete sequence"
21	AF206019.1	15735 (2366.9bits)	0.0	99	"AF206019 Homo sapiens REV1 protein (REV1) mRNA, complete cds Length = 4276"
22	8923709 ref	1547 (238.2bits)	1.7E-63	93	NM_017548.1
23	Z83840.7	4939 (747.1bits)	1.2E-215	85	HS216E10 Human DNA sequence from clone CTA-216E10 on chromosome 22 Contains the NHP2L1 gene for non-histone chromosome protein 2
24	AB028958.1	15904 (2392.3bits)	0.0	98	"AB028958 Homo sapiens mRNA for KIAA1035 protein, partial cds Length = 5124"
25	AF273437.1	16890 (2540.2bits)	0.0	100	"AF273437 Homo sapiens actin binding protein anillin mRNA, complete cds"
26	AB011792.1	6121 (924.4bits)	0.0	99	"AB011792 Homo sapiens mRNA for extracellular matrix protein, complete cds"
27	AF130358.2	2233	1.1E-105	97	"AF130358 Homo sapiens

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
		(341.1bits)			chromosome 21q11.2 PAC 90B5, complete sequence"
28	AC009289. 8	2003 (306.6bits)	6E-108	96	"AC009289 Homo sapiens, clone RP11-44J3, complete sequence Length = 146,010"
29	AC007386. 3	1768 (271.3bits)	1.2E-116	94	"AC007386 Homo sapiens BAC clone RP11-359K10 from 2, complete sequence"
30	AK024129. 1	795 (125.3bits)	1.5E-25	97	"AK024129 Homo sapiens cDNA FLJ14067 fis, clone HEMBB1001315 Length = 4153"
31	AC007999. 11	795 (125.3bits)	4.9E-116	79	AC007999 Homo sapiens 3q25-26 BAC CTB-177N7 (California Institute of Technology BAC Library) complete sequence
32	AB037825. 1	28786 (4325.1bits)	0.0	98	"AB037825 Homo sapiens mRNA for KIAA1404 protein, partial cds Length = 7204"
33	AB023218. 1	12029 (1810.9bits)	0.0	98	"AB023218 Homo sapiens mRNA for KIAA1001 protein, complete cds Length = 4304"
34	AB007144. 1	1275 (197.4bits)	1.2E-51	66	"AB007144 Homo sapiens mRNA for ZIP-kinase, complete cds Length = 2105"
35	AC006241. 1	1031 (160.7bits)	6.9E-48	99	"AC006241 Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence"
36	AC008733. 7	759 (119.9bits)	7.7E-27	96	"AC008733 Homo sapiens chromosome 19 clone CTD-2525J15, complete sequence"
37	AF026813.1	1627 (250.2bits)	2.4E-67	92	AF026813 Homo sapiens topoisomerase III gene promoter region Length = 1361
38	AK022932. 1	3459 (525.0bits)	2.3E-191	99	"AK022932 Homo sapiens cDNA FLJ12870 fis, clone NT2RP2003727 Length = 2566"
40	AF161365.1	2726 (415.1bits)	1.4E-116	99	"AF161365 Homo sapiens HSPC102 mRNA, partial cds Length = 547"
41	AL121934.1 7	687 (109.1bits)	5.5E-41	73	HSBA209A2 Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10)

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
42	AF250238.1	447 (73.1bits)	2.6E-11	57	"AF250238 Homo sapiens macrophage ABC transporter (ABCA7) mRNA, complete cds"
43	AB046641.1	2389 (364.5bits)	1E-181	97	"AB046641 Macaca fascicularis brain cDNA, clone QccE-16161 Length = 2901"
44	AL365224.8	2296 (350.5bits)	9E-107	99	"AL365224 Human DNA sequence from clone RP11-96B21 on chromosome 6, complete sequence [Homo sapiens]"
45	AF168787.1	12094 (1820.6bits)	0.0	99	"AF168787 Homo sapiens vanilloid receptor gene, partial sequence; CARKL and CTNS genes, complete cds; TIP1 gene, partial cds; P2X5b"
46	AC000353.27	821 (129.2bits)	1.2E-29	77	"AC000353 Homo sapiens Chromosome 11q13 BAC Clone 18h3, complete sequence"
47	U37263.1	522 (84.4bits)	2E-16	64	"HSU37263 Human KRAB zinc finger protein (ZNF177) mRNA, complete cds"
48	AJ271735.1	7131 (1076.0bits)	0.0	99	"HSA271735 Homo sapiens Xq pseudoautosomal region; segment 1/2 Length = 240,000"
50	L22009.1	576 (92.5bits)	1.9E-16	79	"HUM49KDA Human hnRNP H mRNA, complete cds Length = 2201"
51	AF249738.1	1537 (236.7bits)	1.8E-63	73	AF249738 Mus musculus Pb99 gene sequence Length = 2127
55	AL138994.3	366 (61.0bits)	0.0000024	57	CNS01DWZ Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC C-2046P20 of library CalTech-D from chromosome 14 of Homo
59	AC010137.3	1325 (204.9bits)	2.7E-112	100	"AC010137 Homo sapiens BAC clone RP11-169D1 from Y, complete sequence"
60	AK024343.1	2098 (320.8bits)	7.5E-89	90	"AK024343 Homo sapiens cDNA FLJ14281 fis, clone PLACE1005611, weakly similar to Mus musculus mRNA for mDj10"
62	AL034375.2	1140	4E-65	97	HS523G1 Human DNA

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
	3	(177.1bits)			sequence from clone 523G1 on chromosome 6p22.3-24.1 Contains part of the mRNA for SCA1 (spinocerebellar
65	AC005740. 1	3048 (463.4bits)	3.1E-130	99	"AC005740 Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence"
69	AL135783.6	1648 (253.3bits)	5.4E-67	99	"AL135783 Human DNA sequence from clone RP3-527F8 on chromosome Xq25-27.1, complete sequence [Homo sapiens]"
70	AL049715.2 5	1824 (279.7bits)	2.7E-87	93	"HSJ646P11 Human DNA sequence from clone RP4-646P11 on chromosome 1, complete sequence [Homo sapiens]"
71	AC006157. 2	1801 (276.3bits)	6.6E-74	99	"AC006157 Homo sapiens BAC clone RP11-414C23 from Y, complete sequence"
75	AC016622. 5	688 (109.3bits)	1.2E-23	90	"AC016622 Homo sapiens chromosome 5 clone CTD-2343F18, complete sequence"
78	AC010627. 5	3031 (460.8bits)	1.8E-129	98	"AC010627 Homo sapiens chromosome 5 clone CTD-2165H16, complete sequence"
79	AL132822.1 5	1257 (194.6bits)	2.5E-49	99	"HSJ1017F8 Human DNA sequence from clone RP5-1017F8 on chromosome 20 Contains STSs, GSSs and a CpG Island, complete"
80	AC012315. 5	1150 (178.6bits)	1.7E-44	100	"AC012315 Homo sapiens chromosome 5 clone CTD-2122K7, complete sequence"
82	AC026425. 3	1196 (185.5bits)	1.4E-46	99	"AC026425 Homo sapiens chromosome 5 clone CTD-2183D23, complete sequence"
83	AP001331.1	2020 (309.1bits)	8.5E-84	100	"AP001331 Homo sapiens genomic DNA, chromosome 8q23, clone:KB1153C10"

Table 1C

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
1	W34081	374 (136.7bits)	1.6e-34	85	W34081 Human monoclonal antibody light chain GM4-IgG4.lambda. Length = 129
3	G03831	104 (41.7bits)	6.6e-06	39	G03831 Human secreted protein, SEQ ID NO: 7912. Length = 165
9	G46687	196 (74.1bits)	3.8e-15	29	G46687 Arabidopsis thaliana protein fragment SEQ ID NO: 58762. Length = 374
10	R94903	136 (52.9bits)	3.9e-08	52	R94903 Human lastin. Length = 675
11	Y70963	687 (246.9bits)	7.2e-70	51	Y70963 Human Ras signalling pathway associated protein CalDAG-GEFII. Length = 797
12	R66286	304 (112.1bits)	4.2e-27	100	R66286 VHL disease gene g7 product. Length = 284
13	G16993	169 (64.5bits)	2.1e-10	31	G16993 Arabidopsis thaliana protein fragment SEQ ID NO: 17846. Length = 464
15	Y94903	1182 (421.1bits)	3.8e-120	59	Y94903 Human secreted protein clone pt332_1 protein sequence SEQ ID NO:12.
16	G33308	291 (107.5bits)	2.3e-39	35	G33308 Zea mays protein fragment SEQ ID NO: 40339. Length = 350
17	W88812	143 (55.4bits)	3.7e-09	39	W88812 Polypeptide fragment encoded by gene 58. Length = 452
19	R90766	178 (67.7bits)	2.3e-09	24	R90766 Tumour suppressor protein HTS-1. Length = 1137
20	R76595	118 (46.6bits)	2.2e-07	27	R76595 MoMLV mutated gag matrix protein. Length = 131
21	G48221	286 (105.7bits)	5.0e-38	43	G48221 Arabidopsis thaliana protein fragment SEQ ID NO: 60872. Length = 1114
24	Y13055	183 (69.5bits)	3.9e-14	97	Y13055 Human secreted protein encoded by 5' EST SEQ ID NO: 69. Length = 39
25	Y03636	3020 (1068.2bits) 6.5e-315	6.5e-315	71	Y03636 Hypoxia-regulated gene RTP220 product. Length = 864
26	Y67598	1051 (375.0bits)	2.9e-106	99	Y67598 Human adipose tissue protein #1. Length = 699
28	Y76628	143 (55.4bits)	4.8e-10	56	Y76628 Human ovarian tumor EST fragment encoded protein 124. Length = 94
33	W75062	359 (131.4bits)	6.2e-33	93	W75062 Human secreted protein encoded by gene 6 clone

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
					HBMCY91. Length = 73
34	Y06921	267 (99.0bits)	9.7e-23	39	Y06921 Human ZIP-kinase (serine/threonine kinase). Length = 454
39	W81727	127 (49.8bits)	1.8e-07	41	W81727 M. tuberculosis immunogenic polypeptide TbH-30. Length = 174
43	G02019	128 (50.1bits)	2.0e-07	38	G02019 Human secreted protein, SEQ ID NO: 6100. Length = 82
44	G02711	411 (149.7bits)	1.9e-38	97	G02711 Human secreted protein, SEQ ID NO: 6792. Length = 81
46	W44195	116 (45.9bits)	4.0e-06	42	W44195 Mouse osteoclast transporter protein. Length = 537
48	W48792	643 (231.4bits)	5.0e-63	46	W48792 Homo sapiens sprouty 2 protein. Length = 315
49	Y32167	184 (69.8bits)	2.2e-14	59	Y32167 Soybean E2F protein fragment. Length = 80
60	Y91941	145 (56.1bits)	1.6e-09	43	Y91941 Human chaperone protein 2 (HCHP-2). Length = 375

Table 1D

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
1	AAA66494.1	413 (150.4bits)	2.0e-38	89	(L29164) immunoglobulin light chain variable region [Homo sapiens]
3	CSRT31	140 (54.3bits)	1.7e-09	58	CSRT31 protein P31 - rat >prf
5	AAF55906.1	141 (54.7bits)	1.3e-09	69	(AE003735) CG6353 gene product [Drosophila melanogaster] Length = 156
7	CAB82724.1	5366 (1894.0bits)	0.0	97	(AL162331) hypothetical protein [Homo sapiens] Length = 2270
8	BAB14447.1	900 (321.9bits)	5.0e-90	98	(AK023176) unnamed protein product [Homo sapiens] Length = 265
9	BAA92672.1	1305 (464.4bits)	6.0e-133	99	(AB037855) KIAA1434 protein [Homo sapiens] >emb
10	AAD45827.1	132 (51.5bits)	1.2e-08	80	AC004890_4 (AC004890) similar to zinc finger proteins; similar to BAA24380 [Homo sapiens]
11	NP_056191.1	1292 (459.9bits)	1.4e-131	91	KIAA0846 protein [Homo sapiens] >dbj|BAA74869.1| (AB020653) KIAA0846 protein [Homo sapiens]
12	BAB14132.1	759 (272.2bits)	4.3e-75	97	(AK022613) unnamed protein product [Homo sapiens] Length = 664
13	NP_057666.1	957 (341.9bits)	4.5e-96	100	peptide transporter 3 [Homo sapiens] >dbj|BAA93432.1| (AB020598) peptide transporter 3 [Homo sapiens]
15	BAA86484.1	2104 (745.7bits)	1.3e-217	99	(AB032996) KIAA1170 protein [Homo sapiens] Length = 838
16	BAA86495.1	1545 (548.9bits)	2.2e-158	100	(AB033007) KIAA1181 protein [Homo sapiens] Length = 336
17	NP_056345.1	143 (55.4bits)	4.7e-09	39	DKFZP434I56 protein
19	BAA74893.2	5332 (1882.0bits)	0.0	99	(AB020677) KIAA0870 protein [Homo sapiens] Length = 1019
20	GAG_AVISN	160 (61.4bits)	3.7e-11	42	GAG_AVISN GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
					PROTEIN P30] >pir
21	NP_057400.1	2952 (1044.2bits)	1.8e-307	100	REV1 protein [Homo sapiens] >gb|AAF06731.1|AF151538_1 (AF151538) deoxycytidyl transferase;
22	NP_060018.1	385 (140.6bits)	1.9e-35	100	hypothetical protein [Homo sapiens] >gb|AAF02423.1|AF103803_1 (AF103803) unknown [Homo sapiens]
23	AAG00552.1	164 (62.8bits)	4.5e-09	25	AF286473_1 (AF286473) retinitis pigmentosa GTPase regulator [Mus musculus]
24	NP_056054.1	1355 (482.0bits)	3.0e-138	100	KIAA1035 protein [Homo sapiens] >dbj|BAA91749.1| (AK001544) unnamed protein product [Homo sapiens]
25	NP_061155.1	5727 (2021.1bits)	0.0	100	anillin [Homo sapiens] >gb|AAF75796.1|AF273437_1 (AF273437) actin binding protein anillin [Homo sapiens]
26	NP_001384.1	1051 (375.0bits)	4.9e-106	99	extracellular matrix protein 2 [Homo sapiens] >dbj|BAA33958.1| (AB011792) extracellular matrix protein [Homo
30	AAF48140.2	168 (64.2bits)	4.5e-08	26	(AE003488) CG2779 gene product [Drosophila melanogaster] Length = 1612
31	B71413	194 (73.4bits)	7.2e-15	39	B71413 hypothetical protein dl3525w - Arabidopsis thaliana >emb
32	BAA92102.1	1661 (589.8bits)	1.1e-170	90	(AK002139) unnamed protein product [Homo sapiens] Length = 893
33	NP_055775.1	759 (272.2bits)	4.3e-75	96	KIAA1001 protein [Homo sapiens] >dbj|BAA76845.1| (AB023218) KIAA1001 protein [Homo sapiens]
34	NP_001339.1	267 (99.0bits)	1.6e-22	39	death-associated protein kinase 3 [Homo sapiens] >dbj|BAA24955.1| (AB007144) ZIP-kinase [Homo sapiens]
38	BAB14313.1	571 (206.1bits)	1.6e-81	94	(AK022932) unnamed protein product [Homo sapiens] Length = 838
39	A56154	149 (57.5bits)	5.9e-07	28	A56154 Abl substrate ena (enabled) - fruit fly

SEQ ID NO:	Accession No	Blast Score	p-value	% Identity	Description
					(Drosophila melanogaster) >gb
43	BAB03558. 1	582 (209.9bits)	2.5e-56	79	(AB046640) hypothetical protein [Macaca fascicularis] Length = 740
45	BAB00640. 1	679 (244.1bits)	1.3e-66	50	(AB036930) hapsin [Mus musculus] Length = 754
46	CAB09724. 1	120 (47.3bits)	2.7e-06	46	(Z97028) renal organic anion transporter [Pseudopleuronectes americanus]
47	AAB09748. 1	133 (51.9bits)	9.4e-09	39	(U37251) Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between
48	CAB96768. 1	1586 (563.4bits)	1.0e-162	100	(AJ271735) sprouty (Drosophila) homolog 3 [Homo sapiens] Length = 288
49	CAC01815. 1	199 (75.1bits)	2.5e-15	42	(AL391146) E2F transcription factor-like protein [Arabidopsis thaliana]
60	NP_060096. 1	145 (56.1bits)	2.7e-09	43	hypothetical protein FLJ20027 [Homo sapiens] >dbj|BAA90896.1| (AK000034) unnamed protein product [Homo sapiens]

TABLE 2

SEQ ID NO:	Accession No:	Description	p-value	Raw Score	Residue Position
9	PD01922B	PROTEIN PHOSPHODIEST ERASE HYDROL.	8.714E-20	21.83	63-99
13	BL01022B	PTR2 family proton/o ligopeptide symporters proteins	6.016E-14	22.19	72-118
13	BL01022A	PTR2 family proton/o ligopeptide symporters proteins	9.135E-12	11.58	42-61
13	PR00490A	SECRETIN RECEPTOR SIGNATURE	6.889E-09	4.58	191-204
20	PF01140A	Matrix protein (MA), P15	2.274E-12	11.51	1-55
26	BL01208B	VWFC domain proteins	1.0E-13	15.83	7-22
26	BL00422C	Granins proteins.	5.765E-09	16.18	132-160
26	BL00422C	Granins proteins.	7.706E-09	16.18	126-154
28	PR00234B	HIV-1 MATRIX PROTEIN SIGNATURE	7.25E-09	17.94	108-127
30	PD00787B	SYNTHASE BIOSYNTHESIS SIGNATURE	8.085E-09	13.26	792-806
33	BL00523A	Sulfatases proteins.	7.5E-17	13.36	36-53
33	BL00523C	Sulfatases proteins.	6.143E-14	12.64	129-140
33	BL00523B	Sulfatases proteins.	8.105E-14	8.64	84-96
48	PR00614A	NI-FE HYDROGENASE SMALL SUBUNIT SIGNATURE	8.373E-09	13.66	159-182
49	PD02910A	TRANSCRIPTION PROTEIN FACTOR REGULATION A.	7.0E-16	15.43	146-181
52	PR00209B	ALPHA/BETA GLIADIN FAMILY SIGNATURE	9.906E-09	4.88	124-143
58	BL01166F	RNA polymerases beta chain protiens	6.049E-09	7.27	175-186
60	PR00625B	DNAJ PROTEIN FAMILY SIGNATURE	1.321E-13	13.48	33-54
60	BL00636B	Nt-dnaJ domain proteins	8.333E-13	15.11	33-54

TABLE 3

SEQ ID NO:	pFam model name	Accession No:	Predicted beginning of domain	Predicted end of domain	pfam Score	e-value
1	ig	PF01812	9	65	16	0.0022
3	pro_isomerase	PF00160	62	78	8.6	0.22
10	KRAB	PF01352	4	34	-12.7	0.29
11	RasGEF	PF00617	146	308	-13	1.10E-05
12	VHL	PF01847	159	217	149.4	6.50E-41
13	PTR2	PF00854	101	185	9.2	0.06
19	DENN	PF02141	117	223	84.8	1.60E-22
19	TPR	PF01365	489	522	10.5	3.6
19	WD40	PF00400	867	904	12.3	1.3
19	WD40	PF00400	908	949	14	0.8
19	WD40	PF00400	1089	1128	6.1	8.7
20	gag_MA	PF01140	2	68	42.2	3.30E-11
21	BRCT	PF00533	44	131	57.3	3.30E-13
21	ODC_AZ	PF02100	333	355	2.2	8.2
25	PH	PF01636	985	1108	60.2	2.00E-15
48	metalthio	PF00131	121	191	-10.5	6.9
51	hormone	PF00103	16	25	1.1	4.7
60	DnaJ	PF00226	23	56	-0.8	0.032

TABLE 4

SEQ ID NO:	Signal peptides position	Mean Score	Cutoff	Conclusion
1	1-55	0.108	0.48	NO
2	1-9	0.116	0.48	NO
3	1-10	0.166	0.48	NO
4	1-143	0.16	0.48	NO
5	1-16	0.135	0.48	NO
6	1-8	0.104	0.48	NO
7	1-746	0.077	0.48	NO
8	1-31	0.63	0.48	YES
9	1-221	0.062	0.48	NO
10	1-22	0.075	0.48	NO
11	1-299	0.117	0.48	NO
12	1-89	0.252	0.48	NO
13	1-177	0.462	0.48	NO
14	1-73	0.458	0.48	NO
15	1-268	0.186	0.48	NO
16	1-46	0.447	0.48	NO
17	1-130	0.119	0.48	NO
18	1-36	0.278	0.48	NO
19	1-508	0.157	0.48	NO
20	1-6	0.293	0.48	NO
21	1-258	0.052	0.48	NO
22	1-37	0.095	0.48	NO
23	1-71	0.036	0.48	NO
24	1-96	0.115	0.48	NO
25	1-623	0.051	0.48	NO
26	1-38	0.125	0.48	NO
27	1-63	0.068	0.48	NO
28	1-14	0.221	0.48	NO
29	1-42	0.402	0.48	NO
30	1-724	0.096	0.48	NO
31	1-150	0.083	0.48	NO
32	1-284	0.103	0.48	NO
33	1-16	0.895	0.48	YES
34	1-136	0.062	0.48	NO
35	1-43	0.233	0.48	NO
36	1-146	0.073	0.48	NO
37	1-66	0.072	0.48	NO
38	1-150	0.253	0.48	NO
39	1-115	0.077	0.48	NO
40	1-79	0.137	0.48	NO
41	1-16	0.914	0.48	YES
42	1-83	0.211	0.48	NO
43	1-132	0.198	0.48	NO
44	1-94	0.059	0.48	NO
45	1-463	0.093	0.48	NO
46	1-61	0.168	0.48	NO
47	1-131	0.094	0.48	NO

SEQ ID NO:	Signal peptides position	Mean Score	Cutoff	Conclusion
48	1-237	0.156	0.48	NO
49	1-77	0.053	0.48	NO
50	1-8	0.274	0.48	NO
51	1-126	0.085	0.48	NO
52	1-37	0.61	0.48	YES
53	1-24	0.551	0.48	YES
54	1-24	0.548	0.48	YES
55	1-77	0.182	0.48	NO
56	1-25	0.55	0.48	YES
57	1-127	0.086	0.48	NO
58	1-89	0.152	0.48	NO
59	1-15	0.702	0.48	YES
60	1-41	0.045	0.48	NO
61	1-61	0.071	0.48	NO
62	1-104	0.163	0.48	NO
63	1-34	0.622	0.48	YES
64	1-36	0.685	0.48	YES
65	1-18	0.226	0.48	NO
66	1-51	0.453	0.48	NO
67	1-51	0.067	0.48	NO
68	1-11	0.064	0.48	NO
69	1-0	0	0.48	NO
70	1-23	0.347	0.48	NO
71	1-43	0.233	0.48	NO
72	1-20	0.864	0.48	YES
73	1-13	0.428	0.48	NO
74	1-55	0.346	0.48	NO
75	1-13	0.108	0.48	NO
76	1-24	0.679	0.48	YES
77	1-61	0.107	0.48	NO
78	1-24	0.375	0.48	NO
79	1-69	0.293	0.48	NO
80	1-22	0.218	0.48	NO
81	1-14	0.088	0.48	NO
82	1-18	0.192	0.48	NO
83	1-0	0	0.48	NO

TABLE 5

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	SEQ ID No: of contig nucleo-tide sequence	SEQ ID No: of contig peptide sequence	SEQ ID NO: in USSN 09/540,217	SEQ ID NO: of nucleotide in USSN 60/250, 583	SEQ ID NO: of peptide in USSN 60/250, 583
1	85	168	252	22974	2565	2
2	86	169	253	20878	2577	14
3	87	170	254	12791	2580	17
4	88	171	255	6072	2588	25
5	89	172	256	16749	2611	48
6	90	173	257	27958	2612	49
7	91	174	258	25431	2613	50
8	92	175	259	53	2623	60
9	93	176	260	14203	2632	69
10	94	177	261	25455	2655	92
11	95	178	262	20399	2663	100
12	96	179	263	18639	2675	112
13	97	180	264	30435	2676	113
14	98	181	265	9819	2682	119
15	99	182	266	23487	2694	131
16	100	183	267	27666	2701	138
17	101	184	268	21075	2703	140
18	102	185	269	5372	2709	146
19	103	186	270	26608	2712	149
20	104	187	271	7050	2714	151
21	105	188	272	10656	2718	155
22	106	189	273	8306	2724	161
23	107	190	274	26811	2733	170
24	108	191	275	19370	2748	185
25	109	192	276	8838	2753	190
26	110	193	277	2975	2776	213
27	111	194	278	28343	2778	215
28	112	195	279	23107	2780	217
29	113	196	280	947	2786	223
30	114	197	281	25499	2787	224
31	115	198	282	26874	2789	226
32	116	199	283	7863	2791	228
33	117	200	284	12385	2808	245
34	118	201	285	9325	2811	248
35	119	202	286	135	2830	267
36	120	203	287	948	2842	278
37	121	204	288	11131	2844	280
38	122	205	289	26590	2848	284
39	123	206	290	29769	2852	288
40	124	207	291	12703	2884	320
41	125	208	292	19931	2888	324
42	126	209	293	12950	2892	328
43	127	210	294	16635	2893	329

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	SEQ ID No: of contig nucleotide sequence	SEQ ID No: of contig peptide sequence	SEQ ID NO: in USSN 09/540,217	SEQ ID NO: of nucleotide in USSN 60/250, 583	SEQ ID NO: of peptide in USSN 60/250, 583
44	128	211	295	11259	2894	330
45	129	212	296	17066	2910	346
46	130	213	297	27046	2917	353
47	131	214	298	28443	2920	356
48	132	215	299	12951	2934	370
49	133	216	300	16401	2937	373
50	134	217	301	2095	2941	377
51	135	218	302	14896	2958	394
52	136	219	303	3942	2969	405
53	137	220	304	18627	2977	413
54	138	221	305	1334	2978	414
55	139	222	306	12612	2986	422
56	140	223	307	26757	2992	428
57	141	224	308	29643	3010	446
58	142	225	309	17502	3024	460
59	143	226	310	15745	3033	469
60	144	227	311	16448	3085	521
61	145	228	312	2700	3097	533
62	146	229	313	3038	3124	560
63	147	230	314	5507	3146	582
64	148	231	315	21158	3203	639
65	149	232	316	30322	3267	703
66	150	233	317	29542	3292	728
67	151	234	318	19566	3358	794
68	152	235	319	180	3399	835
69	153	236	320	2278	3404	840
70	154	237	321	6132	3542	978
71	155	238	322	138	3645	1081
72	156	239	323	29552	3652	1088
73	157	240	324	28639	3658	1094
74	158	241	325	186	3732	1168
75	159	242	326	7065	3765	1201
76	160	243	327	18073	3901	1337
77	161	244	328	513	3985	1421
78	162	245	329	6994	4036	1472
79	163	246	330	189	4080	1515
80	164	247	331	191	4260	1695
81	165	248	332	8767	4798	2226
82	166	249	333	23899	4997	2425
83	167	250	334	533	5057	2485
84		251	335	6903	2835	

TABLE 6

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
252	A	3	744	RQSSGNLTMAWTPLLLPLLTFCTVSEA SYELTQPPSVSVSPGQTATITCSGDALP KK\HPYWYQQKSGQAPVLVIYEDNKR PSGIP\ERFSASSSGTMATLTISGAQVED EADYYCYSTDSSGNHRGVFGGGTRLT VLSQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKA GVETTTPGKQSNNKYAASSYLS\LTPE QWKSHKSYSCQVTHEG\STVEETGAPT EYLLRVY
253	B	1	1617	MEKGSGFIKYSTYKQGTIRVAEEAETA HSSVLIGPEKGVVHLATAAVLNAVWD LWAKQEGKVLAVGRELQEEEKEETG WRKAQAAVEGGVGTWWLTASIRAAN AFTVRKKWGLYTYVLQILSFLLQACLE VTCGHDLIMGCIKSKENKSPAIKYRPE NTPEPVSTSVSHYGAEPTTVSPCPSSSA KGTAVNFSSLSMTPFGGSSGVTPFGGA SSSFSVVPSSYPAGLTGGVTIFVALYDY EARTTEDLSFKKGERFQIINNTPMVLN LGQNHPGDIWQYLETFLVVTVGVLPLS SSASTPVFDRVTNGVTPTIKDLTGCCV ENRLLTSNSSDFFTLINHSNSSKTPFQN TRLVVSRGNSSEKQFAIRFQDGKTDHA IQLSSGKKTALGREALEHPESLDSRKV GQRSRWSSQAASPISGPIQAETALLCPG DQWTQEFHTSPLLTVPHLPDIYTLDCC RKDFSIYIHSFGDITQSYIFKYHLQIDDY QLCAQALKDGWTRPPPFHTAHLHFSL LTLACAETVTSAETPDALAKSRFKVK
254	A	1	717	GTRDATAEENRVLLAMVNPTVFFDIA VDGEPLGRVSFEVRGLDTKK*LLI*SIK LC*QIGGSSIFITSD*KNSCLPLIVQQCL LFLRILP\LFADKVPKTAENFRALSTGE KGFGL*GVPCFHRIIPGFMCQGGDCE/R HHNGTGGKSIYTEKFEDE\NFILKAYG VLGSLSMANA\GPNTN\GSQFFICTAKT EWL\DGKP\VVFGKVKEGMNIVEAME

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				RFGSRNGKTSKKIISIADCGQLE
255	A	253	571	ICHQPTSLSHQ*ERNGWPGRWHSQPRS KFCRLRV\LSQGDHEKKSLPSGQRPHR TGCASSSGSSKGLLLLLPLDGLGVIVLIN PHLVVFPGMRAP*LLPRLWLRRWS
256	A	1	384	VRDYNLTEEQKAIKAKYPPVNRKYEY LDHTADV/QWIVLHRA*IYFFRLHAWG DTLEEAFEQCAMAMFGYMTDTGTVEP LQTVEVETQ/GWGEEFSLSKHPQGTEV KAITYSAMQVYNEENPEVFVIIDI
257	A	675	1010	VTSSCPRKKRRFGGDRPSSSFSPPSKEL LAVKAPREGRRGPGNESRSEPSQPLDS HGPGLRRTFLPPSPRHPTKDRRTAARS GPRRKRGQTNEIRGCKEEEGEKYLVPA QG
258	A	5751	6430	FYFVPSQESVPSASPTGIPKHSLRKTTS TEEPRGTHSQGQFTMPLAGMSLGSLKS EFVPLFSATPFWVPFSSLPLFPWVLVED HVCLLDCVVVDLQD\MD\IFAAERHP\R DYSK\APEDSSGDLIFPSYFVR\QTGGSL L\TEPCRLKLQVERNLDKEISHTVPDISI HGNLSSVHCSLDLYKYKLIRGLLENNL GEPIEEFMRPYDLQRSKNSYCPEWRSV HLYVLPH
259	B	144	638	MIVNLFNMFITYGDTFLPTPSSYDELY YEIIRMHQSFDNLYSMVLRLSTNAGQ WKEAASKVTHALVNIRAIINHFNPKIES YAAVNHISQLSEEQVLEVVRANYDTL TLKLQDGLDQYERYSEQHKEAAFFKE LVRSISTNVRRNLAFHTLSQEVLLKEFS TIS
260	B	30	2477	MTPGQLSNVRAPGSAEKGSGDTGDAR PPSAAPPGGSAGEARTAGARYLCPRSS LSGGAAATRTCGLANPEEEGPSAKCGE NGSAERTDLGGNKYNQERIQIEYVEVL FADFFREVFAICGSCDALGNWNPQNA VALLPENDTGESMLWKATIVLSRGVS VQYRYFKGYFLEPKENIHHRGDFLVTF PSSSRSSFVQTGQFSGRDIDKDPKLSPV GRGWGFEWAIELCMAVKEDVRQEVG

SEQ ID NO:	Me t h o d	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				SHIGLLPDVAMAFVNCRGTDGSVAVR MTRGHSHCHLGFAYCASGFSLEPCVE NDCGASSAEVQQGFVFITSASSSSSYCT EAKRVKLTLEGLEEDDDDRVSPTVLH KMSNSLEISLISDNEFKCRHSQPECGYG LQPDRWTEYSIQTMEPDNLELIFDFFEE DLSEHVVQGDALPGHVGTACLLSSTIA ESGKSAGILTLPIMSRNSRKTIGKVRVD YIIIKPLPGYSCDMKSSFSKYWKPRIPL DVGHRGAGNSTTTAQLAKVQENTIAS LRNAASHGAAFVEFDVHLSKDFVPVV YHDLTCCLTMKKKFDADPVELFEIPVK ELTFDQLQLLKLTHVTALKSKDRKESV VQEENSFSENQPFPSLKMDGMWDGNL STYFDMNLFLDIILKTVLENSGKRRIVF SSFDADICTMVRQKQNKYPILFLTQGK SEIYPELMDLRSRTTPIAMSFAQFENLL GINVHTEDLLRNPSYIQEAKAKGLVIFC WGDDTNDPENRRKLKELGVNGLIYDR IYDWMPEQPNIFQVEQLERLKQELPEL KSCLCPTVSRFVPSSLCGESDIHVDAN GIDNVENA
261	A	1	3257	MEPIEGKRSSCHKTGEATAVVHCPPG WNITMGVEASCAFVGRAGSQDTVRTG RALKALTQLRAAQGRGSQGAAAAETG LGGRRLRRAPGGGPCVGPRAAAATTL SGPRGTAQGHGGGGRSSGKGDQRAHE LAAWIPRATRARHTGAAGAEPYYRA WGSGEQGRGVCRGLLRLPAGPPTPGR ARALAERLSPPRAAPRQDSWPLRGFLP PPQPLNPTSASPHPRLFSLLGARPISPW TMAATIQAMERKIESQAAHLLSLEGQT GMAEKKLADCEKTAVEFGNQLEGKW AVLGTLLQEYGLLQRRLENVENLLHN RNFWILRLPPGSKGESPKVALGRPGVG EAAAKPVSVWFSEQVWGKLEDWQKE LCKHVMRGNCEMLVSLDYAISKSEVL SQIEQGKEPCNWRRPGPKIPDVPVDPSP APVPLPLFCSLYPPGEIHQCSVPAAKQL HVVQRTSPVTAKLSTLQPKPHFHLVLH

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				PTPCQLLKGNTVNPTLTSTPTATACFS APLRGRAPWIYTMEGNRLNQCFQTGC WRAPGHIQAGEEAPGSRVVFTRITGSG ECRRGPEKSCGFGHSREALGEEWMIR KVKVEDEDQEAEEEVEWPQHLSLLP\S PFPAPDLGHLAAAYKLEPGAPGALSGL ALSGWGPMPEKPYGCGECERRFRDQL TLRLHQRLHRGEGPCACPDCGRSFTQR AHMLLHQRSHRGERPFPCSECDKRFSK KAHLTRHLRTHTGERPYPCAECGKRFS QKIHLGSHQKTHTGERPFPCTECEKRF RKKTHLIRHQRIHTGERPYQCAQCARS FTHKQHLVRHQRVHQTAGPARPSPDS SASPHSTAPSPTPSFPGPKPFACSDCGL SFGWKKNLATHQCLHRS\EGRPFGCDE CALGATVDAPAAKPLASAPGGPGCGP GSDPVVPQRAPSGERSFFCPDCGRGFS HGQHLARHPRVHTGERPFACTQCDRR FGSRPNLVAHSRAHSGARPF\ACAQCG RRFSRKSHLG\RHQAVHTGSRPHACAV CARSSFSSKTNLVRHQGI\HTGSRPFSC PQCGKSFSRKTHLVRHQLIHGEAAHA A\PDAALAAPAWSAPPEVAPPP\LFF
262	A	327	2561	ITMGSSGLGKAATLDELLCTCIEMFDD NGELDNSYLPRIVLLMHRWYLSSTELA EKLLCMYRNATGESCNEFRLKICYFM RYWILKFPAEFNLDLGLIRMTEEFREV ASQLGYEKHVSLIDISSIPSYDWMRRV TQRKKVSKKGKACLLFDHLEPIELAEH LTFLEHKSFRRISFTDYQSYVIHGCLEN NPTLERSIALFNGISKWVQLMVLSKPT PQQRAEVITKFINVAKKLLQLKNFNNL IAIVGAL\SHRSISGFKGTHS\HLSSEV\T KNWNVK*QKWVSSNG\NYCNYRKPFA DCDGFKIPILGVHLKDLIAVHVIFPDWT EENKVNI\VKMHQLSVTLSELVSLQNA SHHLEPNMDLINLLTLSLDLYHTEDDI YKLSLVLEPRNSKSQPTSPTTPNKPVVP LEWALGVMPKPDPTVINKHIRKLVESV FRNYDHDHDGYISQEDFESIAANFPFL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				DSFCVLDKDQDGLISKDEMMAYFLRA KSQLHCQI/GAPGFIHNFQEMT\YLKP\T FCEHCAGFIL\GIIKQGYKCKDCGANCH KQCKDLLVLACRR\FARAPSLSSGHGS LPGSPSLPPAQ\D*VFKFPGVTADNSD\L DSRAITLVTGSSRK\TSVRLQRATTSQA T\QT\EPVWSEAGWG\DSGSHTLPYNRY SGSLHKP/AKRHKGFAIWEK*KSPGWH \AGGDV*NPGT\EFE\LAPDEGEKTT\QD G\EDGLTSRLAENLKANNGWLLGGGK NKKLLRKALASQEVILERTP
263	A	4463	4703	RPKMGRRSKHKPPASFQVSSLSNPGFF FFI*HCFF*LYFSYKRNVSL*KITHYRKI LRRKTFTSETKFFPMKTEPKRVSG
264	A	1	1941	MPAPRAREQPRVPGERQPLLPRGARGP RRWRRAAGAAVLLVEMLERAAFFGV TANLVLYLNSTNFNWTGEQATRAALV FLGASYLLAPVGGWLADVYLGRYRA VALSLLLYLAASGLLPATAFPDGRSSF CGEMPASPLGPACPSAGCPRSSPSPYC APVLYAGLLLLGLAASSVRSNLTSFGA D\QVMDLGRDATRRFFNWFYWSINLG AVLSLLVVAFIQQNISFLLGYSIPVGCV GLAFFIFLFATPVFITKPPMGSQVSSML KLALQNCCPQLWQRHSARSKLSQGQQ GNNGSESKLHLLVAKWQHTLGRVELT VAVFGDDYTNIVPFGISKDSARLLDKK RDRQCARVLADERSPQPGASPQEDIAN FQVLVKILPVMVTLVPYWMVYFQMQ STYVLQGLHLHIPNIFPANPANISVALR AQGSSYTIPEAWLLLANVVVVLILVPL KDRLIDPLLLRCKLLPSALQKMALGMF FGFTSVIVAGVLEMERLHYIHHNETVS QQIGEVLYNAAPLSIWWQIPQYLLIGIS EIFASIPGL\EFAYSEAPRSMQGAIMG\IF F\CLSGVGSLLGSSLVGTAVPLPGGWL HCPKDFGNINNCRMDLYFFLLAGIQAV TALLFVW\IAGRYERASQGPASHSRFSR DRG
265	B	46	774	XACSGVPGTKCSPPSGSGYPNPYSKHV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				LTEDIVHREVTPDQKLLSRATLTKTNR NAHAGPERLFPANVAHSVYVLEDSIVD PQNQTLTTFNWNINPRPG
266	A	3	2523	SSLTSSMEDPAAPGTGGPPANGNGN\G GGKGKQAAPKGREAFRSQRRESEGSV DCPTLEFEYGDADGHAAELSELYSYTE NLEFTNNRRCFEEDFKTQVQGKEWLE LEEDAQKAYIMGLLDRLEVVSRERRL KAARAVLYLAQGTFGECDSEVDVLH WSRYNCFLLYQMGTFSTFLELLHMEID NSQACSSALRKPAVSIADSTELRVLLS VMYLMVENIRLERETDPCGWRTARET FRTELSFSMHNEEPFALLLFSMVTKFCS GLAPHFPIKKVLLLLWKVVMFTLGGFE HLQTLKVQKRAELGLPPLAEDSIQVVK SMRAASPPSYTLDLGESQLAPPPSKLR GRRGSRRQLLTKQDSLDIYNERDLFKT EEPATEEEEESAGDGERTLDGELDLLE QDPLVPPPPSQAPLSAERVAFPKGLPW APKVRQKDIEHFLEMSRNKFIGFTLGQ DTDTLVGLPRPIHESVKTLKQHKYISIA DVQIKNEEELEKCPMSLGEEVVPETPC EILYQGMLYSLPQYMIALLKILLAAAP TSKAKTDSINILADVLPEEMPITVLQSM KLGIDVNRHKEIIVKSISTLLLLLLKHF KLNHIYQFEYVSQHLVFANCIPLILKFF NQNILSYITAKNSISVLDYPCCTIQDLPE LTTESLEAGDNSQFCWRNLFSCINLLR LLNKLTKWKHSRTMMLVVFKSAPILK RALKVKQAMLQLYVLKLLKLQTKYL GRQWRKSNMKTMSAIYQKVRHRMND DWAYGNDIDARPWDFQAEECTLRANI EAFNSRRYDRPQDSEFSPVDNCLQSVL GQRLDLPEDFHYSYELWLEREVFSQPI CWEELLQNH
267	A	150	1076	PAWNARPRQVDLKLTHKKQRALLERF DIYRKVPKDLTQPTYTGAIISICCCLFIL FLFLSELTGFITTEVVNELYVDDPDKDS GGKIDVSLNISLPNLHCELVGLDIQDE MGRHEVGHIDNSMKIPLNNGAGCRFE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				GQFSINKVPGNFHVSTHSATAQPQNPD MTHVIHKLSFGDTLQVQNIHGAFNAL GGADRLTSNPLASHDYILKIVPTVYED KSGKQRYSYQYTVANKEYVAYSHTG RIIPAIWFRYDLSPITVKYTERRQPLYRF ITTICAIIGGTFTVAGILDSCIFTASEAW KKIQLGKMH
268	B	264	1999	MLIYSSKTLELRETSVTPSNLWGGQGL LGVSIRFCSFDGANENVWHVLEVESNS PAALAGLRPHSDYIIGADTVMNESEDL FSLIETHEAKPLKLYVYNTDTVYTGNS TWKTCVKSSYSGALVNLNRLFSSAYT RIPCFGALRINSDKHFVNGCWLLSTYT L
269	A	67	906	NLLLGGGGKKKKPPRTRGPFPGLSQPG LLWLFPKRPGCSHLPSTPIKEMGLPKIH HRVGWESFSGVFLEVDFKIYKKKMNE FFSVDDNNEEEEDVEMKEDSDENGPE EKQSVEEMEEQSQDADGVNTVTVPGP ASEEAVEDCKDEDFAKDENITKGGEV TDHSVRDQDHPDGQENDSTKNEIKIET ESQSSYMETEELSSNQEDAVIVEQPEVI PLTEDQEEKEGEKAPGEDTPRMPGKSE GSSDLENTPGPDVEMNSQVDKVNDPT ESQPSCQA*RSRG
270	A	401	881	ERRERSPDQSSGRASRGPPERQSLRMS PSRAAWTSSPCRSCASQGVCAWPLNL RRIASTSWC*PMSAGIGPMAWWPSTT GPCMMSTVSTMAKPHRECPGCFVPFA VCVVSRFPYYNSLKDCLSWHYRRPGA TLLSPSSLVTLLLVKGPGAAAADAGEI PV
271	A	184	581	ASAPVGCLTRAVCGRPPWRTNTVVEP REGTRILEFGHLKLAHVPPLEFLVNQH QPEDHVLIKRWKEEKLEPAWEGPYPV LLTTKTAVRT/DKKKKKKKKRWTHHT QVKKVPPPPESWAIVPGENPTKLKLRK M
272	A	1	3802	MRRGGWRKRAENDGWETWGGYMAA KVQKLEEQFRSDAAMQKDGTSSTIFSG

129

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				VAIYVNGYTDPSAEELRKLMMLHGGQ YHVYYSRSKTTHIIATNLPNAKIKELK GEKVIRPEWIVESIKAGRLLSYIPYQLY TKQSSVQKGLSFNPVCRPEDPLPGPSNI AKQLNNRVNHIVKKIETENEVKVNGM NSWNEEDENNDFSFVDLEQTSPGRKQ NGIPHPRGSTAIFNGHTPSSNGALKTQD CLVPMVNSVASRLSPAFSQEEDKAEKS STDFRDCTLQQLQQSTRNTDALRNPHR TNSFSLSPLHSNTKINGAHHSTVQGPSS TKSTSSVSTFSKAAPSVPSKPSDCNFIS NFYSHSRLHHISMWKCELTEFVNTLQR QSNGIFPGREKLKKMKTGRSALVVTD TGDMSVLNSPRHQSCIMHVDMDCFFV SVGIRNRPDLKGKPVAVTSNRGTGRAP LRPGANPQLEWQYYQNKILKGKAADI PDSSLWENPDSAQANGIDSVLSRAEIA SCSYEARQLGIKNGMFFGHAKQLCPN LQAVPYDFHAYKEVAQTLYETLAS\YT HNIEAVSCDEALVDITEILAETKLTPDE FANAVRMEIKDQTKCAASVGIGSNILL ARMATRKAKPDGQYHLKPEEVDDFIR GQLVTNLPGVGHSMESKLASLGIKTCG DLQYMTMAKLQKEFGPKTGQMLYRF CRGLDDRPVRTEKERKSVSAEINYG\IR FTQPKEAEAFLLSLSEEIQRRLEATGM KGKRLTLKIMVRKPGAPVETAKFGGH GICDNIARTVTLDQATDNAKIIGKAML NMFHTMKLNISDMRGVGIHVNQLVPT NLNPSTCPSRPSVQSSHFPSGSYSVRDV FQVQKA\KKSTEEEHKEVFRAAVDLEI SSASRTCTFLPPFPAHLPTSPDTNKAES SGKWNGLHTPVSVQ\SRLNLSIEVPSPS QLDQSVLEALPPDLREQVEQVCAVQQ AESHGDKK\KEPVNGCNTGILPQPVGT/ MSLLQIP\EPQESNSDAGINLIALPAFS\Q VDPEVFAALS\AELQRELKAAYDQRQR QGENSTHQQS\ASASVPKNPLI\HLKAA\ VKEKKRNKKKKTIGSPKRIQSPLNNKL LNSPAKTLPGACGSPQKLIDGFLKHEG

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				PPAEKPL/EKNSSGFLLSGVPG\LSSLQS DP/SLGCVRPPPP\NL\AGAVEFNDVKTL LR\EWVTTISDPMEEDILQ\VVKYCTDL IEDKDLEKLDLVIKYMKRLMQQSVES VWNMAFDFILDNVQVVLQQTYGSHIK SYINITQRA
273	A	1	785	MAETEERSLDNFFAKRDKKKKKERSN RAASAAGAAGSAGGSSGAAGAAGGG AGAGTRPGDGGTASAGAAGPGAATK AVTKDEDEWKELEQKEVDYSGLRVQ AMQISSEKEEDDNEKRQDPGDNWEEG GGGGGGMEKSSGPWNKTAPVQAPPAP VIVTETPEPAMTSGVYRPPGARLTTTR KTP\QGPPEIYQ*YHSSHPLAVNLPKHV ESRKDKEMEKSFEVVRHKNRGRDEVS KNQALKLQLDNQYAVL\ENQKSSHSQ YN
274	A	463	828	HLRILRDSRTHSYFLTSLRGENNPWTD QSPCAAASRAQHLHPAAVAAATMPKT KAEGDAKGDKAKVKDEPQVTRAAIQT NTFIFKC*IEPQKQIYILYIQNSCQISLLI LPKSTLMKWMQTL
275	A	3	1901	SSVEQASVEVPDGPTLHDPDLYIEIVKN TKSVPEYSEVAYPDYFGHIPPPFKEPIL ERPYGVQRTKIAQDIERLIHQSDIIDRV VYDLDNPNYTIPEEGDILKFNSKFESGN LRRVIQIRKNEYDLILNSDINSNHYHQ WFYF\EVSGMRPGVAYRFNIIN\CE\RC NRLFNYGMQPLMYSVQEALNARPWW IRMGTDIRYYINHFSRSSVAAGGA/QRG KSYYTITFTVQFST*RMDVCYFA/YIHY PYTY\STLQMHLQKLESAHNPQQIYFR KDVLCETLSGNSCPLVTITAMPESNYY EHICHFRNRPYVLMYARVHPG\ET\NAS WGYERERWEYLHEAINPTGFRSLRRN LYY/IFKIVPMLNPDGVINGNHRCSLSG EDLNRQWQSPSPDLHPTIYHAKGLLQY LAAVKRLPLVYCDYHGHSRKKNVFM YGCSIKETVWHTNDNATSCDVVEDTG YRTLPKILSHIAPAFCMSSCSFVVEKSK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				ESTARVVV*REIGVQRSYTMESTLCGC DQGKYKGLQIGTRELEEMGAKFCVGL L\RLKRLTSPLEY\NPALPSPALTFENDL N*IQACKVTSPYPLMSLDEDEP\RF\LEE VDYSAESNDELDIELAENVGDYEPSAQ EEVLSDSELSRTYLP
276	A	1076	3511	IKALSSSAEDASLVNASISSSVKATSPV KSTTSITDAKSCEGQNPELLPKTPISPLK TGVSKPIVKSTLSQTVPSKGELSREICL QSQSKDKSTTPGGTGIKPFLERFGERC QEHSKESPARSTPHRTPIITPNTKAIQER LFKQDTSSSTTHLAQQLKQERQKELAC LRGRFDKGNIWSAEKGGNSKSKQLET KQETHCQSTPLKKHQGVSKTQSLPVTE KVTENQIPAKNSSTEPKEVIREIEMSVD DDDINSSKVINDLFSDVLEEGELDMEK SQ/AGDGSSISR/TAAKNRKMH*ISPQC LYLHHWHKQLV*V*CPHLDWN*KTPA EVMKVQNQENSKELVS/RRAESGDSLG SEDRDLLYRSQRFKETERPSIKQVIVRK EDVTSKLDEKNNAFPCQVNIKQKMQE LNNEINMQQTVIYQASQALNCCVDEE HGKGSLEEAEAERLLLIATGKRTLLIDE LNKLKNEGPQRKN*G*S/APSEFIAIPKD QFTLSEIRLP*KADFVCSTVQKPDAAN YYYLIILKSRS\ENMVATPLASTSNSLN GDALTFTTTFTLQDVSNDFEINIEVYSL VQKKDPSGLDKKKKTSKSKKSNIHSSV MASPGGLSAVRTSNFALVGSYTLSLSS VGNTKFVLDKVPFLSSLEGHIYLKIKC QVNSSVEERGFLGCPGGGRLQPKRQTI FEDVSGFGAWHRRWCVLSGNCISYWT YPDDEKRKNPIGRINLANCTSRQIEPAN REFCARRNTFELITVRPQREDDRETLV\ TNAGTHSVFTKNWLSADTKEERDLW MQKLNQVLCDIRLWQPDACYKPIGKP
277	B	1	2319	MQINETIWDTVGAASRHGEGERQAKS STRGCTHLAEGQGIYLQEEQSPPEMCT RVMEKREGLTIERERDPLLPVWKALGI QAHKCVAHTTNPSKATAVHLPHLTMQ

SEQ ID NO:	M e t h o d	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				PQGCLMSFFPTAAEFSTYGQELYLENN QIEEITEICFNHTRKINVIVLRYNKIEEN RIAPLAWINQENLESIDLSYNKLYHVPS YLPKSLLHLVLLGNQIERIPGYVFGHM EPGLEYLYLSFNKLADDGMDRVSFYG AYHSLRELFLDHNDLKSIPPGIQEMKA LHFLRLNNNKIRGNKQEIKQTSKQASA VQSEKWVTMRRAHWGLRAARRLRPP STAWINSRSRPVPVEQTHCGLAVAEER KDLFMFFRSLHFFVEWFEYRKRTFKHL KWDEDYDQEPDDDYQTGFPFRQNVD YGVPFHQYTLGCVSECFCPTNFPSSMY CDNRKLKTIPNIPMHIQQLYLQFNEIEA VTANSFINATHLKEINLSHNKIKSQKID YGVFAKLPNLLQLHLEHNNLEEFPFPL PKSLERLLLGYNEISKLQTNAMDGLVN LTMLDLCYNYLHDSLLKDKIFAKMEK LMQLNLCSNRLESMPPGLPSSLMYLSL ENNSISSIPEKYFDKLPKLHTLRMSHNK LQDIPYNIFNLPNIVELSVGHNKLKQAF YIPRNLEHLYLQNNEIEKMNLTVMCPS IDPLHYHHLTYIRVDQNKLKEPISSYIFF CFPHIHTIYYGEQRSTNGQTIQLKTQVF RRFPDDDDESEDHDDPDNAHESPEQE GAEGHFDLHYYENQE
278	A	65	262	SRRRGGVSAPTSFYGRDRRMFPAQEE ADRTVFVGNLEARVREEILYELFLQVL CPREMGILSISP
279	A	1	892	MSRWGAAVGQGALREEHFAHAHITER TRRVREGRRKRRSSLLTTSPTSANAQA HFLKLKVSIDKGPQNRAGAIVPWFAK MSFPKYKP\SSLRTLP\ETLDPAEYNISP ETRRAQA\ERLAHR\AQL\KREYLLQYN DPN\RRGLIENP\ALLRWAYARTINVY\P NFKP\TPKSSLMGAFVWDFGPLIFI\YYII KTERWDPNQRWLTDSRILKYEAILLER DDLTLTTDNSLNPAAFLRGNPNPEEPE HKCLDLISYQTRVRLDLSKTPFQTGRH LFIDGSSLVIGGKGHNGYSVVDGETLT K

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
280	B	1	597	MQTFTTCISYSEYSCMLLANASSHGTL YCKLRVGICLLMVPAVKNQASGSARG ATKVRRKCQAGCQNEHLGELDDGTD GKNQLNIRENGGRGQNCEQELEESVA EKDLSQTSRDLEKMMSKHIFLKPMLSI SDLVNFLMQVSKVLVKTAEGIVLQQL PLAFPALHFHAYGNLFPVCSFKHYIYM IDHPIFISIPDFLT
281	A	1	4061	MPVPSRHINIGRSQSWDAAGWYEGPW ENAESLRPLGRRSSLTYGTAEGTWFEP NHRPQDAALPVAAEPYLYREAVYNSV AARKGSTPDFTFYDSRQAVMSGRSPLL PREYYSDPSGAARVPKEPPLYRDPGVS RPVPSYGVLGSRTSWDPMQGRSPALQ DAGHLYRDPGGKMIPQGRQTQSRAAS PGRYGREQPDTRYGAEVPAYPLSQVFS DISERPIDPAPARQVAPTCLVVDPSSAA APEGSTGVAPGALNRGYGPARESIPSK MAYETYEADLSTFQGPGGKRTVLPEFL AFLRAEGLAEATLGALLQQGFDSPAVL ATLEDADIKSVAPNLGQARVLSRLANS CRTEMQLRRQDRGGPLPRARSSSFSHR SELLHGDLASLGAAAPLQTASPRAGDP ARRPSSAPSQHLLETAATYSAPGVGTH APHFPSNSGYSSPTPCALTARLSPTYPL QAGVALTNPGPSNPLHPGPRTAYSTAY TVPMELLKRERNVAASPLPSPHGSPQV LRKPGAPLGPSTLPPASQSLHTPHSPYQ KVARRTGAPIIVSTMLAPEPIQFAGQA VQSDNVRKAYAAGTPVRPTSPGDTDK WGLQARAPGRAVDPRNMISAQEHKV VECMARRSATCFVFGQLCRLHSTSSDP VGVDFILSMEDVGRGKSRNPDSWSPN AVVWDASGVGGERVLQYQLDMNTVP PQGWTTRKTRVCCKHEASPSPISALAA IAKEEGVILLLWTFTLGNKRLGGSATR VGYAEAQAEAPSCKATTVTLSSGSSHE CDSSVSSKTATCRDFMGQPWGHASIPP TPNPPPPAVVPGIFSQHENPLAFLFSRL AMKDLLPGFEPQTLDRSRASLSHVLRA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				RPSGRVEGIRPQIMNGPLHPRPLVALL DGRDCTVEMPILKDLATVAFCDAQST QEIHEKVLNEAVGAMMYHTITLTRED LEKFKALRVIVRIGSGYDNVDIKAAGE LGECEAALAAWSCPELCGPCSGGLGE AAGTGTTEQPLLAVARWLPPGRAVEH LAALPSHDTGIAVCNIPSAAVEETADST ICHILNLYRRNTWLYQALREGTRVQSV EQIREVASGAARIRGETLGLIGFGRTGQ AVAVRAKAFGFSVIFYDPYLQDGIERS LGVQRVYTLQDLLYQSDCVSLHCNL\N EHNHHL\INDFTIKQMRAGSIPLWNAA RGGLVDEKALAQALKEGRIRGAALDV HESEPFSFAQGPLKDAPNLICTPHTAW YSEQASLEMREAAATEIRRAITGRIPES LRNCVNKEFFVTSAPWSVIDQQAIHPE LNGATYRYPPGIVGVAPGGLPAAMEGI IPGGIPVTHNLPTV\AHPSQAPSPNQPTK HGDNREHPNEQ
282	A	29	573	LLKISGIILKTGESQNQLAVDQIAFQKK LFQTLRRHPSYPKIIEEFVSGLESYIEDE DSFRNCLLSCERLQDEEASMGASYSKS LIKLLLGIDILQPAIIKTLFEKLPEYFFEN KNSDEINIPRLIVSQLKWLDRVVDGKD LTTKIMQLISIAPENLQHDIITSLPEILGD SQHADVGKEL
283	A	927	5088	KRKRRRTWKRYRSIIDHLQEKRREVTL RVDTYTLVQPEAEDHVESYRSMPIYPT YNEVHLDERPFLRPNIISGKYDSTAIYL DTHFRLLREEIVRPLREGILELLQSFED QGLRKRKFDDIRIYFDTRIITPMCSSSGI VYKVQFDTKPLKFVRWQNSKRLLYGS LVCMSKDNFETFLFATVSNREQEDLCR GIVQLCFNEQSQQLLAEVQPSDSFLMV ETTAYFEAYRHVLEGLQEVQEEDVPF QRNIVECNSHVKEPRYLLMGGRYDFT PLIENPSATGEFLRNVEGLRHPRINVLD PGQWPSKEALKLDDSQMEALQFALTR ELAIIQGPPG\TGKTYVGLKIVQALLTN ESVWQISLQKFPILVVCYTNHAL\DQFL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				GRHLQLSGRPGIVRVGWKGATVEIPEG SFTLRELRNKREFRRNLPMHLRRAYM SIMTQMKESEQELHEGAKTLECTMRG VLREQYLQKYISPPALGKSHEWPQCRI VNGFSSQHWKHSHDAGVA*VLVSVLS RKVFLQQDLRIQPQAEGDEEEEGEE/RE FRLIRDSQREADPDFKQTG*LRRKRW* GPSGGRRKRVEQTRSWLKCFWP*G*TI VALGQQLDRSKPQESGRPS/DNQKKK MKKRVKDELRKLNTMTAAEANEIEDV WQLDLSSRWQLYRLWLQLYQADTRR KILSYERQYRTSAERMAELRLQEDLHI LKDAQVVGMTTTGAAKYRQILQKVEP RIVIVEEAAEVLEAHTIATLSKACQHLI LIGDHQQLRPSANVYDLAKNFNLEVSL FERLVKVNIPFVRLNYQHRMCPEIARL LTPHIYQDLENHPSVLKYEKIKGVSSN LFFVEHNFPEQE\SKRRKSHQNQHEAH NVVELCKYFLCQEYLPSQITILTTYTGQ LFCLRKLMPAKTFAGVRVHVVDKYQ GEENDIILLSLVRSNQEGKVGFLQISNR ICVALSRAKKGMYCIGNMQMLAKVPL WSKIIHTLRENNQIGPMLRLCCQNHPE THTLVSKASDFQKVPEGGCSLPCEFRL GCGHVCTRACHPYDSSHKEFQCMKPC QKVICQEGHRCPLVCFQECQPCQVKVP KTIPRCGHEQMVPCSVPESDFCCQEPC SKSLRCGHRCSHPCGEDCVQLCSEMV TIKLKCGHSQPVKCGHVEGLLYGGLL VKCTTKCGTILDCGHPCPGSCHSCFEG RFHERCQQPCKRLLICSHKC\QKPCIGE CPPCQRTCQNRCVHSQCKKKCEELCSP CVEPMCSRCQHYQCTKLCSEPCNRPPC YVPCTKLLVCGHPCIGLCGEPCPKKCR ICHMDEVTQIFFGFEDEPDARFVQLED CSH\IFEVQALDRYMNEQKDDEVAIRL KVCPICQVPIRKNLSYGTSIKQRLEEIEII EEKYPGLIRGNGNQPGTA
284	A	381	2040	AERKLSEKSLVVAAVAPDNRNPAFTT MGWLFLKVLLAGVSFSGFLYPLVDFCI

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				SGKTRGQKPNFVIILADDMGWGDLGA NWAETKDTANLDKMASEGMRFVDFH AAASTCSPSRASLLTGRLGLRNGVTRN FAVTSVGGLPLNETTLAEVLQQAGYV TGIIGKWHLGHHGSYHPNFRGFDYYF GIPYSHDMGCTDTPGYNHPPCPACPQG DGPSRNLQRDCYTDVALPLYENLNIVE QPVNLSSLAQKYAEKATQFIQRASTSG RPFLLYVALAHMHVPLPVTQLPAAPR G/RKSLYGAGLWEMDSLVGQIKDKVD HTVKENTFLWFTGDNGPWAQKCELA GSVGPFTGFWQTRQGGSPAKQTTWEG GHRVPALAYWPGRVPVNVTSTALLSV L\DIFPTVVALAQAS\LPQGRRFDGVDV SEVLFGRSQPG\HRVLF\HPNSGAAG\D FGALQTVRLERYKAFYITGGARACDG STGPELQHKFPLIFNLEDDTAEAVPLER GGAEYQAVLPEVRKVLADVLQDIAND NISSPDYTQDPSVTPCCNPYQIACRCQA A
285	A	1	885	PVATTISQPLSLEADMWSIGVITYILLS GASPFLGDTKQETLANITAVSYDFDEE FFS\ETSELAQDFIRKLLG*ETRKRVTIQ EALRHPWITSKGEGRAPEQRKTEPTQL KTKHLREYTLKCHSSMPPNNCYVNFE RFACVVEDVARVDLGCRALVEAHDTI QDDVEALVSIFNEKEAWYRDENESAR HDLSQLRYEFRKVESLKKLLREDIQAT GCSLGSMARKLDHLQAQFEILRQELSA DLQWIQELVGSFQLESGSSEGLGSTFY QDTSESLSELLSRSCTEEFLAGWKL
286	C	187	342	MVPVFSVEKDGEELGSFRPRWADWLT GLLEWVSVESLSIYCISQPVYMWVE
287	C	188	207	MWHLSV
288	A	153	503	HPHSPDPGSALGSSSGGWLPAPLSPCR G*AGAGGGRRCRGRPWSRAG*ACSGH AGSRCCPA*SVCGGLPGGAPGCLCKG GSAGFCCQGPGCSCSGCSGSGHGGYR HRQGRPLSASQ
289	A	1	4964	SVYKADLEWLRGIGWMPEGSVEMNR

SEQ ID NO:	Me th o d	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				VKVAQDLVNERLYRTRPEALSFTSIVD TPEVVLAKANSLQISEKLYQEAWNKD KSNITIPSDTPEMLQAHINALQISNKLY QKDWNDTKQKGYDIRADAIEIKHAKA SREIASEYKYKEGYRKQLGHHMGFRT LQDDPKSVWAIHAAKIQSDREYKKAY EKSKGIHNTPLDMMSIVQAKKCQVLV SDIDYRNYLHQWTCLPDQNDVIQAKK AYDLQSDPLYRNAWEKEKANVNVPA DTPLMLQSKINALQISNKRYQQAWED VKMTGYDLRADAIGIQHAKASRDIAS DYLYKTAYEKQKGHYIGCRSAKEDPK LVWAANVLKMQNDRLYKKAYNDHK AKISIPVDMVSISAAKEGQALASDVDY RHYLHHWSCFPDQNDVIQARKAYDLQ SDTEPCSLAQAGVQWVADMTARGQSP LAPLLETLEDPSASHGGQTDAYLTLTS RMTGEEGKEVITEIEKKLPRLYKVLKV SSIIDSLEILFNKGETHSAVVDFEALNVI VRLIEQAPIQMGEEAVRWAKLVIPLVV HSAQKVHLRGATALEMGMPLLLQKQ QEIASITEQLMTTTLHRSGSFINSLLQLE ELGFRSGAPMIKKIAFIAWKSLIDNFAL NPDILCSAKRLKLLMQPLSSIHVRTETL ALTKLEVWWYLLMRLGPHLPANFEQ VCVPLIQSTISIDSNASPQGNSCHVATS PGLNPMTPVHKGASSPYGAPGTPRMN LSSNLGGMATIPSIQLLGLEMLLHFLLG PEALSFAKQNKLVLSLEPLEHPLISSPSF FSKHANTLITAVHDSFVAVGKDAPGN KKEKPGSEVLTLLLKSLESIVKSEVFPV SKTLGTPALFLIQLIFNNFLECGVSDER FFLSLESLVGCVLSGPTSPLAFSDSVLN VINQNAKQLENKEHLWKMWSVIVTPL TELINQTNEVNQGDALEHNFSAIYGAL TLPVNHIFSEQRFPVATMKTLLRTWSE LYRAFARCAALVATAEENLCCEELSSK IMSSLEDEGFSNLLFVDRIIYIITVMVDC IDFSPYNIKYQPKVKSPQRPSDWSKKK NEPLGKLTSLFKLIVKVIYSFHTLSFKE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				AHSDTLFTIGNSITGIISSVLGHISLPSMI RKIFATLTRPLALFYENSKLDEVPKVY SCLNNKLEKLLGEIIACLQFSYTGTYDS ELLEQLSPLLCIIFLHKNKQIRKQSAQF WNATFAKVMMLVYPEELKPVLTQAK QKFLLLLPGLETVEMMEESSGPYSDGL KLESSSLKVKGEILLEEEKSTDFVFIPPE GKDAKERILTDHQKEVLKTKRFEEQM DSDIVIPQDVTEDCGMAEHLEKSSLSN NECGSLDKTSPEMSNSNNDERKKALIS SRKTSTECASSTENSFVVSSSSVSNTTV AGTPPYPTSRRQTFITLEKFDGSENRPF SPSPLNNISSTVTVKNNQETMIKTDFLP KAKQREGTFSKSDSEKIVNGTKRSSRR AGKAEQTGNKRSKPLMRSEPEKNTEE SVEGIVVLENNPPGLLNQTECVSDNQV HLSESTMEHDNTKLKAATVENAVLLE TNTVEEKNVEINLESKENTPPVVISADQ MVNEDSQVQITPNQKTLRRSSRRR/YR SSRVYH*KPR*GK*SSKKGTT*GRRKTS SEESIAYKR
290	A	2310	2635	KDAYMFKKGLLALALVFSMPVFAAEH WIDVRVPEQYQQEHVQGAINIPLKEVK ERIATAVPDKNDTVKVYCNAGRQSGQ AKEILSEMGYTHVENAGGLKDIAMPK VKG
291	A	2	359	SSPSCHLVKKIKIKMKSPALRGLSRQH TKSPVTFWWMTFGDTSRPSQDTLPMD LQQLLGVTKVCSKATSPTSQRGQEVIS TPTSKSGPFIGRGS*G*SGRWERPSCCL HFSYPQLRGLC
292	A	834	1913	REPAGAGAYMRACARVRRRGDRRPR RSPRPRDPAVRARARSAPPPLFIAAAG GGGSGWRLYADSGEEYGIMAFALFVL LG\FALLGTHGA\SGAAGTVFTTVEDL\ GSKILLTC\SLNDSATEVTGHR\W\LKG GVVLKE\DALPGQKT/ESFKVDSDDHV GMKYS\CVFLP\EPHGHGPTIQASTGPP RVEGL*SSFRTHSTRGKTGLVGSCK\SE FVPP\VTDW/APWYKITDSEPQGPSLNA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				QRTRFF\VGPSAGPVKSYQH*EPEHIGP PPARNRCNGTSSKGLRPRPLQFLRVRT AT*AAL\WPFLGIVG\EVLVL\VTI\IFIYE KRRK\PEDVL\DDDDAGSAPLKE/SAGQ HQN\DKGKKRSARGNFS
293	A	1	936	MKVLLESVKERAEEEKLAAAHLRSFA AKKAKKYDSVKKEKTLQDVDLTQHQ HKQTRALSGGLKRKLSLGIAFMGMSR TVVLDEPTSGVDPCSRHSLWDILLKYR EGRTIIFTTHHLDEAEALSDRVAVLQH GRLRCCGPPFCLKEAYGQGLRLTLTRQ PSVLEAHDLKDMACVTSLIKIYIPQAFL KDSSGSELTYTIPKDTDKACLKGLFQA LDENLHQLHLTGYGISDTTLEEAEGRT AAPEPPMLEDGHAVTQRFSFIQVVGCE DDRTTWVQAQGASAPGGQRPQEDLPS FPQDGRSRAQFKDPHQFSN
294	A	1	1743	MASHAYDKNQNANVLVHLCFYNRIPK TGAYYLDSRSVSISYLIGHHIDMGLET ATSKNEFIFDSASTLLGMLFRKPSQHSL SLFSKKFQENLIYLESDDCLPPPPPPPW SEPPSFLTWTIVTVFQWVSLLLSLPNIQ VILYRAVGVVPSQPKSDNLKGWGSGR VVKEKLRSEIPDWKIKSIHILERTASSST EPSVSRQLLEPEPVPLSKEADSWEIIEG LKIGQTNVQKPDKHEGFMLKKRKWPL KGWHKIQKGKVHGSIDVGLSVMSIKK KARRIDLDTEEHIYHLKVKSVFNSFSAI IRGNDLPTPVVKSQDWFDAWVSKLRH HRLYRQNEIVRSPRDASFHIFPSTSTAE SSPAANVSVMDGKMQPNSFPWQSPLP CSNSLPATCTTGQSKVAAWLQDSEEM DRCAEDLAHCQSNLVELSKLLQNLEIL QRTQSAPNFTDMQANCVDISKKDKRV TRRWRTKSVSKDTKIQLQVPFSATMSP VRLHSSNPNLCADIEFQTPPSHLTDPLE SSTDYTKLQEEFCLIAQKGKGASKKQA KRNAAEKFLAKFSNISPENHISLVSNVD SYDVNVIKHFLQ
295	A	1	1248	MLRTRKAPHSWVKSSSNTVHYRVSVV

SEQ ID NO:	Met hod	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				CLHDHVTDWEWQLTATARHPKRVSH YILWDQEKTKIKIRKDIIRILPSLDVEVK DITDSYDANWFLQLLSTEDLFEMTSKE FPIVTEVIEAPEGNHLPQSILQPGKTIVI HKKYQASRILASEIRSNFPKRHFLIPTS YKGKFKRRPREFPTAYDLEIAKSEKEP LHVVATKAFHSPHDKLSSVSVGDQFL VHQSETTEVLCEGIKKVVNVLACEKIL KKSYEAALLPLYMEGGFVEVIHDKKQ YPISELCKQFRLPFNVKVSVRDLSIEED VLAATPGLQLEEDITDSYLLISDFANPT ECWEIPVGRLNMTVQLVSNFSRDAEPF LVRTLVEEITEEQYYMMRRYESSASHP PPRPPKHPSVEETKLTLLTLAEERTVDL PKSPKRRR
296	A	1	906	MFAFEPLGGCRPWRLSLPGLGSRLFRT YGAADGRRQRRPGREAAQWFPPQDR RRFFNSSGSSDARMGDPSQSDDPDDPD DPDFPGSPVRRRRRCPGGRVPKDRPSL TVTPKRWKLRARPSLTVTPRRLGLRAR PPQKCSTPCGPLRLPPFPSRDSGRLSPD LSVCGQPRDGDELGISASLFSSLASPCP GSPTPRDSVISIGTSACLVAASAVPSGL HLPEVSLDRASLPCSQEEATGGAKDTR MGSVRVLRDPVGVNLYEHSVSKCHVG QPDTDPREKVKAAPEELCLHALQHPRS EQADC
297	A	574	869	QGAFWLLFSSPRSFFLLSVP/WWLPESS RWLLLHGKSQLAVQNLQKVAHRGDW PGSGHPAPQSQHSSLRRSAARSRPPCW ARRWRAPPHTPRVAGGSGC
298	A	225	749	ESVTFEDVAVEFIQEWALLDSARRSLC KYRMLDQCRTLASRGTPPCKPSCVSQL GQRAEPKATERGILRATCVAWESQLK PEELPSMQDLLEEASSRDMQMGPGLFL RMQLVPSIEERETPLTREDRPALQDPP WSLGCTGLKAAMQIQRVVIPVPTLGH RNPWVARDSGAIGNG
299	A	1	591	PLPLDQRLLASITPSPSGQSIIRTQPGAG VHPKADGALKGEAEQSAGHPSEHLFIC

SEQ ID NO:	M e t h o d	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				EECGRCKCVPCTAARPLPSCWLCNQR CLCSAESLLDYGTCLCCVKGLFYHCST DDEDNCADEPCSCGPSSCFVRWAAMS LISLFLPCLCCYLPTRGCLHLCQQGYDS LRRPGCRCKRHTNTVCRKISSGSAPFP KAQEKSV
300	A	1	1569	MKTCLAFPLAFHHDSNGSAVLRLQAT HGISSDSPLPSVEKASHSPDPSEYFRKH PPVRRSGLRTKRTSPGPGARVPGSQSF RSAEACGVAALECWRRRVPVPLSSPA EVQVLLKKALRPESRPFRNQILHNCER NWGNKGWKGLVGRSESQTGQSEKLS MSSHHRGTVREELVVEEYIGGWCLCG SAWKLLVTGLEQLLFSRTRPQEEAVD KTWRTARQLESGTLLCRHCITLPWPSE RNGGCFLSPSNMLVCELRVLSVIVASP EPSTEHTQEHLSGDEFEKSQPSRKEKSL GLLCHKFLARYPNYPNPAVNNDICLDE VAEELNVERRRIYDIVNVLESLHMVSR LAKNRYTWHGRHNLNKTLGTLKSIGE ENKYAEQIMMIKKKEYEQEFDFIKSYT SVNSRKDKSLRVMSQKFVMLFLVSTP QIVSLEVAAKILIGEDHVEDLDKSKFKT GSLVRLFAPCLSGAGSKLPGLVEALAF EVSLAAFSVVASVESFEPVALEEWVVH TVGLRPWGGVTLWWA
301	C	236	481	MDLIVYHKKSDISNQPSIPTCALFFPCV SLEPFQLFPVKQTARRPPPYSSPGKSTG NVIPFGHGFPTLQPKXQITPVGGQY
302	A	1	1755	MRQTKTEYIQEFNQEATVARALEGQE KPTEGPRNTCLGSNNMYDIFNLNDKA LCFTKCRQSGSDSCNVENLQRYWLNY EAHLMKEGLTQKVNTPFLKALVQNLS TNTAEDFYFSLEPSQVPRQVMKDEDKP PDRVRLPKSLFRSLPGNRSVVRLAVTIL DIGPGTLFKGPRLGLGDGSGVLNNRLV GLSVGQMHVTKLAEPLEIVFSHQRPPP NMTLTCVFWDVTKALVGGYDILAIYE VEHFQQEQCVAVISVCSRGGKGSAEC GHWGKGLTTEHSSPVPAVTHLSLARIA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				EKGKAGCPARACRVHSWVLVLSGKRE VPENFFIDPFTGHSYSTQDEHFLGIESL WNHKNYWINMQDCWNCCKVPREGEL GDPEERLAHL/SWWLGLSVHLHGGRS QSAAPELPSHHPVPAALMVYEPLPATT GLDL*PG*PCEMGVHAPGD**VSAVLD *RRRQWDKR*G*CGKSGQGG*G*ELR HAPLV\VEQIEISPEGTNILEIKEWYQNR EDMLELKHINKTTDLKTDYFKPGHPQ ALRVHSYKSMQPEMDRVIEFYETARV DGLMKREETPRTMTEYYQGRPDFLSY RHA
303	A	3	1376	GDQKVHPFSTPSPGTPAFHIPTTFSPAA GPGHHLPMDPGEGLAEGPGLP/GSSG* RPL*VPSRRASHCP\PGATKARGGRCR GPAATTG*AACAGRTAAPG*PGASPPA AQALHHSLQEPGEHRGRPGPSASAPSA GTVDQVGGGAERMPTTPGPRHAVGEC GPTCSASLRGPL*PLPNLAAPAQWGSH QLQGEEQIQVPSCCFAPGIQRLLPRPQT QEPGF*TQTPDPGLKPQDSKPRLPGLQ TQTPDPGPRTRADGFPDQRGPV\GQGQ WEGAPGGHTLGNSGGSCLA/GPPW*RS EGHEECPSSCQSQFGELRLWLPRGGW AEGVSAGSHGPPWPAGPAPPGPQPLG WDAGPHFPEESRTRPGPDPEP*KDHGT VL*LTQRKHRDGHKEPRTKIQLPVPGA EGQTCPPEPWAGAHRRNANWQAQGS RRERPSGFQTPRSHWVPSAGRSGFLGP QFSCL
304	C	215	343	MSGRVFRCQALVAYTVLSELFTEAKE QRLATDEGQKEFSAES
305	C	215	339	MSGRVFRCQALVAYTVLSELFTEAKE QRLATDEGQKEFSAE
306	A	2	2483	GKYYKLSSGTAPTCVSLGWGLARGDS AAPALGSRTSACAPCSHGTWKLSLEPS DRLSPCDRSSEEAHTHAPHRLLALVAS LPWSRLPLLAPQSHSEAEATSQPTGVE NHHQKTRYVKAGGPVICRSLPESRGFL WASEGRKCMLIGSWAAMGRLRKSTIS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				SRFGPQTLAGTGRPQAIPVLKKHSDAV LLGVCFLKLLHQHHQELGENADSQTL PQTHWEFILSEDYNKMTPVKNYQVLE VLARAMRQEKQIKSIQLGKEEVKLSVF ADDMIVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQTESQIIS ELPFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCSWVGRI NIMKMAILPRVIYIFNAISIKLPMTFFTE LEKTTLKFIWNQKRARIAKTILSQKNK AGGITLPDFKLYYKATVTKTAWYWY QNRGVDQWNRIEPSEIIPHIHNHLIFDK PDKNKKWGKDSLFTKWCWENWLAIC RKLKLDPFLTPYTKINSTWIKDLNVRP KTIKTLEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLKSFCTAKET TIRVNRQPTEWEKIFTIYPSDKGLIPRIY KELKQNLQEKIKQPHQKVGKGYKQTF LKRRHLCSQQTHEKMFIITGHQRNAKQ NHNKIHLTPVRMAIIKKSGNNRDMDE AGNHHSEQTIARTENQAPYLLTHRWE LNNENTWTQVEEHHTLGPIVGVICRKV FPGNSGPSKPSGLHFSQPLPQVTSVVA KITIVPWEMKLIAMGVQDELNIAFHKN HLLMNDTTIHMTPYIQPAPKS
307	A	1532	1937	TPLPVCHFTCRKNHLKGMENLCLHKK CMWMSTVAFSIIAKTWKQPRCPSAAPS WKQPTHLTTGDWANGLG*FSTREYVT A*ERTNQSKPDTTTWVNLTDVQLSNSS QAPRGVSTTLQFPVLGTVDKSGVTMT FWV
308	A	1	939	MGNKTYGGQNQMLIFAFTLHSLFLNS GDGRLSFESSSQKPGGFRNIAIQTSPSL RKHFPVFKRKRLTASKSVEEMPTASQS AIHVNGNLSEQDIVSSDLAYLRLAQHL EDGPRRVKVSHAFLPRVPKVQSNGPVS ICLEAGTWRSLEKATAAIQVPDDIYHS PSWEARESALSPDRSAEHNSLSRPSDP GLSLQPQLLPTLCLPFHVLYTRSPQSLG HGPIAVHGLLGTMLRSRRTWSFLYPGF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				LPWCSGRIGSRVGLENECKVSLSGSSS QPMGEPEGRWSSPEVGPLASPGSPLIA WAKLRFVPPVDDLPV
309	A	1	1528	MDSQEVEKYPNTSVACEEIPFSGIHVA GGKSGALEHGKDDLDEPIENPLFCFSSF SNALAILLPKVFLKNIHILQFIYRSFHLL TMAKAKFEGAESVEPVSPSQPKRPSYV PLEELWTRLTKGNSRPQQRDREKGGW MKGVQQGHQGVGKQEEGSENIKEKA GIVVCEVPNNKLDKFMGILSWKDSKH SLNNEKIILRGCILRNTSWCFGMVIFAG PDTKLMQNSGKTKFKRTSIDRLMNTL VLWIMLISQPVVEFIMRGHSYFINWDR KMYYSRKAIPAVARTTTLNEELGQIEY IFSDKTGTLTQNIMTFKRCSINGRIYGE VHDDLDQKTEITQLIHRWLARLKKKK REKNQTDTIKNDKGNITTDLAETQTTI REYYKHLYTNKLENLEEMDKFLDAYT LSRLNQEEVESLSRPITSSEIEAVINSLP TKKSPGPDRFTAELYQKYKEELEKEPV DFSVKSQADREFQFFDHNLMESIKMG DPKVHEFLRLLALCHTVMSEENSA
310	A	104	315	DWTVGFVGNSDTELPGSVGRRSLWES SYSTRTRNQGRQAIQIQHS*LREVERKS GQKATMSSGGGYCQPE
311	A	271	1020	AIRQEKEIKGIQLGKEEVKLSLFADDMI LYLENPIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYKLL LKEIKEDRNKWKNIPCSWVGRINMVK MAILPKVIYGFNAIPIKLPMIFFTELEKT TSKFIWNQKRAHIAKSILSQKNKAGGI TPPDFKLYYKATVTKTAWTRKIYSAK KRKVKISVEPVYSGVTLTTAIQLVPLLC TAL
312	B	1	889	MDYEKADKRPTPWEAAAKSPLGLVD DAFQPKNIQESIVANVVSAARRKVLPG PPEDWNERLSYIPQTQKAYMGSCGRQ EYNVTANNNMSTTSQYGSQLPYAYYR QASRNDSAIMSMETRHLYTRQLYCYS

SEQ ID NO:	Meth od	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				FGDSGNFCENTNGRPAADAVRGLTILS LSTTSIPSSGISEALISENENKNLEHLTH GGYVESTTLQIRPATKTQCTEFFLAPV KTEVPLAENQRSGPDCAGSLKEETGPS YQRAPQMPDSQRGRVAEELILREKVE ASTQNNYYVGELTGVTLQNGYGEKPI LATQX
313	B	471	1448	MLKYTGAHQEVELSAPIVTKMATQYL RENLFGRFDNDNFCLLNGDAVIFRMY VSWKLVEKERTEIMLKYTGAHQETWL KDLEESPLYEALSMRGQDKETLGLWI QLPWCPWGKAVQMHMNPSSFQLDTK PGKGELAGRLIIPHQEASILELSLLLMT CCVEREGKTSVRVAAVGECTASETPN QGAGRLSLWQQLTSKKETIMEKEHTD CVSQTVALISTCVKEGGSRPADKDLEE GGGLEAESPKQSPNLCVILRHNLASRP GQLALVTVGTMQGRPLSHSSEVKGTT FVTHSVPAGKEKDEERGIGDLEHARDL RNSPTPLFY
314	A	1	903	MSELPFTIASKRIKYLGIQLTRDVKDFF KENYKPLLNEIKEETNKWKNIPCSWV GRINIVKMAILPQRLPHGFLPNMKLEV VDKRNPRLIRVATIVDVDDQRVKHSM TASSGSGVSADLNTASQPLWLLKTAL AVSSSVKVHPPVSGLIFSSSRTLLSFMG IMREDLGFSRRQILHFPMALSKSAGRR SKIGQLDALSQDFGLRDRDSSKKGTGY PNPENFSWTEYLEATQTNAVPAKVFK MDSDVGENRKILRDERPNYSQYTPFSR CDNASYKENVFLQKLERNTPDIAERFD CLLLTY
315	A	12	253	MMSWSSAEKGPEGHRRREWP\SQWED EP*NQNGESRKKERKEKRRKET*EERR GEKREKREKKRRREGRMSISFARRYSI L
316	A	2020	3942	SQRTAGNPCLHPVSLCGSASWMPMIM PQRWSSLCSAMEKPASPCL*MPPQATC WCPSRLPMAWA\SGH*HTSTGHSQLPA IPFDNHCGKRCRLGGKWRAPLQHPQW

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				K
317	A	2	271	RRPTRPQEEGGSESSTMTELETAMGLII DVFSRYSGSEGSTQTLTKGELKVLMEK ELPGFLQLSGPGLGHQHTLLLLFRSAS WSRLVPQ
318	A	1	455	MVEGKEEQVTSYVDVQRACAGIRGAF EKPQGAVARVHIGQVIMSICTKLQNKE HVIEALCKANFKFPGRQNIHFSEKWDF TKFSVDEFEDMMAEKQLIP/DNCGVKY TPNRDPPDKRDGVALQHGLLLWQLLQ NKIRLHQGREKKPPKKARR
319	B	1	370	MSRRKQGKPQHLSKREFSPRDREEVTT CFPCPPPTPPGLVTSPPAPRARLGQPCS ARNENLLEADYDPPEPIVLRNTTATHT HSHSVSPSLYNSDSPQPLKHLGAVSAA ETGVRGMMGMYLKPX
320	B	1	3204	MCELDILHDSLYQFCPELHLKRLNSLT LACHALLDCKTLTLTELGRNLPTKART KHNIKRIDRLLGNRHLHKERLAVYRW HASFICSGNTMPIVLVDWSDIREQKRL MVLRASVALHGRSVTLYEKAFPLSEQ CSKKAHDQFLADLASILPSNTTPLIVSD AGFKVPWYKSVEKLGWYWLSRVRGK VQYADLGAENWKPISNLHDMSSSHSK TLGYKRLTKSNPISCQILLYKSRSKGRK NQRSTRTHCHHPSPKIYSASAKEPWIL ATNLPVEIRTPKQLVNIYSKRMQIEETF RDLKSPAYGLGLRHSRTSSSERFDIML LIALMLQLTCWLAGVHAQKQGWDKH FQANTVRNRNLKIYSHMVTLWGNYEG ISQTQAFAKENNQKAYKETYGVSHITR HDMLQIPKQQQNEKYQVPQFDQSTIK NIESAKGLDVWDSWPLQNADGTVAEY NGYHVVFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGKIRLFY TDYSGKHYGKQSLTTAQKAYRLEIVSL EMQKNGAADAAPYRQIEYWALGHGD DIKKAVAFWSSGWPVGFSKMEKAGKI LRSQVKFPEYMEESSCLGRGSLMSLNN

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				TSSSNGSFIFVLPLKLLRVGDTYNSSDQ SRMAWRLTIEFGGSELHLGVREEAGH QKGLVHESGNPARSSGSDPQHARHRQ PSATRAAAAAAAAAAALPAPLSLPVPT SAIQVRVTAYPLLAQCLQAAFPPLLGS GCGQEGTGAGGGGGAAGVREQLEDR RAAAEPGDLPGGKRVRGRGAREGPGV GAEGPPLERNRPSSPLPWLAAPAAGAS QFAEIQGAGKGEMRAKDAERGRAKLR GELSSSGRKIFDPDDLYSGVNFSKVLST LLAVNKATEDQLSERPCGRSSSLSAAN TSQTNPQGAVSSTVSGLQRQSKTVEM TENGSHQLIVKARFNFKQTNEDELSVC KGDIIYVTRVEEGGWWEGTLNGRTGW FPSNYVREIKSSERPLSPKAVKGFETAP LTKNYYTVMSRSLTSTVLKNSKVARIH SKPY
321	A	724	1296	RSPTLSSPPPASKAQALALRSEAQAQM PRLPAPRVRRSSAAASAAARSLAETFS GKECQWTDACLSHPCANGSTCTTVAN QFSCKCLTGFTGQKCETDVNECDIPGH CQHGGTCLNLPGSYQCQCLQGFTGQY CDSLYVPCAPSPCVNGGTCRQTGDFTF ECNCLPETVRRGTELWERDREVWNGK EPDEN
322	C	150	362	MPGPAAASHRASTYVSTWSCPPHHSW HAWQCTVARPHLQTSHCCTSGLPLAD MESRLVASPSEWNKLTWAQ
323	A	1133	1350	ESQSLETGLRALIWSTRKPGGPVLGGL VLIKWAWASRSPASPSDPSPGPNLCCS PTSPATKPRVDGPFVIRN
324	A	1	615	MNWVLQKFITAWKFMGYRKSSNSAR GSTIKEHIELDAQRPVRRSGPIQASGAH PKKGRGVSCSVEEPSDQQSPSPPSPLTF QPKDGEINFSVIGQYVDYLVKEQGVK NIFGKSTLGMSLHVSSSVFRRYILPGYQ PRGHTVMVSQVNIDFQTREATRKNLQ EPSLTCFDQAQGKVHSLMEKDSYPRFL RSKMYLDLLSQSQRRLS
325	B	1	669	MVMSFVKPGVKEKEQVKKRDGEFNSE

SEQ ID NO:	Meth od	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				HAELDVPARDTKRKFWEPTRLSSTLRT SSDPLFSVPISITMVCEPGSKSLQSCCLT AGGANVWEKSTCRKKSRQLVLRNVK VPGKSPCGELLPILKKNQLNILLLQPVD TETLEGPPGLGLDAEGPEKRHSWILLP CPGIDHTSGLEVMSDLYHRKGNSLHPQ GKRTKDARKESFPQKMGQFPLQSLAVI YPEAGT
326	B	1	2043	MEEHSMLMGRKNQYRENGRIAQELEK TTLKFIWNQKRACITKSNLSQKNKAGG ITLPDFKLYYKATVTKTAWYWYQNRD IDQWNRTEPSEIMPHIYNYLIFDKPEKN KQWGKDSLFNKRFWENWLAIFRKLKL DPFLTPYTKINSRWIKDLHVRPKTIKTL EENPGITIQDTGMGKDFTSKTPKAMAT KAKIDKWDLIKLKSFCTAKETTIRVNR QPTKWEKIFATYSSDKGLTSRIYNELK QIHKKKTNNPIRKWAKDMNRHFSKED IYAAKKHMKKCSPSLAIREMQIKTTMR YHLTSVRMAIIQKSGNNRVLPLAPLAL AALWMDPVMPGMDGLLGDSESFQGL SATFFASVFHSALHIDSAPGPCIGPGDS SADSSPTFLPPEAKRKNYLLLWRKNLK KFSDDPKRLIEGFPKLALTFRLIWKDIN VLLGQALLQEERQTICGAAIHCRNDLH LENANYPGGATAVPQLDPNQDYNAK AGIWARNHRLLCLIETTTQQPTNAHSP QTQRQQHDTDKPQPNPPAKTTGVPVS FLAFLYQYLCGHISISWPVVILKYAASV YGISLADRKRQYDRYFRYERLRTIKPN FLPFQIFKSGSVVKLKAGFTIGKVHNTE VTALKVSDTRRAQHLQTGCWSAVVT HPNNLENVVRHPPEALAASYNKPFICS LVTLQGAFVT
327	A	1	1113	MLMVYPRTNKQNQKKKWKVEPPTPQ EPGPAKVAVTTSSSSSSSIPSAEKVPTT KSTLWQEEMRTKDQPDGSSLSPAQSPS QSQPPAASSLREPGLESKEEESAMSSD RMDCGRIPSTPNHRRSQVIEKFEALDIE KAEHMETNAVGPSPSSDTRQGRSEKR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				AFPSKQDFTNEAPPQAPLPDASASPVST PKSQVTGQEGQNISWDMAVVLKATQE APAASTLGSYSLPGTLAKSEILETHGT MNFLDSSPQVRYHPRNLGTACNQAGL DRYYPEGPLPRSGDDTVLSPRPAWSKL AATRSQRLDPRQRGSTEREKGEAHND PLAAAPISAAGSRRGALASWLASPTRS QNPARPPTPDCRAPLTESARPTS
328	C	1	354	MGKWDGGFNFMVFCVLENTCSLNRSL LENLIFATLKISWGGAGIKGWNHMKA QLLTCVVFDAGFQLSPQGSLEQKHLIL YPELTGPIELDPICYHHHLSNLLSQTPK ASFEVLHQNH
329	A	1	768	PIWATRCYGGWRGSLFLELPRCDGPLS RWGWAAPKMAASLLFSDQGFLASWIP RNGTLGHAMSGIALLEAVGHGRELWN PATSAASVISNTSSDANQFPKLPLGEISP DKEKSYWSSNPTKNNPKETTRVAVFA RILDVNDNAPHFAVFYDTFVCENARPG QRDACGRLGDWDSEKQEGRKGFTSTN SVILHKKRTKRSVLGGDKFWQKKSPES PQGDFQDSRSLRSTVKFHKSTRKLQGE VEKSSVARNYGFDPL
330	B	44	329	GCLEHEASSAYEWLWSLCALLDMYTA GPTKTQTLQPMGQPNLKGDGGFTRES TGFMQLPADFISSLICHETWVPGKPSTA MHRGRYWAEPIMLPKX
331	B	3	431	MSEKNTPLVLSGENQKKGREIGVCRK QSQCDHQDNNSHTLRFSSYSSSSGPVT LVSFHSHNYPSKVLLQGNLDTETCTER RQREIWTQRHEGKCGHRDMYREKTK RKYREKAIYKLRKGPETDPSSQPSERT NPANTLISDS
332	A	5	1269	TISWRQGRGGEAGRRLWHTPPQVKHL EPGHP/EQQARKAQIQGQPPAPGWDLT QGEQAG/NIHQHCGQSRG*QQHQKDP* GHRFAEGMQSLSKELQSD*TSRKGGFR VPCSHNREPPTRPGDPCDS\PAGLGLQE CRARYRPGKPSS/PPRGQSRAT/GPVRW HPSPSRN*G/PPGSRPAPGTDPAPGRPP\

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				GRPLAASGLLPNSPPAPG/SP/QGPPPPR GSNR/PRFPHWLRRPAGRGAPC*PQPRS PQ/QHIPEHRTKPVPAPEPPSGSRNTDPP GQPRARGTWKASPGHRADSASRRASF LFRCLANLQRSLKQMRGKLHSQKAQF WFILNGFIGGVIGRRMTDCQACEPRLR SIQCQLPESYTSLCHPAALTQSGPKNVL ERDQPSACSLKTPAQTCLPQCSLHWTL RDDQTQPLTAPSSTMNGAYRMKC
333	A	233	380	PLVVCLLEFYCTHLRDGLNSVQLAYR GCRPTEATFTPARRPWQARAPCR
334	B	220	309	MAEYDLTTRIAHFLDRHLVFPLLEFLS VKE
335	A	577	945	RGARIRYAVCVCVCVCVYPCVHVCTC VRMCLCVCVCVCVCVCGGCKCTC GPTEGGEKAWLFTSIQEGRRCGWSSSL RGSAAGRDLYSARLFAHRLLLLEGRP WQDAGAPSAARISRSEPWS

CLAIMS

WHAT IS CLAIMED IS:

1.   An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-84, or 168-251, a mature protein coding portion of SEQ ID NO: 1-84, or 168-251, an active domain coding portion of SEQ ID NO: 1-84, or 168-251, and complementary sequences thereof.

2.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4.   The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5.   An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6.   A vector comprising the polynucleotide of claim 1.

7.   An expression vector comprising the polynucleotide of claim 1.

8.   A host cell genetically engineered to comprise the polynucleotide of claim 1.

9.   A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10.   An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

        (a)   a polypeptide encoded by any one of the polynucleotides of claim 1;

        (b)   a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-84, or 168-251; and

152

(c)   a polypeptide comprising an amino acid sequence selected from the group consisting

of SEQ ID NO: 85-167, or 252-335; the mature protein portion thereof, or the active domain

thereof.

5   11.   A composition comprising the polypeptide of claim 10 and a carrier.

12.   An antibody directed against the polypeptide of claim 10.

13.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

10   a)   contacting the sample with a compound that binds to and forms a complex

with the polynucleotide of claim 1 for a period sufficient to form the complex; and

             b)   detecting the complex, so that if a complex is detected, the polynucleotide

of claim 1 is detected.

15   14.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

             a)   contacting the sample under stringent hybridization conditions with

nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

             b)   amplifying a product comprising at least a portion of the polynucleotide of

claim 1; and

20   c)   detecting said product and thereby the polynucleotide of claim 1 in the

sample.

15.   The method of claim 14, wherein the polynucleotide is an RNA molecule and the method

further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

25

16.   A method for detecting the polypeptide of claim 10 in a sample, comprising:

             a)   contacting the sample with a compound that binds to and forms a complex

with the polypeptide under conditions and for a period sufficient to form the complex; and

             b)   detecting formation of the complex, so that if a complex formation is

30   detected, the polypeptide of claim 10 is detected.

17.   A method for identifying a compound that binds to the polypeptide of claim 10,

comprising:

             a)   contacting the compound with the polypeptide of claim 10 under

35   conditions sufficient to form a polypeptide/compound complex; and

153

b)   detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18.   A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a)   contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b)   detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19.   A method of producing the polypeptide of claim 10, comprising:

a)   culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-84, or 168-251, a mature protein coding portion of SEQ ID NO: 1-84, or 168-251, an active domain of SEQ ID NO: 1-84, or 168-251, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-84, or 168-251, under conditions sufficient to express the polypeptide in said cell; and

b)   isolating the polypeptide from the cell culture or cells of step (a).

20.   The isolated polypeptide of claim 10 comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 85-167, or 252-335, the mature protein portion thereof, or the active domain thereof.

21.   The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22.   A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-84, or 168-251.

23.   The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24.   The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25.   The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26.   The collection of claim 22, wherein the collection is provided in a computer-readable

5   format.

27.   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

10

28.   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

15   29.   A method of detecting bone marrow cells or tissues in a sample comprising:

        a)   contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form a complex; and

        b)   detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected

20   wherein the presence of the polynucleotide of claim 1 indicates the presence of bone marrow cells or tissues.

30.   A method for detecting bone marrow cells or tissue in a sample comprising:

        a)   contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form a complex; and

25   b)   detecting formation of the complex so that if a complex is detected, the polypeptide of claim 10 is detected,

wherein the presence of the polypeptide of claim 10 indicates the presence of bone marrow cells or tissues in a sample.

SEQUENCE LISTING

<110> Hyseq, Inc

<120>   NOVEL BONE MARROW NUCLEIC ACIDS AND POLYPEPTIDES

<130>   21272-050

<140>   NOT YET ASSIGNED
<141>   2001-03-30

<150>   60/250,583
<151>   2000-11-30

<150>   09/540,217
<151>   2000-03-31

<150>   09/649,167
<151>   2000-08-23

<160>   335

<170>   Custom

        <210> 1
        <211> 516
        <212> DNA
        <213> Homo sapiens

        <400> 1
```
ggaggcagag ctctgggaat ctcaccatgg cctggacccc tctcctgctc cccctcctca     60
ctttctgcac agtctctgag gcctcctatg agttgacaca gccaccctcg gtgtcagtgt    120
ccccaggaca aacggccacg atcacctgct ctggagatgc attgccaaaa aaacatcct    180
tattggtacc agcagaagtc aggccaggcc cctgtactgg tcatctatga ggacaacaaa    240
cgaccctccg ggatccctga gagattctct gggtccaact tagggataat ggccaccttg    300
attatcagtg gggcccaggt ggaggatgaa gctgactact actgttattc aacagacagc    360
agtggtaatc atagggaggt gttcggcgga gggaccaggc tgaccgtcct aggtcagccc    420
aaggctgccc ccttcggtca ctctgttccc gccctcctct gaggagcttc aagccaacaa    480
ggccacactg gtatgtctca taagtgactt ctaccc                              516
```


        <210> 2
        <211> 458
        <212> DNA
        <213> Homo sapiens

        <400> 2
```
tcaagacaaa gctctccttt gtaaaccaga cccttttccat tcagtctatc acagggtggc     60
ttactcggca ccccttttca gccccgctct cctcttcagt tctcactggg gctttttgt    120
tcttaattcc ttttcatggc ccggcaaaaa cggagttaat tatattaaag acctgacttc    180
cctgtctagc tccttaactc caggtcagca gataattgag agtcattgcc ctgatactga    240
atgaagagat aaagttccca ggtttatttc aagtgactta tctgaagatg aggaaagagc    300
aagaggttac taaaaaacat atctgtgaat tgttgacaga gacggtcact tctgcagaaa    360
ctccagatgc ccttgccaag tccaggtaca ggtctaaact agcaaaccaa atgcattttc    420
taggtttaaa gtacaggtgg gtgctcatct tcaggatg                            458
```


        <210> 3
        <211> 922
        <212> DNA
```

&lt;213&gt; Homo sapiens


&lt;400&gt; 3
```
tttttttttt ttgacaattg ttatttagtt tttatttgca taatcataaa cttaactctg   60
caaatccagc taggcatggg agggaacaaa ggaaaacatg gaacccaaaa gggaactgca   120
agcgagagcc acaaaagatt ctaggattac tccgagccaa atggggtgga aggggtgctc   180
tccttgagct acagaaggaa tgatctggtg gttaagataa accacaaagt caaacttatt   240
tcgagttgtc cacagtcagc attggtgatc tccttgctgg tcttgccatt cctgggaccc   300
aaagccgctc catggcctcc acaatattca tgccttcttt cactttgccg aaacaccaca   360
tgctttgcca tccaaccact ccagtcttgg gcagtgcaga tggaaaaact ggggaaccat   420
ttgtgtttgg gtccagcatt tgccatggga caagatgcca ggaccgtat gctttaggat   480
gaagtttctc atccttcaaa tttctcccca tagatggact tgccaccagt gccattatgg   540
cgtgtgaagt caccaccctg acacataaac cctggaataa ttctgtgaaa gcaggaaccc   600
ttataaccaa atcctttctc tccagtgctc agagcacgaa aattttctgc tgtctttggg   660
accttgtctg caaacagaag gcaaaattct aaggaacagc aagcactgct gcacgatcag   720
gggtaaacag ctgttctttt agtcacttgt aatgaaaatg ctactacctc caatctgtta   780
acatagcttt atggattaga tgagcagtca cttcttggta tccaggcccc ttacctcaaa   840
ggagacgcgg cccaaggget cgccgtcgac ggcaatgtcg aagaacacgg tggggttgac   900
catggctaat agtacacggt tt   922
```


&lt;210&gt; 4
&lt;211&gt; 1185
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens


&lt;400&gt; 4
```
gcgcctgtgg ggaggccgcc tgtgcctcgg tacatggtgc caaccgcctc ggggcaaact   60
cgctcttgga cctggttgtc tttggtcggg catgtggcct gagcatcgaa gagtcatgca   120
ggcctggaga gtgaagtccc tccaattaaa ccaaacgctg gggaagaatc tgtcatgaat   180
cttgacaaat tgagatttgc tgatggaaga agcataagaa catcgggaac tgcgactcag   240
catgcacgaa gtcaatgcaa aatcatgctg ccgtgttccg tgtgggaagc gtgttgcaag   300
aaagttgcgg gaaaatcagc aagctctatg gagacctaaa gcacctgaag acgttcgacc   360
ggggaatggg ctggaacaca gacctggtgg agacctgga gctgcagaac ctgatgctgt   420
gtgcgcttca agaccatcta cggagcagag gcacggaagg agtcacgggg cgcgcacgcc   480
ggggaaaact acaaggggcg ccttctcgcc acgcccacct gcacctgcct tttcctcccg   540
cctggtggga ctcaacccca cccctgcatt ttctctgcat tttatgtcgt ttccccaaaa   600
gtatatccaa aaaatgcctt ttttccccct ggtaactttg atccctgggt tctcgccatt   660
ttctggatca ctgtgacctg ttccttgctt tgggtcagca tccactgatg ccagcagtgg   720
catctccaag ccaatgtgct ttgctgttag aaggccaagg ttagaagtgc agccagcgtg   780
gcatgaccag gaaataaatg ccagtttatt aaataacgag taagccaccg tttcaagcct   840
gccctgtgga ggaaatgcca gtttattaaa taacgagtaa gccaccattt caagcctgcc   900
ctgtggagga aatgccagtt tattaaataa caagtaagtc accgtttcag acctgccctg   960
tggaggaaat gccagtttac taaataacga gtaagccacc gtttcaagcc tgccctgtgg   1020
aggaaatgcc agttcattaa ataacaagta ttatagagcc tgtcctgtgg tttgattacg   1080
gagcctgccc tgtggtcact tgttcttcag atgaactgat ttttgtgcaa agcacacgtg   1140
ttggattctg cctggtgcag attgatgagt atgatcactc caagc   1185
```


&lt;210&gt; 5
&lt;211&gt; 416
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; misc_feature
&lt;222&gt; (1)...(416)
&lt;223&gt; n = a,t,c or g

```
        <400> 5
gttagagatt acaatttgac tgaagaacag aaggcgatca aggccaagta tccgccagtc        60
aataggaagt acgagtattt ggatcataca gcagatgtcc atggattgta ttacacagag       120
catgaatata cttctttagg ttacacgcat ggggagatac tctggaggaa gcatttgagc       180
aatgtgcaat ggccatgttt ggttacatga cagatactgg gacagtggag cccctccnnn       240
nnnnnnnnn nnnnnnncaa ggtggggaga agaattttca ttgtccaagc accctcaggg       300
aacagaagtc aaagcaataa catattcagc aatgcaggtc tataatgaag agaacccgga       360
agtttttgtg atcattgaca tttaagacac ccaaaaatan aagactccta cgaaaa         416
```

```
        <210> 6
        <211> 787
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 6
aattcgaggg tgtaaagaag aggaagggga aaaatatctt gtaccagccc aggggtgaag        60
aagccccgg cctgagaaag aaggaggagt gggggaggcg aacagtctcg ttgctgcctc       120
tgtgtacgct gaggggggag ggctcttctt ttcgactacc ctcgctgaag attttctctt       180
ccttccctcg cccaactctc cctcggggcc tctacgagga ccccccccc catgggtgg        240
cccaaaatgg agaacgcgga gcagcgcaag atggaggctc cgcttctctg tgtagcagta       300
gatttaggtt ccttttctcc ggcaggctcc taagcctagg agagcccgaa ctggagagag       360
ggaacaacat tcatgtgacg ggccctctg cttctcccc gccccatcat ctccagcgcg       420
tggtggggga acctgctggg gaaggcgatt ggcatcgatc tctccatccc ttccgaggcc       480
cgacttcgga attgtcttac aagaagaag gcatgccacc attttacccc acgtaaatat       540
atgaatatat·ttctgacatt gaggtgttcc agatgatgat aaagaaatga tagctgctcc       600
agaaacacca actgatttta atctactaca ggagtcagaa tcacattttt cttctgacac       660
agattttgaa cgatatcgca ggaaaaaacc gaactcaggg caaaggcaat acttgtagaa       720
aaggcgaaga gggcccagca gaaaaggtct gaggtggaaa aggaagagga acacctactt       780
ctgcgcg                                                                 787
```

```
        <210> 7
        <211> 10918
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 7
cgctgagtac cgtccggatt ccctggtcga ctattgctgt gcgccattga ggagcggctg        60
tgaggatgcg cacgccgcaa ggtctagact ggacgcgagt ctaccgagac accgaccgac       120
tgttctgtca ccatgaaaga tacagataca gaatgatcct tgacgtctaa acacctttc ·       180
ctgaggatat agtcactgtt ggaaggcctt gtaacctggg ttctcaatac ctatttggga       240
aaatatgtca ataacctgaa cactgaccag ctctcagttg cacttctcac aggtgctgtt       300
gaattacaaa acttgccatt aaagaaagat gccttgaaag aattggaatt accatttgaa       360
gtcaaagctg gcttcattgg gaaagtaacc cttcagattc ccttttatcg cccccatgtg       420
gacccttggg tgatctccat ctccagcctt cacttaattg gagccccaga gaaaatacag       480
gatttcaatg atgaaaagga gaagctgttg gaaagggaac gtaagaaagc actacttcaa       540
gccctggagg agaaatggaa gaatgaccgc cagcagaaag gggagtccta ttggtattca       600
gttaccgcct ccgtagctac aaggattgtg gagaatattg aattaaaaat tcaagatgtc       660
catttacgct tgtgaagatg cgtcaccaat ccctcccatc cttttgcttt tggcatctgc       720
attaagaatg tgtccatgca aaatgctgtg aatgagcctg tacagaaact aatgcggaaa       780
aagcaattag acgtagcaga atttagcatc tattgtgatg tcgattgcac tttactgggg       840
gatttgcctc agatggagtt acaggaggcc atggccagga gcatggagag tcgcagccat       900
cactacgtcc tggagcctgt gtttgcatct gctcttttga agagaaactg ctccaagaag       960
cccctgcggt ctcggcacag tcccgtatt gattgtgata ttcagctgga gaccattccc      1020
ttgaaactct ctcagctgca ataccggcaa atcatggaat cctcaaggaa gctggaacga      1080
aaggagaggc aggtgaagtt ccgaaggtgg aaacccaagg tggcgatatc taagaactgc      1140
cgagaatggt ggtattttgc tttgaatgct aacttgtatg agatcagaga gcagaggaaa      1200
cgttgcacct gggactttat gttgcaccgc gctcgtgatg ctgtatctta cactgacaaa      1260
tatttcaaca agttaaaagg aggcctgctg tccacagatg acaaggagga aatgtgtcgg      1320
```

```
attgaagagg aacagagctt tgaggaattg aagattttgc gtgaactggt tcatgatcga   1380
tttcacaaac aggaagaact agcagagagt ctgcgggagc ctcagtttga ttctccagga   1440
gcctgtccgg gagccccaga acccggtgga ggcagtggga tgctgcagta tctccagtcc   1500
tggtttcctg gatggggtgg ctggtacggg cagcagaccc cagaaggaaa tgtggttgag   1560
ggactgtcag cagagcaaca ggagcagtgg attcctgaag agatcctggg cactgaggag   1620
ttttttgacc ccactgcaga tgcctcgtgt atgaacacgt atacaaagcg agatcatgtc   1680
tttgccaaac tgaatttgca gttgcagcga ggtacagtga ctctgttaca caaggagcaa   1740
ggaactcctc aaatgaatga aagtgctttc atgcagctcg agttttcaga tgtaaaactt   1800
ctagcagagt ctcttcctcg aagaaattcc tcgttgcttt cagtccggtt gggtggactg   1860
tttcttcgag acctggctac agaaggaact atgtttcctc ttctagtctt ccctaatcca   1920
caaaaagaag ttggcagagt ctcacaatct tttggtctac aaactacatc tgcagacaga   1980
agtgatcatt acccagctgc agatccagat ggcccgtttt ttgagatgct gtatgagaga   2040
aatccggcgc acagccactt tgagaggcgg ctcaatgtca gcacaaggcc cttgaacatc   2100
atatacaatc cgcaggccat taaaaaagta gcagactttt tctacaaggg aaaggttcat   2160
acctcaggtt ttggttatca gtctgaactt gagctgagag tggctgaagc tgcccgaaga   2220
caatataaca agctgaagat gcagaccaag gcagaaatcc ggcaaactct tgatcgtttg   2280
ctagtgggtg atttcattga ggagagtaaa cgatggaccg tgcggctgga tatttctgcc   2340
cctcaggtga tatttcctga tgatttcaaa ttcaagaatc ctgtgttagt tgtcgtggat   2400
ctaggaagaa tgctttttgac gaacacccaa gataactcca ggaggaaaag tagggatggg   2460
tcagcatctg aagagaccca gtttagtgat gatgaatata agaccccct ggccacacct   2520
cctaacaccc cacctcccga gtcaagcagc agcaacggag agaaaacacc tcccttttct   2580
ggagttgagt tcagtgaaga acagcttcaa gcacatttaa tgagcacaaa gatgtatgag   2640
aggtactcgc tgtcatttat ggacctccag atcatggttg gacgagtgaa agacaattgg   2700
aagcatgtcc aggatattga cgtgggacca acacatgtgg tagagaagtt caacgttcac   2760
ctacagttag agcgtcgatt gatttatact tcagatccca aatatccagg agccgtgctc   2820
tcaggcaact taccagactt aaaaatccac attaatgaag ataaaatatc tgcactaaag   2880
aattgctttg ctctcctcac cacccccagaa atgaaaactt ctgacactca gattaaagaa   2940
aagatttttc cccaggagga gcagcgggga agtttgcaag actccgtaat gaatttaacc   3000
cagagcattg tgttgttgga gcagcatacc cgcgaggttc tggtggagtc gcagctcctc   3060
ctggcggaat ttaaagtgaa ctgtatgcag cttggtgttg agagcaatgg ccggtacatt   3120
tctgtgctca aggtgtttgg taccaatgct cactttgtga agaggcctta tgatgctgaa   3180
gtctccctaa ctgttcatg tttgctcctg gtggatacca tgcagacata tggtgctgat   3240
tttgaccttt tgatggcttc acataagaac ttgagctttg atattccaac gggaagcctt   3300
cgggatagca gggcccagtc tcctgtctct ggaccgaatg tggcccactt aactgatgga   3360
gctacactga acgaccgatc agctacgtga ggtgtctcac ttggcaggat tcgttccaaa   3420
gagcgagagt cccttagtaa gttggaatat cagtgtggga gttcagagcg cccatcgatg   3480
aatttacaca gtactcttca ggtgatttcc ctgcaggtga ataatttaga tattatcgtc   3540
attccagaga cgagtgtgga gctaagtggt tttcttcaaa aatcctttcc caaggaaaaa   3600
gatgatctaa gtcctcaacc tttaatgact gtttgtgaaa gaagcttcag agaacaagga   3660
tcgttccagt ctacacatga acgaatcact gaggttgcag tggaaatcca tagaatgaac   3720
ttagtgcttc ttcggacagt gggcatggca aatagagaga aatatggcag aaaaattgca   3780
actgcaagta taggtggcac caaagttaat gtctcaatgg gtagcacgtt tgacatgaat   3840
ggttctcttg gctgtttaca gcttatggat ttgacacaag ataacgttaa aaaccagtat   3900
gttgtcagca ttgggaattc tgtaggctat gaaaatatca tcagtgatat tggctacttt   3960
gaatctgtgt ttgtcagaat ggaagatgca gccctcactg aagctttgag tttcacgttt   4020
gttgagagat ctaaacagga gtgttttctc aacctgaaga tggcttcttt acattataac   4080
cactctgcta gtttttgaa ggagttgacg ttatccatgg atgaactgga agaaaatttt   4140
cgaggtatgc tgaaaagcgc agccaccaaa gtcaccacag tactagctac caagactgcc   4200
gagtatagcg agatggtatc gctctttgaa actccaagga gactcgggga accctttatc   4260
ttagaggaaa atgaaatata tgggtttgac ctagcttcgt ctcatttgga cactgtaaag   4320
ctaatcttga acataaacat tgaatcacca gttgtttcta tccctcggaa gccggggagt   4380
cctgagttgt tggtgggaca cttgggacag atattcatcc agaattttgt ggcgggagat   4440
gatgaatcca gaagtgaccg tctgcaggtg gaaatcaagg acattaaact gtattctttg   4500
aattgcaccc agttggcagg tagagaagct gttgggtctg aaggaagccg gatgtttttgc   4560
ccaccttccg ggtctggcag tgccaacagt caggaggaag ctcatttcac acgacatgat   4620
ttctttgaat cttttgcatag aggtcaagct tttcacatcc tgaacaacac caccattcag   4680
tttaaactgg agaagatccc tatagagaga gaatctgaat tgactttttc tcttagccca   4740
gatgacctgg gaacttctag catcatgaag attgaaggaa aatttgtcaa tccagttcag   4800
gtggtgttag caaagcatgt atatgagcag gtttttacaaa ccctggacaa tctcgtgtac   4860
agtgaagatc tgaataagta tccagccagt gctacctcct ccccttgccc tgattctcct   4920
ctgcctcccc tcagtacctg tggagaatct tctgttgaaa ggaaggagaa tggattgttc   4980
agccactcca gcctttctaa cacctctcag aagtcattgt cagtgaagga agtcaaatcc   5040
tttactcaga ttcaagccac cttttgtata tcagagcttc aggttcagct aagtggagat   5100
ctgactttgg gggcccaagg tcttgtgagc ttaaagtttc aggactttga ggtggaattc   5160
```

```
agtaaagacc  atccccagac  tttatctatt  cagattgccc  tgcattctct  gctgatggag  5220
gacttattgg  agaagaatcc  agattctaaa  tataagaacc  tgatggtgtc  tcgaggagcc  5280
cctaagccat  ctagtttagc  acaaaaagaa  tacctttctc  agtcttgccc  ctcagtgtcc  5340
aatgtggaat  atcctgatat  gcctcggtct  ctcccttccc  acatggaaga  agctcctaat  5400
gtcttccagt  tgtatcaaag  gcccacctct  gcgtcccgga  aaaagcaaaa  ggaagtccaa  5460
gacaaggact  atcccttgac  cccacctcct  tctccaacag  tggatgagcc  caagatactt  5520
gttggaaaga  gtaaatttga  tgattcctta  gtccacatca  acatattctt  ggtagataag  5580
aaacatccag  aattctcttc  cagttacaat  cgagttaacc  ggagcattga  tgttgatttt  5640
aattgcttgg  atgtgctgat  cacactgcaa  acctgggttg  tgatattaga  ctttttttgga  5700
atcggctcca  ctgcagacaa  ccacgcaatg  aggctgcctc  ctgagggcat  tctgcacaac  5760
gtgaagttgg  agccacatgc  ctccatggag  tctggacttc  aggatccagt  gaacaccaaa  5820
ctggatctca  aggttcattc  actttctcta  gtgctgaata  agaccaccag  tgagcttgcc  5880
aaagcaaatg  tgtccaaatt  agtagcacac  ctggaaatga  ttgagggaga  cctggcctta  5940
cagggcagca  ttgggagtct  gtctctaagt  gacctcacat  gccatggaga  gttctacaga  6000
gaacggttca  ctaccagtgg  tgaagaagca  ctcatcttcc  agacttttaa  atacggacgg  6060
cctgaccctc  tgctccggag  agaacacgac  attcgcgtga  gcctccggat  ggcctctgtg  6120
cagtatgtgc  atactcagcg  tttccaggca  gaggtggtgg  ccttcattca  gcatttcact  6180
cagctgcagg  atgtcttagg  gcgccagcga  gctgctattg  aggggcagac  ggtgagagat  6240
caagcccagc  gctgttcacg  ggttctcctg  gatattgagg  ctggtgctcc  cgttctcttg  6300
atcccagaaa  gttccagatc  aaataatctg  attgtagcaa  atttggggaa  gttgaaagtc  6360
aaaaataagt  ttctgtttgc  tggtttttcct  ggcaccttttt  ccctacaaga  taaggaatct  6420
gtgccttcag  cttccccaac  gggtattccc  aaacacagtc  tgaggaaaac  gacaagcacg  6480
gaggagccca  ggggaaccca  ttcccagggg  cagttcacga  tgcctcttgc  tggaatgagc  6540
ctaggaagcc  tgaagagtga  gtttgtgccc  agtacctcca  ccaagcagca  agggccgcaa  6600
cccacactgt  ctgttggcca  agagtccagt  agtccagaag  accatgtctg  cctgctggat  6660
tgcgttgtcg  tggatctcca  ggaccatgga  ccatctttgc  tgcggagaga  catccggaga  6720
gattactcga  agggcaccag  aggatagtag  tggagatctg  atcttccctt  cctattttgt  6780
gcggacagac  aggaggaagc  ctccttaacc  ggaccttgta  ggctgaaatt  gcaggtggaa  6840
aggaatttgg  acaaagaaat  aagtcatact  gtgccagaca  tatctatcca  tggcaatctc  6900
tcctcagtcc  actgctctct  ggatctgtat  aaatacaagc  tgatccgcgg  cttattagag  6960
aacaacctgg  gagaacccat  agaggaattt  atgcggcctt  atgatttaca  aagatccaag  7020
aattcatact  gtcctgagtg  gagaagtgta  cacctgtatg  tgcttcctca  ttgatatggt  7080
gaatgtaagt  ctggagctta  aagatccaaa  aagaaaagaa  ggtgctgggt  ccctagccag  7140
atttgacttc  aagaaatgca  aactgctcta  tgaaagtttt  tccaaccaaa  ccaagtccat  7200
taacttggtt  tcccattcca  tgatggcttt  tgacacccgt  tatgctgggc  agaagaccag  7260
ccctggcatg  acgaatgtgt  tcagctgtat  cttttcagccc  gctaagaaca  gcagcaccac  7320
ccaagggtcc  attcagattg  aactacattt  cagatctacc  aaggattcct  cctgctttac  7380
agtagttctc  aacaatctcc  gtgtgtttct  catatttgac  tggctactgt  tagtccatga  7440
ttttctccac  actcccagtg  atattaagaa  acaaaatcat  gttactcctt  ctcgccaccg  7500
taactctagc  agcgaatctg  ctatagttcc  caaaactgtg  aagagtggag  tagttaccaa  7560
gcggtcttcc  cttcctgtgt  ccaatgaaag  gcacctggag  gtcaaggtca  atgtaacagg  7620
tacggaattt  gtggtcattg  aagatgtgtc  ctgcttcgac  accaatgcca  ttattctgaa  7680
aggcaccaca  gtgctcacct  ataagccccg  gtttgttgat  cgcccctttt  caggaagttt  7740
gtttggcatt  gaggtgtttt  catgccgact  agggaatgag  catgatacag  ctctttcaat  7800
tgtggatccc  gtacaaattc  aaatggagtt  ggtggggaat  tcttcttatc  aaaatagttc  7860
aggattgatg  gatgcattca  atagtgaaga  tttcccacct  gtcctggaga  ttcagttaca  7920
agccctggat  atcagactct  cctataatgg  tgttcagctg  tttcttgcca  ttgcaaaatc  7980
catcccagag  caagctaatg  ctgcagtgcc  agactcagtg  gccctggagt  cagactccgt  8040
tggcacttac  cttccaggtg  catctcgcgt  tggagaggaa  atcagagaag  ggacaagaca  8100
caccttagat  cctgtcttgg  agttacagct  ggctaggctg  caggagctgg  gattcagcat  8160
ggatgattgt  cgcaaagctc  ttttggcgtg  tcaaggccaa  ttgaaaaagg  cagcaagttg  8220
gttgtttaag  aatgcggaac  ctctgaagtc  tctttccttg  gcctccacca  gccgagatag  8280
cccagggggct  gtggcagcgc  cattgatctc  tggcgtggag  atcaaagctg  agagtgtgtg  8340
catctgtttc  atcgatgact  gcatggattg  tgatgttcct  ctcgctgaac  tcacctttttc  8400
ccgtctgaat  tttcttcagc  gtgtaagaac  tagccctgaa  ggctatgccc  acttcaccct  8460
ttctggagat  tattataacc  gtgctctttc  aggctgggag  ccatttattg  agccttggcc  8520
atgctctgta  tcctggcaac  agcaggcagc  tggtcgtctc  catcctcctc  gactgaagct  8580
agaagccaag  gccaaacctc  gtttggatat  caatatcact  tctgtgctaa  ttgaccagta  8640
tgtaagtacc  aaggaatcgt  ggatggcaga  ttactgtaaa  gatgacaagg  acatagagtc  8700
agctaaatca  gaagactgga  tgggctcttc  ggtggatcct  ccatgtttttg  gacaaagtaa  8760
gagttttcac  tacatgtgtt  taactaaatc  acttttgacc  tacaaagcaa  tgcttcactg  8820
agaaattcaa  atggaaccat  cattctgcgt  ggaaaaacct  acaggaaatt  ctgactatct  8880
tctgtagttc  tgttttagtc  tttgcaggag  acagttttct  ggcatgaact  actgaactta  8940
taaatgtggg  ctgtaattcc  acctttgcgg  gggagaaaag  atctgcaaca  cgtaattcct  9000
```

                                                5

```
aaatcctggt aataatgcat atgaactggt gcacctgaga atgcatcagg atcagctgtg    9060
gtttgtgttt tactctgcaa aacattggtt ttctaattga tcggattttt ttggccagat    9120
ttttaaaagc atctaaaatg gtcttctaaa tctagagata gagggtttgg acatattctt    9180
gaaaagaggg cgagcaggag cccatgtgga aaaagttgtt aaaaagggag ccctgtgctg    9240
ttcatagagt ataaaagaat tgaatgccct gcctcttgaa gaaagaggag tcagcttgct    9300
ctctattgat gatgctttct ttccttattt aatgcctcgc cggctctgtt ttcctcagag    9360
ctggggagat ggtgatggac aactgcatgg tcttagttgt tccacaagcc attgtcatcc    9420
aaattcaact cagctccaac tcttacaatg tggtttcttt ggggagtctt ggctggactt    9480
cacatagctc atgaatactt aaatattcca tctggtctgc aaacgtgtca tgggaagatt    9540
gggtgttctt agtgtgtgaa gtaattgtac tggttcatct ctcctcaggg tgaataagtg    9600
gactttctgt ctgccttgta cttctagaaa gagacacaaa gaaatgtcag catgtgcttg    9660
ttctctgttt tcccaggctg ttgcttctga gtctcaaggt cattacttag gagccagggc    9720
ttttcagata ttgtcagctt tgatttagc tcctcctcca accttcccaa tttgtgtgtc     9780
aagaaaatgt aacataagtc tacccagaag actctagata atctttgtaa tatgtccaag    9840
agagtgtgtt tctaaaacat tattcatgca ggggcatctt caattcagag tcaaactcta    9900
gcaaggcctg gtctgcaaga ttctgatgaa agattttctt gtccctctct ttcttctttc    9960
cttcttccct ccctgcctcc ctttcttcct tccttttaa aattttgtcc ctctctcttt    10020
ctctatagtt aaaaggcttc ctcatctata ttaaatgctg gtgctgagtt aaagcttgat    10080
ttttatttat ttaaagattt ttatgattac ttaggcttat aaaagtgtaa tctatctttt    10140
taataagaca taacttgaat atgcataaat ttccaaacct ctttcttat tggaaattcc     10200
tggatggtag tacagtacat tccaggattg tattctttta gcaggcctac taaaatgatc    10260
attgggaatt tattttgaaa gtgagtaggg ttcaaccttg ttgaactaat cataaacttt    10320
caggtcttat tcaagaatag taagtcatat tcctacaaaa gttatgcttc ttattcagac    10380
tggccttaaa acaagctctt gggaatagcc cttaacatga aatttagcct aagggacctg    10440
ctgctttctc actgtttctt tatcagggga aagaaaatac cagcctcctt ttgacaaaat    10500
tgttggcttt gttcagtcag ggctgagatt ttgcaggtaa acctgggcgg tgtggcactt    10560
cattgaattt attagttttg tattccaagg acattttatg aaaatatcaa atattctgaa    10620
aacttccatg cttgatttag aatttaaata aacactatga ggcaactcct tggtagagat    10680
tgtttaaatt tggaacacat actgactctt cccctgaatt tttgagatcc cctgagactg    10740
gcattttact tctgtgtttt accagttgga atggagcaac cttcactaaa atctgtactg    10800
atggattttc gtaacttttt aatgccattt aagaacataa cacctttaaa ttaaaaatct    10860
tcaaaaggct cgtcattctg ttcaagagaa ggttcaatac atattcttct aattcagg      10918
```

```
        <210> 8
        <211> 1187
        <212> DNA
        <213> Homo sapiens


        <400> 8
tttcgtgcta ccagaagaag tgtcgggtac gtctgcatta cacctggcgg gagctctggt      60
cagccttgat aaatttgctg aagttcctta tgtcaaatga gactgtactt ttggccaaac     120
acaacatttt tacattagcc cttatgattg tgaacctatt aatatgtttt atcacatatg     180
gcgacacatt tctgccaacc cccagcagct atgatgaact ttactatgag attatccgca     240
tgcaccagag ctttgacaac ctctactcca tgggcctgag gctttctacc aatgcaggcc     300
agtggaagga agcagctagc aaggtgaccc atgcattggt taatatcaga gccatcatca     360
accactttaa ccccaaaatt gagtcctacg ctgctgtgaa tcacatatcc caactgtcag     420
aggagcaggt gctggagggg gtgagagcca actatgacac gctcacgctg aagctgcagg     480
atggcctgga ccagtatgag cgctactcag agcagcacaa ggaagctgcc ttcttcaaag     540
agctggttcg atccattagc accaacgtcc ggagaaacct ggccttccac acactcagcc     600
aagaagtcct gctcaaggag ttctccacta tctcctgagg ccacgcctac ctgagcagcc     660
tctgactgcc cttacccatg aggatcatgg gctggagggg gagcgagggg agaggggggct     720
gcccccgagg ttggagagaa acacagatac caagttctct tggtgaagac cgcacttcaa     780
tggagcttgg gcagcagggg caggagggtc aagccaggga taatcttatt tggggaggaa     840
tgggtgggca cagtggggag aggcctccag gaatgtgggg acttccagag tgggctccct     900
aaacagcccc tcacatttcc aatcttgagg ttacaagctg tagctactga ctaattttcg     960
ggagctggtg aggcaagcct cagggtaatg ccagcaccc gaaagtcagt ggctctgctc    1020
ggcttctgaa aacagatcaa ctctcagata tagctacgagc tacatcctgc ttcctttggg    1080
cctggggctg tgcttggctt gaaatctgtg tcccctgcct gcactggcac tttgtccagt    1140
catcgggacc tttggctcag atttagggta agataggaat agggtac                   1187
```

```
        <210> 9
        <211> 1978
        <212> DNA
        <213> Homo sapiens


        <400> 9
aagaaggagt tatcgttgtc cagcaacctg tgagtcttgt acattggtta gtgtagaagt      60
taatcccagt gcctatagag cacctttctg aagagttttc tttttcttct ttttaacata     120
atggacaatc aacgaagtat gtaagaacca ttactgtttg ctagcctcct ttaaagggaa     180
ttctttattg agggctacaa taaatatgct tattcacctt gggctgcttt taagctgtag     240
atttaatatt ataaacgatc tttaaggtgg gtaatttctc agttgttcac tgggtatgca     300
tcaagagttt taactaaatt ttctattttc cttaaattct agaaagcgaa attattattg     360
acgatggaca atttggaatc cacaatggtg ttgaaactct ggattctgga tggctgacat     420
gtcagactga aataagatta cgtttgcatt attctgaaaa acctcctgtg tcaataacca     480
agaaaaaatt aaaaaaatct agatttaggg tgaagctgac actagaaggc ctggaggaag     540
atgacgatga tagggtatct cccactgtac tccacaaaat gtccaatagc ttggagatat     600
ccttaataag cgacaatgag ttcaagtgca ggcattcaca gccggagtgt ggttatggct     660
tgcagcctga tcgttggaca gagtacagca tacagacgat ggaaccagat aacctggaac     720
taatctttga tttttcgaa gaagatctca gtgagcaccg taagttcagg ggtgatgccc     780
ttcctgggac atgtgggtac agcttggtct ccttatccat cccaccattg ctgaagagtg     840
ggaaagagtg ctggaattct tactcttccc atcatgagca gaaattcccg gaaaacaata     900
ggcaaaggga gagttgacta tataattatt aagccattac caggatacag ttgtgacatg     960
aaatcttcat tttccaagta ttggaagcca agaataccat tggatgttgg ccatcgaggg    1020
gcaggaaact ctacaacaac tgcccagctg gctaaagttc aagaaaatac tattgcttct    1080
ttaagaaatg ctgctagtca tggcgcagcc tttgtagaat ttgacgtaca cctttcaaag    1140
gactttgtgc ccgtggtata tcatgatctt acctgttgct tgactatgaa aaagaaattt    1200
gatgctgatc cagttgaatt atttgaaatt ccagtaaaag aattaacatt tgaccaactc    1260
cagttgttaa agctcactca tgtgactgca ctgaaatcta aggatcggaa agaatctgtg    1320
gttcaggagg aaaattcctt ttcagaaaat cagccatttc cttctcttaa gatggtttta    1380
gagtctttgc cagaagatgt agggtttaac attgaaataa aatggatctg ccagcaaagg    1440
gatggaatgt gggatggtaa cttatcaaca tattttgaca tgaatctgtt tttggatata    1500
atttaaaaaa ctgtttttaga aaattctggg aagaggagaa tagtgttttc ttcatttgat    1560
gcagatattt gcacaatggt tcggcaaaag cagaacaaat atccgatact attttttaact    1620
caaggaaaat gtgtagattg atggccagtg catggacttc aggtgtcgga caacccccat    1680
tgcaatgagc tttgcacgag tttgaaaatc tgctgcggat aaatgtacat actgaagact    1740
tgctcagaaa cccatcctat attcaagagg caaaagctaa gggactagtc atattctgct    1800
ggggtgatga taccaatgat cctgaaaaca gaaggaaaat tgaaaggaaa cttggagtta    1860
atggtctaat ttatgatagg tatttgtttt tcatgaaaaa ttttcatgga atttagaagt    1920
atagatttca tcttacgaaa ttataaataa aattaaactt agttaagtta aaaaaaaaa    1978




        <210> 10
        <211> 241
        <212> DNA
        <213> Homo sapiens


        <400> 10
gtgcccgtga cctttgatga tgtggccgtg tatttctccg agcaggagtg gggcaagctg     60
gaggactggc agaaggagct ctacaagcac gtgatgaggg gcaactacga gacgctggtc    120
tccctggact acgccatctc caagcccgag gtcctctccc agattgaaca agggaaggag    180
ccctgcaact ggcgccgccc tggccccaag attccagatg ttcctgtgga ccccagtcca    240
g                                                                   241




        <210> 11
        <211> 4464
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 11
gtgtgctccg gcacttggca gctggacagg cacagtgctg atgtgaaaaa taccacgaca      60
aaaccaccct agttctccaa aatacttatc attcaggttg aataaaccag ttctacagac     120
tgcttcttcc atgcatttcc caatgatgct aactgccctt aaaattcttt cagatttgga     180
actgtatctg tatggaaaca acagagtttt cttgaagtac aactaaggac aggtcaccac     240
taggcactaa catcgctgac ttgcatgatt atggagatgg tctatctgat gctgaaaatg     300
tctctagttt tttgacaacg gctaaataac catgggatca agtggccttg ggaaagcagc     360
aacattagat gaactgctgt gcacttgcat tgagatgttt gatgacaatg gagagctgga     420
taatagttat ttgccaagaa tagttctact gatgcaccga tggtatttat cttccactga     480
attggcagaa aaacttctct gcatgtatcg aaatgccact ggagaaagct gcaatgaatt     540
tcgattaaag atctgctact tcatgaggta ctggattctg aagtttcctg cagagtttaa     600
tttggatctt ggtttgattc gtatgactga ggaatttcgg gaagtagcta gtcaactagg     660
atatgaaaaa cacgtcagcc tcatcgacat atccagcatt ccttcctatg actggatgag     720
aagagtcaca cagaggaaaa aagtatccaa gaagggaaaa gcctgtctgc tgtttgacca     780
tctggagccc attgaattgg ctgagcacct cacttttctg gagcataaat cttttagaag     840
gatctcattc actgattacc aaagctatgt catccatggc tgcctggaga ataatccaac     900
cttgaaaga tcgattgctt tatttaatgg aatctctaag tgggtccagt tgatggttct     960
tagcaaacca acccccccagc aaagggcaga agtcatcaca aagtttatca atgttgcaaa    1020
gaagctcctt cagctcaaaa attttaacaa ccttattgca attgcaggga gccctcaagt    1080
cataggtcca tttcaggctt caaagggacc cattcctcat ctttcctcag aagtttacaa    1140
agaactggaa tgtgaaatga cagaagtggg tctcctccaa cgggcaatta ctgcaattac    1200
cgcaagccct ttgccgactg cgatggcttc aaaatcccca tccttggagt acacttgaaa    1260
gacttgatag ctgtccatgt cattttccca gactggacag aggagaacaa agtgaacatt    1320
tgtgaaaatg caccagctct ccgttaccct gagtgaacta gtctccctgc agaatgcctc    1380
tcaccacttt agaacccaac atggatttga tcaacctgct cacgctttcc ctggacctct    1440
atcacactga agatgatatt tacaaactgt cactggtgct ggagcctaga aattctaaat    1500
cgcagcctac ctcccctacg acgcccaaca agcctgtggt acccctggag tgggcattag    1560
gggtgatgcc aaagccagca cccacggtca tcaacaagca cataaggaaa ttagtggagt    1620
ctgtatttag aaactatgat cacgaccatg atgggtacat ttcccaagag gactttgaaa    1680
gtatagctgc caatttttcc cttcttggat tccttctgtg ttctggacaa agatcaggat    1740
ggcctaatta gtaaagatga aatgatggcc ttacttccat gagagctaaa tcccaactac    1800
actgtcaaat cgcgcaccag gatttatcca caatttcag gagatgactc tatctcaagc    1860
cagaccttct gcgaacactg tgcgggattt attctgtggc ataatcaagc aaggatacaa    1920
atgcaaagac tgtggagcca attgtcacaa acagtgcaaa gacctcctgg ttctggcctg    1980
caggagaatt tgcccgggcg ccctccttga gcagtggtca tgggtcactg cctggaagcc    2040
cctcgctgcc cccagcgcag ggattaggtg tttaagttcc ctggagtcac tgctgacaac    2100
agcgatttta gacagcagag ccatcacact ggttacaggc tcttctcgca agaacttctg    2160
tgaggctaca gagggccacc accagccagg ccaccccaga ctggaacctg tctggtcaga    2220
ggctggctgg gggggactcg gggtcccaca cccttcccta taatagatat tcaggttcct    2280
tgcacaagcc accaaaaggc acaagggctt tgcaatatgg gaaaaatgaa aaagcccagg    2340
gtggcatggc tggtgggat gtttaaaacc cgggcaccgg agtttgaacc ttgccccgga    2400
tgaaggagag aagaccacac acggatgggt gaggatgggc tgacttcaag gctggcggaa    2460
aacttgaagg ccaataatgg ttggcttttt ggaaggggc aagaacaaga aactcttgag    2520
gaaagctctt gcctctcagg aagttatctt ggaaagaacc ccctgatgtt aacttgcctt    2580
ggggacactg tgggatctcc atgtttggac tatgggacag agaattgacc ctaactaaac    2640
tatgaattat tatgtgcctc ctcccctacc cctagttaat gtgccacaaa gactgtgtta    2700
tgtagtcagt acttttttct catgtatctt tctctagaac atttatatac gggctgaaat    2760
gaaagccttt ttgcatgtac ttgatactca gtctgtaaac tcagacttcg cttttttgt    2820
gagactatcc tttcaatatt tttataaact tttgtgtgtg ctgtggcagg gaacagttaa    2880
caaggagttt attttagaggg gtttttttca ttttttgttt ttcttgtttt gttttgtttt    2940
gttttgttct tcttggtgtg cttttttggat gggaccagaa cttaacattt ctcctgacga    3000
ctaggacgct catcagacac tgggaatgca gtgattcttc taatgatggt caactgcaag    3060
gagaaactgt ttacatcctt cccactacac agttgctatg atatgtaaca attcacacat    3120
gtatatatca cacaagtctt accaattctg cgtcactagg aagctatagc atggtcgtga    3180
aagctctcct aatacttact tacttaaata gccatggaag aaaattatgc ttgtcccttc    3240
tgactgggtt aagccatctt tcttaaagat tcctgaagta gaaatagcaa ttaagaaatt    3300
aattcaagtt ttgacggtta acaaacattt agcagaaaaa caaaccattg aataagctac    3360
taggtgaaat gcaaacaac catcaatttt tttaaactca ataattttgt gaaaaaaaaa    3420
accaccacca aacttttggt tgtaaaagag aacccttgtt cccttcctaa gaaactgcct    3480
tccacaatta aagaatactc atagaaagaa ataatcata aatcatattt gattaacatt    3540
tcatttaagc ttttaaaata tcaattttt aaatagctcc catttaccca aaataactag    3600
ttatgggtct atttcttcca tgattagagg agagagaact tgattcaaga tactgaaaaa    3660
tagagctggg actgagcctg tgaatgacag gaatgatcta ttaccaggtg actagtcgga    3720
```

```
aactacacag accgtgcact ggtctgcatt tgggggctaa agtgtatata ttccatttaa    3780
aatggaattt ggtttggaat tggggcagtc ttcagtaaaa gcctttctcc tttcttttct    3840
ccattgagga ccagttctgc tcagcaaaaa ttgttgagta ccctggttct gggccaggtc    3900
ccacgctata tgcaccaaag ttaggaaaaa cttgggtctt aagcccttgg ggagcttgac    3960
cagcccatgg gcattaaggc aaagtagttc ccagtgattt aaaatacggg ttccaaatac    4020
gctaaaacca aacttgtgcc aacccagatt tacagattgg aaatactgca gatgatgtga    4080
agttataagt tggaggagct gtgatttagg ctggataata agagaacgtg ccatctgtaa    4140
agcactcaga aggcagccat ccctagatgt tggtttcgat gtatattaca ctatctacta    4200
ctatccataa atgcaataat atgcatgtta acaacattaa aaacagcaaa cagcaatcta    4260
agtacagaaa agcttttgt gtgtttaaaa aaattgaaga aaattcagga agaaacgtgt    4320
taataaacat tgtactgttc ttttgcttct caaaggaatt attcacttgc cactttggtt    4380
atttttgagt tttcgtacat aggaagtttt atattgccag ccttcctgtg ataaagatat    4440
taaatgtaac ttgagtaaaa aaaa                                           4464
```

```
        <210> 12
        <211> 1299
        <212> DNA
        <213> Homo sapiens


        <400> 12
        caattctgtc attatctgat acaaacttca gaatacccctt cacctcagcc acagctgccc    60
        agtcccacag cttctttcct cccaacccca gcaccctgc accctagct ccaaaattcc    120
        taaaaggttc actgtttgtt cttctaattt ctccccatga tgttgcgttt gaaattggtt    180
        tgctctagtg ggtttccctg tagccttgcg tattcctgag ctgcaacatc agattctggt    240
        ttttctccgc agtgactttc catttcctgt gaaaagcact gtacggactg gaagaatacg    300
        acactcagga tgggattgcc ataaacctcc tgcccgctgc tgttttctca ggactttgca    360
        aaaaaatggg ggtcccggtg acctcacagg aatcaggcca aaaattggtg tctccgctgt    420
        gcctggctcc gtatttccgg ttactgaaac tttgtgtgga gagacagcat aacggaaact    480
        tggaggagat tgatggtcta ctaaattgtc ctatattcct aactgacctg gagcctggag    540
        agaagttgga gtccatgtct gctaaagagc gttcattcat gtgttctctc atatttctta    600
        ctctcaactg gttccgagag attgtaaatg ccttctgcca ggaaacatca cctgagatga    660
        aggggaaggt gctcactcgg ttaaagcaca ttgtagaatt gcaaataatc ctggaaaagt    720
        acttggcagt cacccccagac tatgtccctc ctcttggaaa ctttgatgtg gaaacttag    780
        atataacacc tcatactgtt actgctattt cagcaaaaat cagaaagaaa ggaaaaatag    840
        tgtatactct gaaagagcga tgcctccagg ttgtccggag cctagtcaag cctgagaatt    900
        acaggagact ggacatcgtc aggtcgctct acgaagatct ggaagaccac ccaaatgtgc    960
        agaaagacct ggagcggctg acacaggagc gcattgcaca tcaacggatg ggagattgaa    1020
        gatttctgtt gaaacttaca ctgtttcatc tcagcttttg atggtactga tgagtcttga    1080
        tctagataca ggactggttc cttccttagt ttcaaagtgt ctcattctca gagtaaaata    1140
        ggcaccattg cttaaaagaa agttagctgt cttctgtagg cattgtgatg tttaggggca    1200
        aacatcacaa aatgtaattt aatgcctgcc cattagagaa gtatttatca ggagaaggtg    1260
        gtggcatttt tgcttcctag taagtcagga cagcttgta                         1299
```

```
        <210> 13
        <211> 1417
        <212> DNA
        <213> Homo sapiens


        <400> 13
        atgcccgcgc cgcgcgcccg ggagcagccc cgcgtgcccg gggagcgcca gccgctgctg    60
        cctcgcggtg cgcggggccc tcgacggtgg cggcgggcgg cgggcgcggc cgtgctgctg    120
        gtggagatgc tggagcgcgc cgccttcttc ggcgtcaccg ccaacctcgt gctgtacctc    180
        aacagcacca acttcaactg gaccggcgag caggcgacgc gcgccgcgct ggtattcctg    240
        ggcgcctcct acctgctggc gcccgtgggc ggctggctgg ccgacgtgta cctgggccgc    300
        taccgcgcgg tcgcgctcag cctgctgctc tacctggccg cctcgggcct gctgcccgcc    360
        accgccttcc ccgacggccg cagctccttc tgcggagaga tgcccgcgtc gccgctggga    420
        cctgcctgcc cctcggccgg ctgcccgcgc tcctcgccca gcccctactg cgcgccgtc    480
        ctctacgcgg gcctgctgct actcggcctg gcgccagct ccgtccggag caacctcacc    540
```

```
tccttcggtg ccgacgcagg tgatggatct cggccgcgac gccacccgcc gcttcttcaa        600
ctggttttac tggagcatca acctgggtgc tgtgctgtcg ctgctggtgg tggcgtttat        660
tcagcagaac atcagcttcc tgctgggcta cagcatccct gtgggctgtg tgggcctggc        720
attttcatc ttcctctttg ccacccccgt cttcatcacc aagcccccga tgggcagcca        780
agtgtcctct atgcttaagc tcgctctcca aaactgctgc ccccagctgt ggcaacgaca        840
ctcggccaga gaccgtcaat gtgcccgcgt gctggccgac gagaggtctc cccagccagg        900
ggcttccccg caagaggaca tcgccaactt ccaggtgctg gtgaagatct tgcccgtcat        960
ggtgaccctg gtgcccctact ggatggtcta cttccagatg cagtccaccct atgtcctgca       1020
gggtcttcac ctccacatcc caaacatttt cccagccaac ccggccaaca tctctgtggc       1080
cctgagagcc cagggcagca gctacatgat cccgtgagcc tggctccttc tggccaatgt       1140
tgcgtgggag ctgagtctgc gccctctgaa cgaccgcttg agcgacccctt tactgctgcg       1200
gtgcaagctg cttccctctg ctctgcagaa gatggcgctg gggatgttct ttggttttac       1260
ctccgtcatt gtggcagcca cagcccagct agcccaggcc aagggagtcc gacccccacc       1320
ccgaagcaca gggaagttgc tgcccttccc cgcagtgaca ggaatcctct caaaggttct       1380
ggaaggcaag gatgcggcca tccctggaga cgccaag                                 1417


        <210> 14
        <211> 620
        <212> DNA
        <213> Homo sapiens


        <400> 14
ttttttttca gggctggaag ttgattttta atgataaagt acaatgaagg gagggcagag         60
gggctaagcc tagctgtccc ggggtgctgt ggtggtggta gactggctac acaaactgtt        120
gctgctgctg ctgcttcttg gtggccgcct tgctggcgag ggtccttggc cttctctgta        180
gctgccagtg cggtctcctt tgccttctcc ttggcttcct tggctgtctc aacagggggg        240
ttggaagggg cctcgccttg cagcttagcc aagatatatt caaaacccctt cataggtctt        300
ggtcacgttg cttttgaacc gggcaagacc aaattcctgg gacagctctt ggagacacca        360
aattaagcta ggaggagacc caggcttccc ggcggatttt cagtccagcc cactgttgtc        420
aagagttcac aacagtaaaa cacatcgttt cctccaccac catcagccgg ggctgtggtt        480
ggatgttcca ggtgaaggta gtcatggtct gattctgtgg gtccacaata gagtcctcca        540
ggatgtacac tgaatgaaga acattggcag gaaacagttg cttggcccag tgggacatcc        600
ctgtggtctt ggtcaggagt                                                     620


        <210> 15
        <211> 2528
        <212> DNA
        <213> Homo sapiens


        <400> 15
tttcgtcgct gaccagcagc atggaggacc ccgccgctcc tgggaccggg ggccccgcccg        60
caaatggcaa tggcaacgtg tggcggcaaa gggaagcagg cggcgcccaa gggccgcgaa        120
gcgttccgaa gccagcggcg ggagtcagag ggctctgtgg actgtcccac tctggagttt        180
gagtatggag atgcagatgg gcatgcagcc gagttgtcag aattgtatag ttacactgag        240
aacctggaat tcaccaataa caggaggtgc tttgaagaag atttcaagac tcaagtgcag        300
ggcaaggaat ggctggagtt ggaagaagat gcccaaaagg cctatataat gggactcttg        360
gaccggctag aggtggtcag tagggaacgg cggctgaagg cggcccgggc tgttctctac        420
ctggcccaag gtactttttgg ggaatgtgat tcagaggtcg atgtgctaca ctggtccagg        480
tacaactgct tcctgctgta tcagatgggg accttctcca ccttcctgga gctactccac        540
atggaaattg acaacagcca ggcctgtagc agtgcccttc ggaaaccagc tgtctccata        600
gctgatagca cagagctcag ggtgctgctg agtgttatgt acctaatggt ggaaaatatt        660
cgcctggagc gagagacaga ccccctgtggg tggagaacag cccgggagac cttccgcact        720
gaattaagct ctccatgca taatgaggag ccttttgccc ttttactctt ctccatggtt        780
accaagttct gcagtggcct ggctcctcac ttccccataa agaaggtcct gctcctgctc        840
tggaaggtgg tcatgtttac cctcggtgga tttgagcatc tgcagactct caaagtacag        900
aagcgggcag aattgggcct gcctccactg gctgaagaca gtatccaggt ggtgaagagc        960
atgcgtgctg cctcccccgcc ctcttacact cttgacctgg gagagtctca gctggcaccc       1020
ccaccctcca agctgcgagg ccgccgtggc tctcgaaggc aactcctcac taagcaggac       1080
```

```
agcctggaca tctacaatga aagggatctc ttcaagactg aggagcccgc cacagaggag   1140
gaagaggagt ctgctggtga tggagaacga accttggatg gagagctaga cctgctagag   1200
caggaccctc tggtgccacc tccaccctca caggcacccc tctctgctga gcgggtggct   1260
tttcccaagg gcctgccctg ggccccaaag gtcagacaga aggggacatt gagcacttct   1320
tggagatgag caggaacaag ttcatcggat tcaccctggg tcaggacaca gatacattgg   1380
ttggattacc caggcccatc catgagagtg tgaagaccct aaagcagcac aagtatatct   1440
ccatcgcaga tgtgcagatc aagaatgaag aggagctgga gaagtgccct atgtctttgg   1500
gggaagaggt ggtaccagag acgccatgtg aaatcctcta ccagggaatg ctgtacagcc   1560
ttccgcagta tatgatcgct ctgcttaaga ttctgctggc tgcagctccc acctctaagg   1620
ctaagacaga ctctatcaat atcctggcag atgtcctacc tgaggagatg cccatcactg   1680
ttctccagag catgaagctg ggcatcgatg tgaacaggca caggagatt attgtaaaga   1740
gtatctctac cctgcttctg ctactcctca aacacttcaa actcaaccat atctaccagt   1800
ttgaatatgt atcgcaacat ttggtatttg ccaactgcat ccccttgatc ctgaagttct   1860
tcaatcaaaa tatcttgtca tacatcactg ccaaaaacag catctcagtc ctggattatc   1920
cttgctgtac catccaggat ttgccggagc ttactactga aagtctggaa gctggagaca   1980
acagccagtt ctgctggagg aacctctttt cctgcatcaa cctcctgagg ctgctcaata   2040
aactgaccaa atggaaacat tcccggacca tgatgctggt agtgtttaaa tcggcaccaa   2100
tcttaaagcg ggccctcaag gtcaaacagg ccatgctgca actttatgtc ctaaagctac   2160
taaagttaca gaccaagtac ctggggcgcc aatggaggaa aagcaacatg aaaaccatgt   2220
cagccattta ccagaaagtg cgtcaccgca tgaacgatga ctgggcttac gggaatgaca   2280
tcgatgccag accatgggac ttccaagcag aagaatgtac cttgagggcc aacattgagg   2340
cttttaacag ccgtcgctat gacagacccc aggactctga gttttcacct gtggataact   2400
gcttgcagag cgtactgggg cagaggttgg atctgcctga agatttccac tattcatatg   2460
agctctggct cgagagagag gtgttttcac agcccatctg ttgggaggag ctgctccaga   2520
atcactga                                                           2528
```


        <210> 16
        <211> 2447
        <212> DNA
        <213> Homo sapiens

        <400> 16
```
gagcgggagg cgagtggcga gtggcgagtg gcgagtgtca ggggggcggc cggcggtggc     60
gggcggccg gaggaggcgt tggcagcggg ctcggaccca cgcggcgccg cggcccgcct    120
ggcctgcagc gctcccaccc ccggcggcgg cacgatgccc tttgacttca ggaggtttga    180
catctacagg aaggtgccca aggaccttac gcagccaacg tacaccgggg ccattatctc  · 240
catctgctgc tgcctcttca tcctcttcct cttcctctcg gagctcaccg gatttataac    300
gacagaagtt gtgaacgagc tctatgtcga tgacccagac aaggacagcg gtggcaagat    360
cgacgtcagt ctgaacatca gtttacccaa tctgcactgc gagttggttg ggcttgacat    420
tcaggatgag atgggcaggc acgaagtggg ccacatcgac aactccatga agatcccgct    480
gaacaatggg gcaggctgcc gcttcgaggg gcagttcagc atcaacaagg tccccggcaa    540
cttccacgtg tccacacaca gtgccacagc ccagccacag aacccagaca tgacgcatgt    600
catccacaag ctctcctttg gggacacgct acaggtccag aacatccacg gagctttcaa    660
tgctctcggg ggagcagaca gactcacctc caaccccctg gcctcccacg actacatcct    720
gaagattgtg cccacggttt atgaggacaa gagtggcaag cagcggtact cctaccagta    780
cacggtggcg aacaaggaat acgtcgccta cagccacacg ggccgcatca tccctgcaat    840
ctggttccgc tacgacctca gcccccatcac ggtcaagtac acagagagac ggcagccgct    900
gtacagattc atcaccacga tctgtgccat cattgtgcggg accttcaccg tcgccggcat    960
cctggactca tgcatcttca cagcctctga ggcctggaag aagatccagc tgggcaagat   1020
gcattgacgc cacacccagc ctaatggccg aggaccctgg gcatcgccag ccttgcctcc   1080
agtgccctgt ctcctttggc cctcaatctg gtcccaaatc tggctgtgtc caaagggtg   1140
tgtgggaagt ggggggaaag tagaggatgg ctcgatgttt gcagctacc tctttttcccc   1200
gtgtttcttt ttagacaaat tacactgcct gaagttgcag ttccccttc cctggggagc   1260
cccaagaaca gagtcaggca aggggtgggg agtccaggga tcttggggac ccctcctagg   1320
agagctgcag tctcttccct caggggaaca tcccagaatg catatcgatc agctctcagc   1380
caggcttcga caatctcgca gcccccacta ggtggacaca ttaatgattt ggtttctccc   1440
ctgggcagcc aacctgcccc agaggcacca gacctgggct ttcagctttg gaccaggct    1500
gcccaaaggt actcctttat acacccggca ccttccacga aagatggtac ttcccaagca   1560
agccccatg atttgtcact atagatggaa ccctgacttc tgccccatcc cttcctgccc   1620
aacctagaac ccaggcctca agtctttacc ccacccctt cttgttcttc caagaagcag   1680
atgcccagtt gctcagcagc agcggtagag acttgaatct gcccaccagt cacaaggcgg   1740
```
```

                                    11
```

```
gtcacagatt cctcttcctc tcttctcctc gttcctctga accctccacc aatgtgcctc   1800
agcctgtgtg ctgtgtggca acagcattct ggttcccact gccaagatct cccaccactc   1860
tgctgggatc tgcagtggca gggagtgggg gttgtgtaaa ggggaagtca tcttttgaga   1920
tccagataga catggtttgt gcacttacgt ccagatggga agcatccttc ctgcaaccct   1980
aaaataatca tgcagcctct cagacggacg ccatcggtcc caaggcctta ggtggaggaa   2040
gcaaagcagg ccaggcctgt cctgtccgtg gacctctacc ttctggactc cctacgggtg   2100
cagagcactt gggtttctct acagccatcg tggcccactt gacactgtgc tcctccatca   2160
gctggtcaca tgccaacacg ttcccagccc ctgaggcagc tccagggtgc cccacctgct   2220
cctgaggtgg gtccctaccc tgctgctcct cttcatcctt tcccttttgt cctgaaaggg   2280
aggagcaatg gtccaggcat taattccacc cagggaattt tagctatgcc ctcatgtccc   2340
agggagagag ccacacgcct gttttccatt tatagcaaga ttgtttgcat acttttgtaa   2400
tgaaggggag tgtccagtgg aaggattttt aaaattatct tatggat             2447
```

```
                    <210> 17
                    <211> 2657
                    <212> DNA
                    <213> Homo sapiens


                    <400> 17
         ctgggctcgg ccacaactgt gttccacacc agagtgggtg ctagggatag ggagaggcca     60
         gggagtggga gcaggcactt ctgagcttgt gggggaagga ggcttcctga gccctttaca    120
         ttgcatcaca taggaatcca cataatacct ggttgacgca acatcagtcc aactgaccac    180
         aaagcaacta ggggtttcag agggagtaca cgtaaggggc aaaagcagca acggaatacg    240
         acaacggaat aagcatgaat acgacctggc tacctgaagg aggtacaaga aaattcccca    300
         ggacacagag ctggtttgga gcctttcttt gattttattg tttctattaa tggttcaaga    360
         ttaaataaag acaatgacac tcttaaggat ctgctgaaag caaacgttga aaagcctgta    420
         aagatgctta tctatagcac caaaacattg gaactgcgaa agacctcagt cacaccaagt    480
         aacctgtggg gcggccaggg cttattggga gtgagcattc gtttctgcag ctttgatggg    540
         gcaaatgaaa atgtttggca tgtgctggag gtggaaatca aattctcctg cagcactggc    600
         aggtcttaga ccacacacgt gattatataa ttggagcaga tacagtcatt gaatgagtct    660
         gaagatctat tcagccttat cgaaacacat gaagcagaac acattgaaac tgtatgtgta    720
         ccacacagac acgtgagtaa cggtcgagaa gtgattatta caccaaattc tgcatggggt    780
         ggagaaggca gcctaggatg tggcattgga tatggttatt tgcatcgaat acctacacgc    840
         ccatttgagg aaggaaagaa aatttctctt ccaggacaaa tggctggtac acctattaca    900
         cctcttaaag atgggtttac agaggtccag ctgtcctcag ttaatccccc gtctttgtca    960
         ccaccaggaa ctacaggaat tgaacagagt ctgactggac tttctattag ctcaactccc   1020
         accagctgtc agtagtgttc tcagtacagg tgtaccaaca gtaccagtta ttgccaccac   1080
         aagtaaacca gtccctcact tctgtgccac caatgaatcc agctactaca ttaccaggtc   1140
         tgatgccttt accagcagga ctgcccaacc tccccaacct caacctcaac ctcccagcac   1200
         cacacatcat gccagcgggt tggcttacca gaacttgtaa acccaggttt tgccacctct   1260
         ttcttccatg cctccccgaa acttacctgg gcattgcacc tctccccctg ccatccgagt   1320
         tcctcccgtc attccccttg gttccagaga gctcttctgc agcaagctca ggagagctgc   1380
         tgtcttccct cccgcccacc agcaacgcac cctccgaccc tgccacaact actgcaaagg   1440
         cagacgctgc ctcctcactc actgtggatg tgacgccccc cacctgccaa gggcccccc    1500
         accgttgagg acagatgtcg gcgactccac cccattcaga gagaaacctg tttctgcggc   1560
         tgaggatgcc aatgcttctg agtcacccct aactttgaac cattctttgg aaatggggt    1620
         ggtatattta accacggggg ccgttctgg aaaacgcaaac tatcattaat ttcatactag   1680
         tttgtaccgt atctgtcagg catcctgtaa ataattccca aggggaaaac taaacgagga   1740
         cgtgggttgt atcctgccca ggttgagtgg ggctcacacg ctagggtgag attgtcagaa   1800
         agcgcttgta ttttaaacaa ccaaaaagaa ttgtaagggt ggcttgctgc ccaggctttg   1860
         cactgcccgt tccctggggg tgtgcatctt cgggaaaggt ggtggcgggg cgtccactag   1920
         gtttcctgtc cccgtgctgc tcccttccgg taaggaaaat gaaatattct atgcctaata   1980
         ctccacaggc aacatttctt ggtactttgg taagtcgttt tgcggagaat gcagaccacc   2040
         tcacttaaac ttgtaaaccg gtaaaagaga tttttacttt tgggtctccg gtgagtcgca   2100
         tcttcttact tagggtttac acaggaaatt ccacctggaa gacttgtgtt aaaagttcta   2160
         cagcggcgca ctggttaacc tgaaccgtct tttttcttca gcctatacgc ggatcccttg   2220
         ttttggagct ctcagaatca actcagacaa acattttgta aacggctgct ggttgctttc   2280
         tacatacacc ttataaagtg acatttcaaa aagaaatcaa ggtgccacag ttttaaacca   2340
         gaaggtggca ctttttcttc ttttgggggt gggggcctcc cttgtagtat tatagctata   2400
         ctggggaaag ccataggtac aggcaattaa agtaccagta attttacttt ttttcttgtg   2460
         ttacatctaa attacaaccc ttaattgcca cgtgtgcact tactactctc cagtatgtct   2520
```

```
tattactctc cagtatgtca cgcatcttta acttttcacg tcctatgttt gctttctccc    2580
atttttaaga gatggtaagt taactggaat tgatttactg aatgaaatta aatgcagata    2640
tccctgtttt tgaaata                                                    2657
```

```
<210> 18
<211> 298
<212> DNA
<213> Homo sapiens
```

```
<400> 18
gaatcctcac tatgggaaat atttgtatct taaaaggaaa ttaaatgtag ttaacccata     60
cagcccagaa attattgtaa aatttgaaaa tttccaggtt gtgtcctcta tccatatcct    120
gtgcattcat aagctaaaac tttcatcaaa ccaagaagat gccgtgattg tggagcaacc    180
agaagtgatt ccattaacag aggaccaaga agaaaaagaa ggtgaaaaag cagaaattgt    240
tggctctgtt tatggcattt caagaaatgc aaatggtaaa gaggaaaatc aaacagct     298
```

```
<210> 19
<211> 3892
<212> DNA
<213> Homo sapiens.
```

```
<400> 19
cctcccatct cccttccccg aaggcagcaa catccccagc ttctacacag tcgcaccata     60
ggcaagcgtc cttggacctc gccactgtcc ccagagcaac tcttggagaa caacagtgca    120
gataaagcct ctggttctgt gtccaccacg ttgccggttg cttataaaaa gggagtcaaa    180
catctttctg ctcttcttga tccagaggtc ctgtccattt tcgtgcctcc ttttatcagt    240
aaagaggaca gtcaaacggc cggtgccaac tgcggcactc tcggtaaaac ccggatgcgc    300
tccttgagaa agaagagaga gaagcccaga ccagagcagt gggagggcct cccggggccc    360
cccagagcgc cagagcctga ggatgtcgcc gtcccggggcg gcgtggacct cctcaccctg    420
ccgcagctgt gcttcccagg gggtgtgtgc gtggccactg aacctaagga ggattgcgtc    480
cacttcctgg tgctgaccga tgtctgcggg aataggacct atggcgtggt ggcccagtac    540
taccggcccc tgcatgatga gtactgtttc tacaatggca aaaccgcacc gggagtgtcc    600
tggctgcttc gtgcccttcg cggtgtgcgt ggtctccagg tttccctatt acaactccct    660
caaggactgc ctttcctgtt tattggctct tctgaagccc tgtaaagatt ttgaagtgga    720
caatcatata aaagatttcg ctgcgaagct gtctttaata cccagcccgc cacctggacc    780
gctccatttg gtatttaaca tgaagtcgct ccagattgtg ttacctgccc gagcagaccc    840
cgaaagcccc atcctggacc tggaccttca cctgcccttg ctgtgcttcc ggcctgagaa    900
ggtgctacag atcctgacat gcatcctgac ggaacagcgg atcgtcttct tctcctcgga    960
ctgggtctg ctgacgctgg tcactgagtg cttcatggtc tacctgtatc cgctgcagtg   1020
gcagcacccc ttcgtgccca tcctgtcgga ccagatgctg gattttgtca tgggccccac   1080
atccttcctg atgggctgcc atctcgacca cttcgaagaa gtcagcaagg aagccgacgg   1140
tttagttctg ataaatattg atcatgggag catcacctac tccaagtcca cggacgataa   1200
cgtggacatt cctgatgtcc ccctcctggc agcccagacg tttattcaga gggtgcagag   1260
cctccagctc caccatgagc tgcacgccgc ccacctcctc tccagcacag acctgaagga   1320
gggccgagcc caccggcggt cctggcagca gaaactcaac tgccagatac agcagaccac   1380
cctgcagctg ctcgtgagca tcttcaggga tgtaaagaat catttaaact atgaacacag   1440
agtctttaat agtgaagaat ttctcaaaac cagggctcca ggggaccatc agttttataa   1500
gcaggtctta gacacctaca tgttccattc ttttcttaaa gcccggctca ataggaggat   1560
ggacgccttt gctcagatgg acctcgacac ccagtcggag gaggacagaa taaatggaat   1620
gcttctaagt ccaaggagac cgaccgttga gaaaagagcc tcccggaagt cctcgcacct   1680
gcatgtcacc cacaggcgca tggtggtcag catgcccaac ctgcaggaca ttgccatgcc   1740
tgagctggca cccaggaact cctcgctccg gctgacggac accgcaggct gtaggggcag   1800
cagcgcagtt ctgaatgtca cgccgaagtc cccgtataca ttcaagattc ccgaaatcca   1860
cttttccgctg gagagcaagt gcgtgcaggc ataccatgcc cactttgtct ccatgctgag   1920
cgaggccatg tgctttctgg cccccgataa ctctctgctc ctggcccgct atttgtacct   1980
ccgagggctc gtttatctga tgcagggaca gctgctgaac gccctcttgg acttccagaa   2040
tctgtataaa acagacatac ggatctttcc cactgatttg gtgaagagga cggtggaatc   2100
catgtctgcc cctgagtggg aggggggctga gcaggcgccg gagctgatga ggctcatcag   2160
```

```
cgagatcctg gacaagccgc acgaggcctc gaagctggac gaccacgtga agaagttcaa    2220
gctgcccaag aagcacatgc agctgggcga cttcatgaag cgggtccagg agtcagggat    2280
cgtgaaggac gccagcatca tacaccggct gttcgaggcc ttgactgtag gacaggagaa    2340
acaaatcgac ccagaaacat tcaaagattt ctacaactgc tggaaggaga cggaagcaga    2400
agcccaggag gtcagtctgc cgtggctggt gatggaacac ctggataaaa acgagtgtgt    2460
gtgtaagttg tccagctccg tcaagacaaa cctaggcgtt ggcaagatcg ccatgaccca    2520
gaagcgcctg ttcctcctaa ccgaaggaag gccaggctac ttggagattt ccaccttcag    2580
aaatatagag gaggtcagga gaaccactac tacatttcta cttcggagaa tacccacttt    2640
aaaaatcaga gtggcgtcca agaaagaagt cttcgaagcc aacctgaaaa ccgagtgtga    2700
cctttggcac ctgatggtga aggagatgtg ggctgggaag aagctggccg atgaccacaa    2760
ggaccctcac tacgtccagc aggcgctgac caacgtcttg ctgatggacg ccgtcgtggg    2820
cacactgcag tcaccaggcg ccatctacgc tgcctccaag ttatcctact ttgataagat    2880
gagtaacgaa atgcccatga cgcttccgga gacaaccctg gaaacactga agcataaaat    2940
caacccctcg gcggggggagg cgttcccaca agcggtggac gtgctgctct acactccagg    3000
gcatcttgac ccagccgaaa aagttgaaga tgctcacccc aagttatggt gtgctctgag    3060
cgaaggcaag gtgaccgtgt tcaatgcttc ttcatggacc atccaccagc actcctttaa    3120
agtgggcact gcaaaagtga actgcatggt gatggccgac cagaaccagg tgtgggttgg    3180
ctcggaagac tccgtcatct acatcatcaa cgtccacagc atgtcctgca caagcagct    3240
cacagcccac tgctccagtg tcacggattt gattgtgcag gacggacagg aggcacccag    3300
caacgtgtac tcgtgcagca tggacggcat ggtgctggtg tggaatgtga gcacactgca    3360
ggtgaccagc cgcttccagc tgccgcgagg tggcctgacg tccatcagac tgcacggcgg    3420
ccgcctgtgg tgctgcacag gtaacagcat catggtcatg aaaatgaatg gatccctcca    3480
tcaagaattg aagattgagg agaacttcaa agacaccagt acctccttcc tggccttcca    3540
gctccttcct gaggaggagc agctgtgggc ggcctgtgca ggacgcagcg aggtttacat    3600
ctggagcctg aaggacctgg cccagccccc gcagaggtg ccctcgagg actgctctga    3660
gatcaactgc atgatccggg tgaagaagca ggtctgggtg ggcagccgag ggctggggca    3720
gggaacaccc aaggggaaaa tctacgtgat tgacgccgag aggaagaccg tggagaagga    3780
gctggtggcg cacatggaca ccgtgaggac gctgtgctcg gctgaggaca gatacgtgct    3840
gagtgggtcg ggcagggagg aggggaaagt cgccatttgg aaaggcgaat aa    3892
```

```
        <210> 20
        <211> 1205
        <212> DNA
        <213> Homo sapiens


        <400> 20
        atgcagccta cacctggttg actggacgac cactttagtg gaaaggagac agtctgggcc      60
        tctggcctgc catgtgcaca agcataacaa ttattttttgt ttaacatgca gatggaatat     120
        ttgatccctt ttaaccaggc atttgcacct tggtatcttg tcttaattgc caaagtttgt     180
        tttaagtctt taacttctat gatcctctag taaaaatgaa aggtatgggt ttaacgaaaa     240
        ttgcaaaaaa cctggtgggg ccagtccatc cttgctcttt actggtccac agaacgttgg     300
        accaactatg gcataaaaag ctctacattg gtgggacaag actcctggtt gacactgggg     360
        tctttatcaa aatctccccg gattaaatg tcccaattct ctaatgccaa gtctgacgag     420
        agtcaggagg gacagaggta cttttctgaa gtagagagct gtctttgcct tggcaagtcc     480
        ccacagggta taacaaggca agcattaaat gcaaaagttt gaagcaaaat tgacttggtt     540
        atgttaataa ctagatggtc agcaatagag tgaggaaaga agaaagagta ttacaataga     600
        agaaagagag agagttacat ttttcttagc tttagcttgg tagggttttc ccctgggact     660
        atgggcccacg actctggagg gggtggcact ttcttgactt gggtgtgatg agtccatctt     720
        tttttttttt ttttttttttt tttgctgtac gaacagcagt cttggtggtt agcagcacag     780
        ggtagggtcc ttcccaggct ggctcgagtt ttctttcttt ccaccctttg atgagaatgt     840
        gatcctcaag ctggtgctgg tttactggaa attcagttac tttgtgccat acctttgaaa     900
        ctagggactt gtctagactt ccttctgatg gccatcccac tctaatgcc ggccaatcta     960
        tctcacacaa agccttaagc tttccaggtg tcatagcaat tccatagtcc ccattggatc    1020
        ctttcttgaa attctttaac acagttccta gtggggtggg cttactttgt gcctgaccca    1080
        tgcttcctca agacaaaaca ccacactcac accatacaca caccacaaaa caaagaacag    1140
        gtaaaaaggg cacacacaca cttttacagt ttataccaaa ccagaatcaa aaccaaagtc    1200
        agaat                                                               1205
```

```
        <210> 21
```

```
<211> 4289
<212> DNA
<213> Homo sapiens


<400> 21
agagccaccg cggagcgcgc gcggggttgg ttgccgcgag cgtggggggag cgtggaccgc    60
ggcgctgctc agcggtgggg ctgccttccc ccggccctcc tccctggtcc ctggcgaggg   120
cactggcggc ggcgggtccg gggtccgcaa ggccggagaa ggccgccggg cccgggcatg   180
gtggtctggg gcaacgcgga agaagctcca ccatgaggcg aggtggatgg aggaagcgag   240
ctgaaaatga tggctgggaa acatggggtg ggtatatggc tgccaaggtc cagaaattgg   300
aggaacagtt tcgatcagat gctgctatgc agaaggatgg gacttcatct acaattttta   360
gtggagttgc catctatgtt aatggataca cagatccttc cgctgaggaa ttgagaaaac   420
taatgatgtt gcatggaggt caataccatg tatattattc cagatctaaa acaacacata   480
ttattgccac aaatcttccc aatgccaaaa ttaaagaatt aaaggggggaa aaagtaattc   540
gaccagaatg gattgtggaa agcatcaaag ctggacgact cctctcctac attccatatc   600
agctgtacac caagcagtcc agtgtgcaga aaggtctcag ctttaatcct gtatgcagac   660
ctgaggatcc tctgccaggt ccaagcaata tagccaaaca gctcaacaac agggtaaatc   720
acatcgttaa gaagattgaa acggaaaatg aagtcaaagt caatggcatg aacagttgga   780
atgaagaaga tgaaaataat gattttagtt ttgtggatct ggagcagacc ctccgggaa    840
ggaaacagaa tggaattccg catcccagag ggagcactgc catttttaat ggacacactc   900
ctagctctaa tggtgcctta aagacacagg attgcttggt gcccatggtc aacagtgttg   960
ccagcaggct ttctccagcc tttttcccagg aggaggataa ggctgagaag agcagcactg  1020
atttcagaga ctgcactctg cagcagttgc agcaaagcac cagaaacaca gatgctttgc  1080
ggaatccaca cagaactaat tctttctcat tatcaccttt gcacagtaac actaaaatca  1140
atggtgctca ccactccact gttcaggggc cttcaagcac aaaaagcact tcttcagtat  1200
ctacgtttag caaggcagca ccttcagtgc catccaaacc ttcagactgc aattttattt  1260
caaacttcta ttctcattca agactgcatc acatatcaat gtggaagtgt gaattgactg  1320
agtttgtcaa taccctacaa agacaaagta atggtatctt tccaggaagg gaaaagttaa  1380
aaaaaatgaa aacaggcagg tctgcacttg ttgtaactga cacaggagat atgtcagtat  1440
tgaattctcc cagacatcag agctgtataa tgcatgttga tatggattgc ttctttgtat  1500
cagtgggtat acgaaataga ccagatctca aaggaaaacc agtggctgtt acaagtaaca  1560
gaggcacagg aagggcacct ttacgtcctg gcgctaaccc ccagctggag tggcagtatt  1620
accagaataa aatcctgaaa ggcaaagcag cagatatacc agattcatca ttgtggggaga  1680
atccagattc tgcgcaagca aatggaattg attctgtttt gtcaagggct gaaattgcat  1740
cttgtagtta tgaggccagg caacttggca ttaagaacgg aatgtttttt gggcatgcta  1800
aacaactatg tcctaatctt caagctgttc catacgattt tcatgcatat aaggaagtcg  1860
cacaaacatt gtatgaaaca ttggcaagcc tacactcata acattgaagc tgtcagttgt  1920
gatgaagcgc tggtagacat taccgaaatc cttgcagaga ccaaacttac tcctgatgaa  1980
tttgcaaatg ctgttagaat gagaaatcaa agaccagacg aaatgtgctg cctctgatgg  2040
aattggttct aatattctcc tggctagaat ggcaactaga aaagcaaaac cagatgggca  2100
gtaccaccta aaaccagaag aagtagatga ttttatcaga ggccagctag tgaccaatct  2160
accaggagtt ggacattcaa tggaatctaa gttggcatct ttggcaatta aaacttgtgg  2220
agacttgcag tatatgacca tggcaaaact ccaaaaagaa tttggtccca aaacaggtca  2280
gatgctttat aggttctgcc gtggcttgga tgatagacca gttcgaactg ataaggacag  2340
aaaatctgtt tcagctgaga tcaactatgg gaataaggtt tactcagcca aaagaggcag  2400
aagctttttct tctgagtctt tcagaagaaa ttcaaagaag actagaagcc actggcatga  2460
agggtaaacg tctaactctc aaaatcatgg tacgaaagcc tggggctcct gtagaaactg  2520
caaaatttgg aggccatgga atttgtgata acattgccag gactgtaact cttgaccagg  2580
caacagataa tgcaaaaata attggaaagg cgatgctaaa catgtttcat acaatgaaac  2640
taaatatatc agatatgaga ggggttggga ttcacgtgaa tcacctggct tccatctaat  2700
ctgaaccctt ccacatgtcc cagtcgccca tcagttcagt caagccactt tcctagtggg  2760
tcatactctg tccgtgatgt cttccaagtt cagaaagctt aagaaatcca ccgaagagga  2820
gcacaaagaa gtatttcggg ctgctgtgga tctggaaata tcatctgctt ctagaacttg  2880
cactttcttg ccaccttttc ctgcacatct gccgaccagt cctgatacta caaggctga   2940
gtcttcaggc aaatggaatg gtctacatac tcctgtcagt gtgcagttcg agacttaacc  3000
tgagtataga ggtcccgtca ccttcccagc tggatcagtc tgtttttagaa gcacttccac  3060
ctgatctccg ggaacaagta gagcaagtct gtgctgtcca gcaagcagag tcacatggcg  3120
acaaaaaaga aagaaccagt aaatggctgt aatacaggaa ttttgccaca accagttggg  3180
acgagtcgtt gttgcaaata ccgagaacct caagaatcga acaagtgacg caggaataaa  3240
tttaatagcc cttccagcat tttcgacagg tggaccctga ggtatttgct gccctttctt  3300
gctgaacttc agagggagct gaaagcagcg tatgatcaaa gacaaaggca gggcgagaac  3360
agcactcacc agcagtcgag ccagcgcatc tgtgccaaag aatcctttaa tatcatctaa  3420
aggcagcgag tgaaagaaaa gaaaagaaac aagaagaaaa aaaccattgg ttcaccaaaa  3480
```

```
aggattcaga gtcctttgaa taacaagctg cttaacagtc ctgcaaaaac tctgccaggg    3540
gcctgtggca gtccccagaa gttaattgat gggtttctaa aacatgaagg acctcctgca    3600
gagaaacccc tggaagaact ctctgcttct acttcaggtg tgccaggcct ttctagtttg    3660
cagtctgacc cagctggctg tgtgagacct ccaccacccc aatctagctg gagctgttga    3720
attcaatgat gtgaagacct tgctcagagg aatgggtaac tacaatttca gatccaatgg    3780
aagaagacat tctccaacgt tgtgaaatac tgtactgatc taatagaaga caaagatttg    3840
gaaaaactgg atctagttat aaaatacatg aaaaggctga tgcagcaatc ggtggaatcg    3900
gtttggaata tggcatttga ctttattctt gacaatgtcc aggtggtttt acaacaaact    3960
tatggaagca cattaaaagt tacataaata ttaccagaga gcctgatgct ctctgatagc    4020
tgtgccataa gtgcttgtga ggtatttgca aagtgcatga tagtaatgct cggagttttt    4080
ataatttta atttcttta aagcaagtgt tttgtacatt tcttttcaaa aagtgccaaa    4140
tttgtcagta ttgcatgtaa ataattgtgt taattatttt actgtagcat agattctatt    4200
tacaaaatgt ttgtttataa agttttatgg atttttacag tgaagtgttt acagttgttt    4260
aataaagaac tgtatgtata ttttgaaaa                                     4289
```

```
        <210> 22
        <211> 686
        <212> DNA
        <213> Homo sapiens


        <400> 22
ctctcattca agtaaattct actcattagt caatgatttc tcctcacatc gattttgtgg      60
gagtggatct gattagatca ggtaaagaaa ctcgagtgtg gtgaatcact gccctcccaa     120
ggtcccttac acattcttta agacagagca gaggagcaag tccacgtgga ggtttaaatt     180
caagccagct gtgctctcaa agtggtgaaa aggctgggat ttattttaaa agccacccca     240
aaaaacacat ttccatctga tgtcatttac atttcttccc attttattta ttttaaaaaa     300
ttcatgtccc taaagtaaga tgtagatgtg ccatatgtag tcatttaatt ccacgtagca     360
ttcattttaa gtacctgttc cggctttata catgcttggc agttgactgc agggatggga     420
actgtgtatc actgtagatt tctggtggtc cttgtggtgt tttccttgtt gtggttaacc    ·480
tggccccagg aggcctatac acaccactag tcatcgctgg ttctggggtt tctgtaacaa    ʼ540
ttactggagc aggaggtgct tgtactggag ctgtttattt ccagggacct gaagattttt    ʼ600
ccatacctcc accaccacct ccacttctt cccagttatc acctggatct tgtctctttt    ʼ660
cattatcgtc ttcttccttt tcactg                                        686
```

```
        <210> 23
        <211> 1528
        <212> DNA
        <213> Homo sapiens


        <400> 23
gagatgaaga tgctaaggaa acccagatag cttccaagaa gaagctcagg gagataagag      60
agaaggattg ggtggtgatc caggcactat ggtggggaaa ccggagacaa gtagcaagtg     120
aaatttatag agaatttgag atactatgtt gggagaatca gaactggatt ggaggtgaac     180
atagagcaga aattcaggca tcagagaaga gagaccacag aacgtggatg gatgtgagga     240
tggcacatat attctgtctc ccgaggctga gatccaggaa caattaaaag gagaaactga     300
tgtggatact caaagcaatg acccacttag agaagaggat ggtacagaca ttcagtcact     360
agggaggaga gaggttaaag gtgaggatga taaagacacc caggaacttg ggaggaaaaa     420
tcagggtcag ttaggaaatg aatttagtgg aaagattcac ataccaaagg gaagaatca     480
ggaacatatt agaggcgaag atggtgcaca tacccagata tctgagtcag ggaactgggg     540
caaattaaca agtcaaattg atggagaaat gcattcagca gaatggaaga aagatcagca     600
gattggaggt gagaatgggg cagaaattca gatacaaggg aagagaaacc tgagagaagt     660
tggaggtgag gacggtgtaa agacctgggc acctgggaaa gaaacccaga gtcagtttag     720
aagtgatctt ggtagaaaga tcctttttatc agagtggaag agccagaagc agatgggaag     780
tgagaatgga acagaaattc aggctccagt ggagagaaac cagagagaac ctggaggtga     840
ggacggtgta aagactcaga gacctaagag agagaacgag gaccagttag atagtgaaat     900
tggagggagc cattcaccag ggaggaggaa ctgggagctg attggaaagg atgttgcaga     960
aaatcaggca tcagagaaga gaaaccagag agaggttgga aacgaggacg agtggaagaa    1020
ccaggaacag ggtggaggtg ggaatgatga agaaattcaa atacagggga agagaaacct    1080
```

```
gagagggacc acagctgatg atggtacaga gacccaggct cctgcaggag atgaccaggg    1140
acagttaaga gttgaaattg ctgaagagat ccaggtacaa gggcaaggaa ataagaatga    1200
cggtggagtt gaggatgttg cagaactcca ggatatagga agccagagaa agtgcacaga    1260
tgaggatgtt ggagagcctc gagcaccaag gggaggaaac aaggatctgg tcagaggaga    1320
ggatgctgtg agggacagtc tccaagtcga ctgttctggg agtgagaggc ccacaggcag    1380
gaagcacagc ctaccatggc ctccagcctt cactggctat ggatgtggga cccgggaaca    1440
ggaacaggca gtggctgtga atggtttcat ctctgccccc tgtcctgaga tgaatcctgt    1500
cccccactgg ggtgaagtct tcctgctg                                       1528
```

```
        <210> 24
        <211> 7268
        <212> DNA
        <213> Homo sapiens


        <400> 24
        tttcgtctcc gcctcgcctg ccaccggggt ttgtatgaaa acaccgggcg gcgggcggcg     60
        agggatccgc cgtgatccag gtgctgagcc gggtgctgcg gctctgcgcg gtccccgcca    120
        gcgccccatc ctgagccgat tatctgcaat tatgaaatga agtaactcaa gatgagcaag    180
        ttaaaagtga taccagaaaa aagccttacc aataattcta ggatcgtagg actcctggct    240
        caactggaga agatcaatgc tgagccttca gaatcagaca ctgcccgata tgttacatca    300
        aaaattcttc atctggctca gagtcaagaa aaaacaagga gagaaatgac agccaaaggt    360
        tctacaggaa tggaaattct gctgtcaaca ttagagaaca caaaagatct tcaaactaca    420
        cttaatatct taagcattct tgttgagctg gtgtcagctg gtggaggtcg aagagtgagt    480
        ttcttagtca ccaaaggtgg ttcacaaata ttgttgcagt tacttatgaa tgccagcaaa    540
        gaatctcccc cacatgagga cttaatggta cagattcatt ctattcttgc aaagattgga    600
        ccaaaagata aaaaatttgg agtaaaggct agaattaatg gggctctgaa tataaccctg    660
        aatttggtca agcagaattt gcagaatcat cgcttggttc taccttgcct tcagctttta    720
        cgagtatatt ctgccaactc tgtgaattca gtatccttag ggaaaaatgg agttgtggaa    780
        ctgatgttta aaatcattgg accatttagt aagaagaatt ccagtcttat aaaggttgct    840
        ttagacactc ttgctgcatt gctaaaatca aaaacaaatg ccaggagagc tgtagacaga    900
        ggatatgtcc aagtgctttt aacaatttat gtagattggc accgccatga taaccggcat    960
        agaaacatgc tcattcggaa aggaatttta cggagtttaa acaagcgtct acaaacatca   1020
        tgttgggaag aaaagcattt attgatgcca atgggatgaa aattctgtat aatacttcgc   1080
        aattgcctgt tattcctgtg actggtcctg tggctcagct ctacagctta cctcctgaag   1140
        tggatgacgt agtagatgaa agtgatgaca cgatgatat  tgatgtagaa gctgaaaacg   1200
        aaactgagaa tgaagatgac ctagatcaaa attttaagaa tgatgatatt gaaacagata   1260
        ttaacaaact aaaaccccag caagaaccgg gacgaacaat agaagatcta aaaatgtatg   1320
        aacacctttt ccctgagctt gttgatgatt tcaggacta  tgatttaatc tccaaagaac   1380
        caaagccttt tgtatttgag ggaaaagtac gtggtcctat tgttgttcct acggcaggcg   1440
        agggaacatc tgggaattct ggcaatttaa gaaaagttgt aatgaaggag aacatatctt   1500
        ctaaaggaga tgaaggtgaa aagaagtcta cctttatgga tctagcaaaa gaagatatta   1560
        aagataatga tagaacatta caacagcagc caggtgatca aaatagaact atttcatcag   1620
        tccatggttt aaacaatgat attgtaaagg ccttggaccg aattacattg cagaatattc   1680
        cttctcaaac agccccaggt tttactgcag aaatgaagaa ggactgcagt cttcctctta   1740
        ctgtccttac ctgtgctaaa gcatgtccac acatggctac ttgtggaaaa tgttctgttt   1800
        cgagggaaga acagttcagc tagggaagct ttgctgcact ggagttgaaa ccgaagatga   1860
        tgaacgatac tgagtcaaat tcatcggtag aacaagcatc ggttgaagta cctgagtgga   1920
        ccaacactcc atgacccaga cctctatatt gagattgtga acatacgaa  gtctgtccca   1980
        gaatattccg aggtggctta tcccgattat tgtggtcaca ttccgcctcc attcaaagag   2040
        cccattttag aaaggcctaa atggtgtacc aaaggacaaa aattgctcaa ggatattgga   2100
        aaggctaata acatcagagg tgatatcata gatcgtgtgg tatatgactt ggctaacccc   2160
        aaattacacc attccagaag agggagatct cttgaaattt aactccaaat tagagtctgg   2220
        gaatctgcgc aaagtaattc aaaattagaa aaaatgaata tgatcttatt ctgaactcag   2280
        acataaacag ccaatcatta tcatcagtgg ttttactttg aagaaagtgg aaccgcgacc   2340
        aggtggtgct tacaggctta acatcattaa ctgtgaaaag gccaacagtc agtttaatta   2400
        tgttatgcat cccactcatg tattcggttc aggaagcatt aaatgccata ccatggtgga   2460
        ttcgtatggt gactgacatt tgttactata aaaatcattt ctcaagaagt tcagttgctg   2520
        caggtgttcc aaagggaaaa tcctactata caattacatt tactgtcaat tttccacata   2580
        tagatgatgt ttgctactat gcttatcact atccatatac gtattcaact ttacagatgc   2640
        atcttcaata attggaatca gcacacaatc ctcagcaaat ctattttcgg aaagatgtgt   2700
        tatgtgaaac ccttgtctgg aaacagctgc cccttggtga ctataacagc aatgccagag   2760
```

17

```
tctaattatt atgaacatat ctgccatttc agaaatcgcc cttacgtttt cttgtctgct 2820
cgggtacatc ctgggagaaa ctaatgcaag ttggggttat gaaagggaac gttgggaata 2880
tctccatgag gcaattaacc ccactggctt caggagctta cggaggaatc tttattattt 2940
tttaaaattg tccctatgtt aaatccagat ggtgtcatca atggaaatca tcgctgttct 3000
ttaagtggag aggatttgaa taggcagtgg caaagtccaa gtccggattc acatcctaca 3060
atttaccatg ctaaggggct gttgcaatac ttggctgcag tgaagcgttt acccttggtt 3120
tattgtgatt accatggcca ttcccgaaag aagaatgtat ttatgtatgg ttgcagcatc 3180
aaagagacag tgtgcatac caatgataat tcgccttcat gtgatgttgt ggaggatacg 3240
ggatacagga cattgcctaa gatactgagc catatcgccc cagcattttg catgagcagc 3300
tgtagcttcg tagtggaaaa atctaaagaa tccacagcac gtgttgtagt ttggagggaa 3360
ataggagtac aaagaagtta taccatggag agtactttat gtggctgtga tcaggaaaaa 3420
tacaagggtt tacagattgg tacccgagaa ctggaagaga tgggagcaaa attttgtgtt 3480
ggtctttttac agtttgaaaa gactgacctc tccattggaa gaataatctg ccctcccagc 3540
cctgcttgac tttgaaaatg atttaaattg aatccaagcc tgcaaagtaa ctagccccta 3600
cccacttatg tccttggatg aagatgaacc ctcgattccc ttgaagaagt tgattacagt 3660
gcagaaagta atgatgagtt agatattgag ttggctgaaa atgtaggaga ttatgaacct 3720
tctgctcaag aagaagtact ttctgactct gaattatcaa gaacatacct accttgagcc 3780
cgctcgccat ctctttgtta actgcaaaga ataaatgaaa tatcttggtg ttttattctc 3840
ccaggaagct tgagagaaat gagtttatac agagctgact caaaaagaca aaaagtaact 3900
tgggccagtt tggtttcaag ataataaatg tgttattaat taatgattaa aattggcgcc 3960
tggtttttatt ttcggatatt ccaatgcact ttatggtagc cattgaatga tccaaatatt 4020
ggatttaccc tttaaaaaaa aaaaacctga gtatcattgc atgaattttt atctccctat 4080
ggttatatcc tgcatcaagg gggataattt tgaagtgtgt tcagaatata aaattgaaat 4140
tttagagttg ttgaaaatcc tgacttgttg aaaactaata tatatgtaca tggatttcta 4200
tagatgtgtt tgtttagaag tgggtagata ttgcagataa gactgttctt cagaatcatg 4260
ttaactattg ggttgtgact gaagtagtcc agggtttgcc ttgaaaccat tacattctac 4320
atttaccaaa ttaaacaaat aaaaactgta ttaaatgttg cattcatttt gtcatcttct 4380
ttaaccagct cagattattt gatgtataga actttgtgag aatgtgataa aaacccagaa 4440
ttggacacag tgataaaaag ttgtttttaa gaaagtgctg ggattacagg cgtgcgccac 4500
cgtgcctggc taaatccttt cttgtaatga aacctacctg ggttttagcc ctcttgctgc 4560
aagaatgact ttattttttaa ataaaataaa gcaaatccat tgactttgga taagtgtttt . 4620
aagaactaag tttctgatat aataaaacaa cctccaaaag atacctcatt gcagattttc · 4680
gccaggattc aggtgcttag gtttttggcac atatcttcct cacttttccc tatagtgttt 4740
ttaacctgtt ataattggaa tgatagagat gtatttcaga attttgcatg gtccaaatca 4800
atgattttttc tttttaatat gtaaagtatt tcattaacag tgtagattct ttctgatgtt . 4860
tggggagcca tgtttaaaaa tgtagtatgg agcaattgaa aaagggtct ttttccctag 4920
cctaattctt actaatctca gaaaacaaag atcaaataga ctgtgaagtt gaactagtcc . 4980
tcttagtgta gtaaccaaat ttaggaaaga tcaggataat ttaggaagga aagtaatcat . 5040
ttatttaatt atttataatt ataaacaatt attttatgtt ttgtatattt tatgtataaa 5100
acaattacat gtttttattat agttatactt cttcagagag tagattatgg agccaccatg 5160
tccatacagt tagttgttcc ttggtattct tggattgatt ccaggacccc ccacagttac 5220
ccaaatccac agatgctgaa gtctctgata taaaatggag tagtatttgc atttaaccta 5280
tggacatcct cctgtatgct ttaaatcatc tctagattac ttataatacc taatacaata 5340
taaatataaa tgctctgtaa atagtttat tgtatagtgt gtgtgtgtgt tttaagagac 5400
gaggactcac aatgggacac tttgaccagg ctggtctcga actcctgggc ctacacaatc 5460
ctcccacctc ggcgtcgcaa gtagctggga ctacaggtac tcaccactat gcctggcagt 5520
ttttttaaatt tgcgttttta aaaattgttt attatttatt gaatatttttc tacctgagat 5580
tgacttaatc tgtggatatg gaacctatag atatggaggg ctggctgtat atgaatttgt 5640
ttttggcttt tacaaaatta gaaattaaaa gtaactacag ttactataat gtgcagaatg 5700
actcaaatat ttccatttat tatgttagtg taaaaactcc taactacgta ttataatatt 5760
ttatattaat gaagtacttt agcatacatt atgagcctga ataaagcttt ttattaaata 5820
ttcacaagat tgaaggagaa attctttata gttaggaaat gattttttca taaacaataa 5880
atagctttga aaatataaaa aaaaatttag ggctgggtgc agaggctcat gcctgtagtc 5940
ccagcactct gagaggccga ggcgggtgga tcacttgagg tgaggagttc aagatcagca 6000
tggccaacat ggtgaaactc cacctccacg aaaaatacaa aaattagcca ggcatggtgg 6060
catgcgcctg taatcctagc tacttgggtg gctgaggcat gagactcact tgaacctggg 6120
aggcagaggt tgcagcagtg agccgagatc aagccgctgc actccagctg gggcgacaaa 6180
gcaagactgt ctcaaaaaat aaaaacaaaa aaattaaaat aaaatcctaa ctttcctagt 6240
tagaaatata attaactttt attggctatt agtagctaaa attgccctta ttttttgcttc 6300
tgtggcctca tttttttttct cggttattca gtatttaaat tatggcttag atgtcttcaa 6360
tgctatagtc ctgaaaatta atgatctacg ttgtgcagca gtgatgggat ctgataaact 6420
gagtctgatg atggagttta gatttatttc ctttaccttg catttggaac tttgaatctc 6480
ttaaatgtgg ttttggtcta gtccactggt tctcacgttg taatgtgcat cagaatcttc 6540
tgaagacaca gattgctgat tatgtagacc tggggtggag gtccaagaat gtgcattcct 6600
```

18

```
tgcaaattcc caggtggtga tgctgcagag ccacactttg agaatcacta gtataatcca      6660
gtatgctctt ccagcatcac accttccttc ctgagaatca caggagttgt gaactgcaga      6720
ttagcattgg ggagaattta gatcaaacta atttgtagaa tcaaggaggt caagtaaggt      6780
cacaggggca cttgggttga gccaggggttt tagcccaggt cttctgacaa ctgcctcatg      6840
tccttaccac aaaggagctg ctatcctttg cctttcccca aagagtgaag actgcttaaa      6900
gctcaaggat ctttcttgaa tttgtgaaat ttgttcaggc aaggtgaaaa gcaaaaacct      6960
atggttcaca ttgacttttt gtattgatca ttgtcttttg aagacaggaa gtatgatcag      7020
tctctgccac ttgtgctagt ttttgtgtgg tgtttagaaa catgggcatt tgtctggatc      7080
ctaattacaa ataagtaacc tagaattctc ttcgagatag tggactaacc accgatgaat      7140
ctattctaaa atttcaaata tccaaattaa aatggactgt attaggcatt aaggtactgg      7200
aaatgggata atacattaaa tgtattaatg gaattgtttt tgtgcatgat acagaaataa      7260
atgatagt                                                               7268
```

```
        <210> 25
        <211> 3378
        <212> DNA
        <213> Homo sapiens


        <400> 25
atggatccgt ttacggagaa actgctggag cgaacccgtg ccaggcgaga gaatcttcag        60
agaaaaatgg ctgagaggcc cacagcagct ccaaggtcta tgactcatgc taagcgagct       120
agacagccac tttcagaagc aagtaaccag cagcccttct ctggtggtga agagaaatct       180
tgttcaaaac catcgccatc aaaaaaacgc tgttctgaca cactgaagt agaagtttct       240
aacttggaaa ataaacaacc agttgagtcg acatctgcaa aatcttgttc tccaagtcct       300
gtgtctcctc aggtgcagcc acaagcagca gataccatca gtgattctgt tgctgtcccg       360
gcatcactgc tgggcatgag gagagggctg aactcaagat tggaagcaac tgcagcctcc       420
tcagttaaaa cacgtatgca aaaacttgca gagcaacggc gccgttggga taatgatgat       480
atgacagatg acattcctga aagctcactc ttctcaccaa tgccatcaga ggaaaaggct       540
gcttcccctc ccaaacctct gctttcaaat gcctcggcaa ctccagttgg cagaagggggc       600
cgtctggcca atcttgccgc aactatttgc tcctgggaag atgatgtaaa tcactcattt       660
gcaaaacaaa acagtgtaca agaacagcct ggtaccgctt gtttatccaa attttcctct       720
gcaagtggag catctgctag gatcaatagc agcagtgtta agcaggaagc tacattctgt       780
tcccaaaggg atggcgatgc ctctttgaat aaagccctgt cctcaagtgc tgatgatgcg       840
tctttggtta atgcctcaat ttccagctct gtgaaagcta cttcttctcc agtgaaatct       900
actacatcta tcactgatgc taaaagttgt gagggacaaa atcctgagct acttccaaaa       960
actcctatta gtcctctgaa aacggggggta tcgaaaccaa ttgtgaagtc aactttatcc      1020
cagacagttc catccaaggg agaattaagt agagaaattt gtctgcaatc tcaatctaaa      1080
gacaaatcta cgacaccagg aggaacagga attaagcctt tcctggaacg ctttggagag      1140
cgttgtcaag aacatagcaa agaaagtcca gctcgtagca caccccacag aacccccatt      1200
attactccaa atacaaaggc catccaagaa agattattca agcaagacac atcttcatct      1260
actacccatt tagcacaaca gctcaagcag gaacgtcaaa aagaactagc atgtcttcgt      1320
ggccgatttg acaagggcaa tatatggagt gcagaaaaag gcggaaactc aaaaagcaaa      1380
caactagaaa ccaaacagga aactcactgt cagagcactc ccctcaaaaa acaccaaggt      1440
gtttcaaaaa ctcagtcact tccagtaaca gaaaaggtga ccgaaaacca gataccagcc      1500
aaaaattcca gtacagaacc taaaggtttc actgaatgcg aaatgacgaa atctagccct      1560
ttgaaaataa cattgttttt agaagaggac aaatccttaa aagtaacatc agacccaaag      1620
gttgagcaga aaattgaagt gatacgtgaa attgagatga gtgtggatga tgatgatatc      1680
aatagttcga aagtaattaa tgacctcttc agtgatgtcc tagaggaagg tgaactagat      1740
atggagaaga gccaagagga gatggatcaa gcattagcag aaagcagcga agaacaggaa      1800
gatgcactga atatctcctc aatgtcttta cttgcaccat ggcacaaac agttggtgtg       1860
gtaagtccag agagtttagt gtccacacct agactggaat tgaaagacac cagcagaagt      1920
gatgaaagtc caaaaccagg aaaattccaa agaactcgtg tccctcgagc tgaatctggt      1980
gatagccttg gttctgaaga tcgtgatctt ctttacagca ttgatgcata tagatctcaa      2040
agattcaaag aaacagaacg tccatcaata aagcaggtga ttgttcggaa ggaagatgtt      2100
acttcaaaac tggatgaaaa aaataatgcc tttccttgtc aagttaatat caaacagaaa      2160
atgcaggaac tcaataacga aataaatatg caacagacag tgatctatca agctagccag      2220
gctcttaact gctgtgttga tgaagaacat ggaaaagggt ccctagaaga agctgaagca      2280
gaaagacttc ttctaattgc aactgggaag agaacacttt tgattgatga attgaataaa      2340
ttgaagaacg aaggacctca gaggaagaat aaggctagtc cccaaagtga atttatgcca      2400
tccaaaggat cagttacttt gtcagaaatc cgcttgcctc taaaagcaga ttttgtctgc      2460
agtacggttc agaaaccaga tgcagcaaat tactattact taattatact aaaagcagga      2520
```

```
gctgaaaata tggtagccac accattagca agtacttcaa actctcttaa cggtgatgct     2580
ctgacattca ctactacatt tactctgcaa gatgtatcca atgactttga aataaatatt     2640
gaagtttaca gcttggtgca aaagaaagat ccctcaggcc ttgataagaa gaaaaaaaca     2700
tccaagtcca aggctattac tccaaagcga ctcctcacat ctataaccac aaaaagcaac     2760
attcattctt cagtcatggc cagtccagga ggtcttagtg ctgtgcgaac cagcaacttc     2820
gcccttgttg gatcttacac attatcattg tcttcagtag gaaatactaa gtttgttctg     2880
gacaaggtcc ccttttatc ttctttggaa ggtcatattt atttaaaaat aaaatgtcaa      2940
gtgaattcca gtgttgaaga aagaggtttt ctaaccatat ttgaagatgt tagtggtttt     3000
ggtgcctggc atcgaagatg gtgtgttctt tctgaaaact gtatatctta ttggacttat     3060
ccagatgatg agaaacgcaa gaatcccata ggaaggataa atctggctaa ttgtaccagt     3120
cgtcagatag aaccagccaa cagagaattt tgtgcaagac gcaacacttt tgaattaatt     3180
actgtccgac cacaaagaga agatgaccga gagactcttg tcagccaatg cagggacaca     3240
ctctgtgtta ccaagaactg gctgtctgca gatactaaag aagagcggga tctctggatg     3300
caaaaactca atcaagttct tgttgatatt cgcctctggc aacctgatgc ttgctacaaa     3360
cctattggaa agccttaa                                                   3378
```

```
        <210> 26
        <211> 3688
        <212> DNA
        <213> Homo sapiens


        <400> 26
aggtaggggg agtaatagga gaagctacga gagcgggaca cggtcaggta gatgtggaag      60
atcaagcagg agcagtttgc gtctatagaa aaaatcaaaa gtcatttaga tctgatagaa     120
gcattcgaga ttatgatttg gcaataatac tatagcatat agtccatatg tcataagtgt     180
aatttgtcaa agacttgcgt actgaggcat acaagcaaat atataagcca attttcagaa     240
gtaaaaattt agtcaccact aactttgaaa tattgtttca ttttagaaat tggctggtgg     300
aaaaaaatca aacatgaaga ttgcagtttt gtttgtttt tttctgctta tcattttca      360
aactgacttt ggaaaaaatg aagaaattcc taggaagcaa aggaggaaga tctaccacag     420
aaggttgagg aaaagttcaa cctcacacaa gcacagatca aacagacagc ttggaattca     480
gcaaacaaca gttttacac cagatagcaa gacttcctac tgttaacttt gattatagca     540
tggaggaaaa gtttgaatcc ttttcaagtt ttcctggagt agaatcaagc tataatgtgt     600
taccaggaaa gaagggacac ttgttgggaa aagggcttaa ccatgtacaa caaagctggg     660
ggggcggctt aagccctgca ctacctgcct ctgctcagat ggaagagttc tttgtgatga     720
aaccatgtgc catccccaga ggtgccccca aacagttata cctgaagggg aatgctgccc     780
ggtctgctcc gctactgtct cctattctct actcagtggt atagcattaa atgatagaaa     840
tgaatttttct ggtgattctt cagaacaaag agaacctacc aatttacttc ataagcaact     900
gccacctcct caggtgggaa tggaccgaat agtaagaaaa gaagcacttc aatctgagga     960
ggatgaagaa gtgaaagaag aagatacaga gcaaaagaga gagacccctg aatctagaaa    1020
tcaggggcaa cttttacagtg aggggagacag cagaggagga gacagaaagc agaggcctgg    1080
agaggagagg aggctggcac accagcaaca acgccaagga agggaggagg aggaggatga    1140
ggaggaggag ggtgaggagg gtgaggagga tgaggaggac gaggaggacc cggtaagagg    1200
agatatgttc cgaatgccct ctcgatcccc gcttctgct cctcccagag gcacactgcg    1260
cctgccaagc gggtgctctc tgtcctacag gaccatcagc tgcatcaacg ccaagcttac    1320
tgcaaatacc accgctgaca gcaccacaga taacaagtct gggagcctca cttggcaata    1380
tccatctgcc tccatctcca gatgaagcat ttatatggat taccaaattt ggaaagggct    1440
tgatctgagt aaaaataata tcactttctt tcaggcatag gtccaaaagc attcaagcgt    1500
tctgaagaag ttaatgcgtt tgaatatgga tggaaataat ttgatacaga ttccttcaca    1560
attgccatct acattagaag aacttaaagt caatgagaac aatcttcagg ctatcgatga    1620
aaaaaggtta ttcaaactta aatcagttgg tcaccttaga attggaagga aacaatctca    1680
gtgaagccaa tgtcaatcct ttagctttca aacctttgaa gagcctagcc tacttgcgtc    1740
tgggaaaaaa taaatttaga attataccgc agggtcttcc tggttctatt gaggaattat    1800
acctagaaaa taaccaaatt gaagaaataa ctgaaatttg tttcaatcat accagaaaga    1860
tcaatgtcat tgtactacgt tataacaaaa ttgaagaaaa taggattgct cctttagcct    1920
ggataaatca agaaaatcta gaatccattg atctctccta caacaagctc tatcacgtcc    1980
ccgtcctatc tacccaagtc cttgctgcac ctagtactcc ttgggaacca gattgaacgg    2040
atccctggct atgtgtttgg ccacatggaa ccaggcctgg aatacttgta cctgtcattt    2100
aacaagactt gctgatgatg gcatggaccc gtgtctcctt ctatgggca tatcattctc    2160
tgagagaatt atttctggga tcacaatgga cttaaaatct ataccacctg gggataccaa    2220
gaaatgaaag cactacattt tctgaggctg aacaacaaca agatacggga acattcttcc    2280
agaagaaatt tgcaatgctg aagaggatga tgactcaaat ctgggaacat cttcatcttg    2340
```

```
aaaacaattt atattaaaat taggggaaat accatcttac acattttcca tgcataagat    2400
catactccaa gtatcgttct taaaccacaa aacatcaagt aattccaagt tttcctttgc    2460
tgtttataaa ctttactcat gtatttgtag tagctgcatt tgtcattaat aagagagaca    2520
taatcctcct gttatactca gtatcattat atgctagtca acctgattca ctaacacaca    2580
gatgaacaac caaaatatac ctaaaaggta tagtctctag gagtttattt aatagtaaag    2640
gtaaaatctc tcagtttcct acctctagaa agaggccatc tcactagaat aggatattat    2700
gcatactgag ctagaccaga agagtctgga acaaaataaa cacagccttt ataatcaact    2760
tgaatactgg tgttagctga gaactctgta agtcccttta aaaattatgt atcttttggt    2820
tcaagattaa gaagcataat gacaacaaaa aaagcaggca gaatttatga ataagtgttg    2880
tttattatta aaacaataat ttgttaattt cttataaggt cctgtgctat aattactggt    2940
ataaatataa ctgaatattg gggtagcttt catttcttcc attaattaca tgtgtaaaat    3000
taaaacacta ctgtaatgtt aatttcctgg ttttggaaaa tcatattatg gttatgtaca    3060
ttgttaacat taaggaaagc tggcagaagg gtgtgcataa attctatact cttttttgaaa    3120
cttttctata attctaaaat tatttttttaa agttaaacag tatattaaga ttaccttcac    3180
tattcctcac tcaagattaa gacattttttt gaaaagcagt agagtttgct taaaatacaa    3240
attaattatt cttgactata accttgtaaa ggtaaatcta atgtataaat ttttgaaaaa    3300
ttttgcacca ctggtcatag catctatctc ctttgcctta atttactgaa atacatcatt    3360
ttattcggtt caattgaaat aaagctatgt ctttactatg tattggccct accaaaatca    3420
tatattaaaa ttttctaaca taatgatttt tatctttgta ttgctaaagt aatttataag    3480
acacatatag aaactatgtt gacttctttt gttactctca gttttatgtc ttggctagga    3540
acttaagtgc cagtgttggc ctcattgcat aggtttctct aatttttttaa gctttagtta    3600
tttaatcatt taatagttct ttcaccactc taggaacctt ccatccccac ttcacaaagc    3660
tattataaga actagaaaag aatgtaaa                                        3688
```

```
<210>  27
<211>  580
<212>  DNA
<213>  Homo sapiens


<400>  27
tcatgcttta gtcagttccc actctagcct tccctgcatg gctctctgcc taggagtgtc    60
ctccccattt cctgcttctt gaccatctag gtactcaggt cccagaattc tctgctcaaa    120
tgatggaagc ttgttcctgg gacctgggtt ctcattcctc aggtttgttc tctcatggac    180
agactgccct gtggcatgca tcattctttg gcctgaggat gtttctcttg caggtgggag    240
agtgggaaga gtctggacgt ggcagctgag gtatctgcag atgtacagag cttctgagag    300
tgcaaagtgg agcttgggag ggggagaaga gcagcaaaag ccttggctga gactgactca    360
tcaaggactg ccatgtcccc cagaggaagt ctcaggaatc cagacattct catcagatcc    420
ttgccttcca ggtggcttgg aagctcatgc tctaaagcaa gtcagtgcaa tcaactccag    480
aactagacca aaagacaaaa tcctggagca aaaacatagg ccctcattgg atcaaggaaa    540
acagctctca atgaaaaaag aaaagatccc tgttggtggg                          580
```

```
<210>  28
<211>  737
<212>  DNA
<213>  Homo sapiens


<400>  28
atgagtaggt ggggagcggc ggtggggcag ggcgcactgc gagaagagca cttcgcgcat    60
gcgcatatca ccgagcgaac gcgccgtgtt cgggaaggta ggagaaagag gcggagctcc    120
ttgttaacga catccccaac ctctgctaac gcgcaggcgc acttcctgaa gctgaaggtc    180
agcatagaca aagggcctca gaatcgcgca ggcgcaattg tgccctggtt cgccaagatg    240
tcgttcccaa agtataagcc gtgcgagcct gcgcactctg ccgtgagacc ctcgacccag    300
ccgaatacaa catatctccg gaaacccggc gggcgcaagc cggagcggtt ggcccatagg    360
agcccagctg caaacgagag tacactgctt cagtacaacg atcccaacac gccgagggct    420
catcgaaaat ccgtgccttg cttcgttggg cctatgcaag aacaataaat gtttattcct    480
aatttcaagc cccactccta aaagctcact catgggagct tttgtgtggg attttgggcc    540
cctcatcttc attttattat attatcaaaa ctgagaggga taggaaagaa aaacttatcc    600
acgggaggaa aattgggatc agagacattt tcacctactc atattaagtc tggcaatgat    660
```

```
gaccattatg aatcctgccc taaataaatc atctattaat cattaaaaaa aaaaaaagaa    720
aaaaagaaaa aaagtcg                                                   737
```

```
        <210> 29
        <211> 585
        <212> DNA
        <213> Homo sapiens


        <400> 29
atgcagttcc gcagggcacc attcatgtat tctgtgcgaa tggagcttgc aggagttcca    60
tgcgaattga catgtttct tccccaaggc atttgtttgt tgatggtacc agctgtcaaa    120
aaccaagcaa gtggcagtgc tagaggtgcc acaaaagtgc gaaggaagtg tcaggctgga    180
tgtcaaaatg aacaccttgg agaactggat gatggaacag acggtaaaaa tcagctaaac    240
atcagagaaa atggaggaag aggtcaaaac tgtgaacagg aactagaaga aagtgtagca    300
gaaaaagact tgtcacaaac ttcgagagat ttggagaaaa tgatgtcaaa acacatcttc    360
ctcaagccca tgctgagtat ctctgatttg gttaatttct tgatgcaagt ttccaaagtt    420
ctggtgaaaa cggctgaagg aatagtgtta cagcaactgc ccttggcttt tccagcttta    480
cacttccatg cctatggaaa tctcttccct gtctgtagct ttaagcatta catctatatg    540
atcgaccatc ccatcttcat ctccatccct gacttcctaa cttga                   585
```

```
        <210> 30
        <211> 2610
        <212> DNA
        <213> Homo sapiens


        <400> 30
ctctgcagaa tccccgggtc gacgatttcg taggatcact taaatgctca ggtacagtat    60
cgaaaccatt tagcatggtt accaggaatg gagggtgagc cgactctgtt taaaatctgc    120
agaaaacatt cagaatccaa aggaaagctt gtaagtaagt acttctccat ggagtgctta    180
atcgtggaag tggttttcat cacaggagag aggattgcaa tttctaaatc agtctccctg    240
catcatgaga atgcggagta tggcattcgc aggactgaat ccctagattt taagtttgga    300
aggagatcca accgggcaga tgaattgacc ggtggtgaat attctgtagc attttcctcc    360
ctggagagga atgccgccac cgctgggaac cgtggactgg catttcccag caggcatata    420
aatattggtc gttctcagag ctgggatgct gctgggtggt acgagggccc ctgggagaac    480
gccgagtccc tgcggcctct ggggaggaga agctccctga cgtatggcac agcagagggg    540
acttggtttg agccaaacca ccgaccacag gacgctgccc tgcccgtggc cgccgagccc    600
tacctgtacc gggaggccgt ttataactca gtggctgcaa gaaaggggtc tactcctgac    660
ttcaccttct acgacagcag acaggcagtg atgtctggtc gcagcccct gctgccacgg    720
gagtactaca gtgatccgtc tggagctgct agggtaccca agagcctcc cctctatcgg    780
gacccaggag tcagccggcc ggtccccagc tacggagtgc ttggcagcag aacgtcatgg    840
gatccaatgc aaggccggtc acctgccctg caggacgccg gtcacctgta ccgggatcct    900
ggaggtaaaa tgatccctca ggggcggcag acacagagca gggctgcatc tcccgggcgg    960
tatggacggg agcagcccga caccaggtat ggggcggagg tgcctgccta ccccctcagc    1020
caggtcttca gcgacatcag cgaaagaccc attgaccctg ccctgccag acaggtggcc    1080
ccgacgtgcc tggttgtgga ccccagttca gctgctgccc cgaaggcag cacagggtg    1140
gccccaggg ccctgaatcg tggctacggg cctgcccggg aaagcatccc atccaagatg    1200
gcttacgaga cttacgaagc tgacctgtcc accttccagg gtcctggtgg caagaggacc    1260
gtgctccctg agttcctggc ctttctgcgg gcggaggggc tggcagaggc cacgctggga    1320
gccctactg agcagggctt tgactccccg gccgtcctgg ctaccctgga ggacgcggat    1380
atcaagtctg tcgcacccaa cctgggccag gcccgtgttc tgagccgcct ggccaatagc    1440
tgcaggaccg aaatgcagct gcggaggcag gaccgggggg gcccgctgcc ccggcgcgcg    1500
tccagcagct tcagccaccg aagcgaactg ctccatggtg acttggcttc tctgggcgct    1560
gcggctcctc tgcagacagc atccccccga gctggagacc cggctcgccg tccctccagc    1620
gcaccatctc agcacctcct ggagacggca gccacctatt ctgccctgg cgtgggcacc    1680
catgccccac acttcccctc caactccggg tacagctctc ccaccccttg cgccctgaca    1740
gcgcgtctga gccccacgta ccccctgcag gcaggggtgg ccttgactaa cccgggcccc    1800
tcaaacccc ttcacccagg ccccagaaca gcctactcca cggcatacac ggtgcccatg    1860
gagctgctaa agagggagcg caacgtggcc gcctctccgc tgcccagccc tcacggcagc    1920
```

```
cccaggtct  tgcggaagcc  aggtgcaccc  ctggggccat  ccaccctgcc  gccggccagc    1980
cagagcctcc  acacgcctca  ctcaccgtac  cagaaggtgg  cccggcgcac  aggggcaccc    2040
atcatcgtgt  ccaccatgct  tgcaccagaa  ccaatccagt  ttgctggcca  agcagtccag    2100
agtgacaacg  tgaggaaggc  gtatgctgcg  gggacccccag  tgcggcccac  cagccccggt    2160
gacacagaca  aatgggggct  ccaggcccgc  gtgagtggca  gcacctggca  ggtggtgggg    2220
tcggctgtcg  ctctcaggct  gacctggccg  gctatggcac  aagtcgcgga  gccctccggc    2280
ggtggctgcg  agccagcaat  ctcccgtgt   cacgtgctgt  cacccgagcc  ctgcctgcac    2340
cagatgcagc  agggatcatc  agaaacaacg  aacgaatggg  gctgcggcca  ttttcatatc    2400
tttgtcttca  caaaatacag  ccaagcctgc  agcctgcaca  gggctcagct  caggacacac    2460
cctgtcacca  gagctggtca  ctctcatggc  ttcttttcgt  gtggcctcgg  tttccagcaa    2520
ctggaggtgt  gaacgctgat  ctcctaggta  gaaagcacct  ccatcaataa  ttttagccct    2580
atcagaatct  gtatagaggg  tcgccgccat                                        2610
```


```
          <210> 31
          <211> 797
          <212> DNA
          <213> Homo sapiens


          <400> 31
cccggaattt  ccgggtcgac  gatctcgtcg  gcttctcgga  agtaatttaa  gtgcacaaga      60
cattggtcaa  aatggtttcc  aaaagaagac  tgtcaaaatc  tgaggataaa  gagagcctga     120
cagaagatgc  ctccaaaacc  aggaagcaac  cacttccaa   aaagacaaag  aaatctcata     180
ttgctaatga  agttgaagaa  aatgacagca  tctttgtaaa  gcttcttaag  atatcaggaa     240
ttattcttaa  aacgggagag  agtcagaatc  aactagctgt  ggatcaaata  gctttccaaa     300
agaagctctt  tcagaccctg  aggagacacc  cttcctatcc  cacaataata  gaagaatttg     360
ttagtggcct  ggagtcttac  attgaggatg  aagacagtct  caggaactgc  cttttgtctt     420
gtgagcgtct  gcaggatgag  gaagccagta  tgggtgcatc  ttattctaag  agtctcatca     480
aactgcttct  ggggattgac  atactgcagc  ctgccattat  caaaacctta  tttgagaagt     540
tgccagaata  tttttttgaa  aacaagaaca  gtgatgaaat  caacatacct  cgactcattg     600
tcagtcaact  aaaatggctt  gacagagttg  tggatggcaa  ggacctcacc  accaagatca     660
tgcagctgat  cagtattgct  ccagagaacc  tgcagcatga  catcatcacc  agcctacctg     720
agatcctagg  ggattcccag  cacgctgatg  tggggaaaga  actcaggtgg  ataaaccctc     780
tgtcatcatc  taagtga                                                       797
```


```
          <210> 32
          <211> 5933
          <212> DNA
          <213> Homo sapiens


          <400> 32
gacgcgcctg  agccggagtt  tcagataaca  taaagtaacg  tgtaggaatt  caggtgactc      60
acacatggtg  gagagaagac  cttatctgga  tgccaggccc  aggaattccc  ataccaacca     120
cagaggccct  gtggatggag  agttaccacc  aagagctaga  aatcaggcca  ataacccacc     180
agccaatgct  ctccgaggtg  gagccagcca  ccctggaagt  gatcctaggg  ccaacaacca     240
tcctgctgct  tactgtcaga  gggaagagag  atttagggcc  atgggctgga  acccacatca     300
aggaagtgag  gaacaggagt  ggcatgtctg  cgacgaagct  agagaccaaa  gacattgcca     360
ggggaatgac  accaggtgga  gaaatggcaa  ccaggactgt  aggaaccgca  gaccaccatg     420
gtccaatgac  aacttccagc  agtggcggac  tccccaccag  aagcctacag  aacagccaca     480
gcaggcgaag  aaactgggct  acaagttctt  agaaagtctt  ctgcagaaag  acccttctga     540
ggtggtcatc  acacttgcca  caagtttagg  gctgaaagct  ctcctttctc  attcttccat     600
gaaatctaac  ttccttgagc  tcatctgtca  ggttcttcgg  aaggcttgta  gctccaaaat     660
ggatcgccag  agtgttctcc  atgtactggg  catattgaaa  aactccaaat  ttctcaaagt     720
ctgcctgcct  gcttatgtgg  tagggatgat  cactgaaccc  atccctgaca  tccgaaacca     780
gtatccagag  cacataagca  acatcatctc  cctcctccag  gaccttgtaa  gtgtcttccc     840
tgccagctct  gtgcaggaaa  cttccatgct  ggtttcccct  ctgccaacct  ctcttaatgc     900
tctgagagcc  tctggtgttg  acatagaaga  gggaaacggag  aagaacctgg  aaaaggtaca     960
gactatcatt  gaacatctgc  aggaaaagag  gcgagagggc  actttgagag  tggataccta    1020
cactctagtg  caagcagagg  aacgaggacg  catgttgaga  gctacgctga  ccatgcccag    1080
```

```
atacccctacc  tacactgaag  cgcacttggg  tgaagaggcc  cttccttcgc  cccaatatca  1140
tttctggaaa   atacgacagc  actgctatct  atctggatac  ccacttccgg  cttctgggag  1200
aagatttcgt   cagacctta   cgggaaggta  ttttggaact  tctccaaagc  tttgaagacc  1260
agggcctgag   gaagagaaag  tttgatgaca  tccgaatcta  ctttgacacc  aggattatca  1320
cccccatgtg   ttcatcatca  ggcatagtct  acaaggtgca  gtttgacaca  aaaccactga  1380
agtttgttcg   ctggcagaat  tccaaacgat  tgctctatgg  gtctttggta  tgcatgtcca  1440
aggacaactt   cgagacattt  cttttgcca   ccgtatctaa  cagggagcag  gaagatctct  1500
gccgaggaat   tgtccagctc  tgcttcaatg  agcaaagcca  acagctgcta  gcagaggtcc  ·1560
agccctctga   ctctttcctc  atggtagaga  caactgcata  ctttgaggcc  tacaggcacg  1620
tcctggaagg   actccaggag  gtccaggagg  aagatgttcc  cttccagagg  aatatcgtgg  1680
agtgtaactc   tcatgtgaag  gagccaaggt  acttgctaat  ggggggcaga  tatgactta   1740
cccccttaat   agagaatcct  tcagccactg  gggaatttct  aagaaatgtc  gagggtttga  1800
gacatcccag   aattaatgtc  ttagatcctg  gccagtggcc  ctcaaaagaa  gccctgaagc  1860
tggatgactc   ccagatggaa  gccttgcagt  ttgctctcac  aagggaactg  gctattattc  1920
aaggacctcc   tggaacaggc  aaaacctatg  tgggtctaaa  aattgttcag  gccctcctaa  1980
ccaacgagtc   tgtttggcaa  attagcctcc  agaagttccc  catcttggtt  gtgtgttata  2040
ctaatcatgc   tttggaccag  tttctggaag  gcatctacaa  ttgtcagaag  accagcattg  2100
tgcgggtggg   tggaaggagc  aacagtgaaa  tcctgaagca  gttcacccta  agggagctga  2160
ggaacaagcg   ggaattccgc  cgcaacctcc  ccatgcacct  ccgaagggcc  tacatgagta  2220
tcatgacaca   gatgaaggag  tcagagcaag  agcttcatga  aggagccaag  accctggagt  2280
gcaccatgcg   tggtgtccta  cgggaacagt  acctgcagaa  gtacatctca  ctccagcact  2340
gggaaagtct   catgaatgga  ccagtgcagg  atagtgaatg  gatttgcttc  cagcactgga  2400
agcattccat   gatgctggag  tggcttaggt  cttggtgtcg  gttctttcac  gcaaagtgtt  2460
tctccagcag   gacctgagaa  tacagcccag  gcagaagggg  atgaggagga  agaaggggag  2520
gaggagagtt   cgctgataga  gatcgcagag  gaagctgacc  tgattcaagc  agaccgggtg  2580
attgaggagg   aagaggtggt  gaggccccag  cggcggaaga  aggaagagag  tggagcagac  2640
caggagttgg   ctaaaatgct  tctggccatg  aggctagacc  actgtggcac  tgggacagca  2700
gctggacagg   agcaagccac  aggagagtgg  cagacccagc  gcaaccagaa  aaagaaaatg  2760
aaaaaaagag   tgaaggatga  gcttcgcaaa  ctgaacacca  tgactgcagc  cgaggccaac  2820
gagatcgagg   atgtttggca  cctggacctc  agttctcgct  ggcagcttta  taggctctgg  2880
ctacagttgt   accggctga   caccgccgg   aagatcctca  gctatgaacg  ccagtaccgc  2940
acatcagcag   aaagaatggc  cgagctgaga  ctccaggaag  acctgcacat  tcttaaagat  3000
gcccaggttg   taggaatgac  aaccacaggt  gctgccaaat  accgccagat  cctacagaag  3060
gtggagccga   ggattgtcat  agtggaacaa  gctgcggaag  tccttgacgc  ccataccatt  3120
gccacattga   gcaaaagctt  gccagcacct  cattttgatt  gcggaccacc  agcagctgcg  3180
ccccagtgcc   aacgtgtatg  atctggccaa  gaacttcaac  cttgaggtgt  cccttttttga  3240
acggctagtg   aaagtaaaca  ttccctttgt  ccgtctgaat  taccagcacc  gtatgtgccc  3300
tgaaattgcc   cgccttttga  cccccacat   ttaccaggat  ctggagaatc  atccatctgt  3360
tcttaagtat   gagaagatta  aggggggtgtc  ttccaacctt  ttctttgtag  aacacaactt  3420
tcctgaacag   gaaatccaag  aggcgcaaaa  gccatcagaa  ccagcatgag  gctcacaatg  3480
tggtagagct   gtgcaagtac  ttcctgtgcc  aggaatacct  gccttcccag  atcaccatcc  3540
tcactaccta   taccgggcag  ctcttctgcc  tgcgcaaact  gatgcctgcc  aagacatttg  3600
ctggcgtcag   ggtccatgtt  gtggacaaat  accaagggga  agagaatgac  atcatcctcc  3660
tctcgctagt   gcggagcaac  caagaaggca  aggtgggttt  tctgcagata  tccaaccgca  3720 ·
tctgtgtggc   cttgtcccga  gccaagaagg  gaatgtactg  catcggaaac  atgcagatgc  3780
tggccaaggt   gcccctgtgg  agcaagatca  ttcatacact  tcgagagaac  aatcaaatag  3840
gccccatgct   ccggctctgc  tgccagaacc  accctgaaac  ccacacctta  gtatccaaag  3900
cttctgactt   ccaaaaagta  cccgaaggag  gctgcagcct  gccctgcgag  ttccgcctgg  3960
gctgtgggca   tgtctgcacc  cgtgcctgcc  acccttatga  ctcttcacac  aaggagttcc  4020
aatgcatgaa   gccatgccag  aaggtcatct  gtcaggaagg  gcaccggtgt  cccccttgttt  4080
gcttccagga   gtgtcagcct  tgtcaggtga  aggtgcccaa  aaccattcct  cggtgcggcc  4140
atgaacaaat   ggtcccttgt  tccgtgcctg  agtcagattt  ctgctgccag  gagccttgct  4200
ccaagtctct   gagatgtggg  cacagatgca  gccacccatg  tggtgaggac  tgtgtgcagc  4260
tgtgttcaga   aataaaactca  ataaaactca  agtgtgggcc  cagttaaacc  ggtaaaatgt  4320
ggttatgtgg   aaggcctcct  gtatggtggt  gtggtagtca  agtgtacaca  caagtgtggc  4380
actatcttgg   actgcgggca  tccttgccca  ggctcctgcc  acagctgctt  cgaagggcgt  4440
ttccatgaac   gctgtcatca  gccagtgcta  gcgcctgctt  atctgctcac  acaagtgccc  4500
agaaaccatg   cattggtgag  tgcccaccct  gccagcggac  ctgtcagaac  cgctgtgtcc  4560
acagccagtg   caagaagaaa  tgtgaggagc  tgtgtagtcc  ctgcgtggaa  cccatgtgct  4620
cgcgctgcca   gcactaccag  tgcaccaaac  tctgctctga  gccctgcaac  cgacccccat  4680
gctatgtgcc   ttgtactaag  ctgctagttt  gtggccaccc  ctgcattggt  ctctgtgggg  4740
agccatgccc   caagaaatgc  cggatctgcc  acatggatga  ggtcacccaa  atattctttg  4800
gctttgagga   tgagcctgat  gcccgctttg  tgcagctgga  agactgcagc  cacaattttt  4860
gaggtgcaag   ccctagaccg  ctacatgaat  gaacagaagg  atgatgaagt  cgccatcaga  4920
```

```
ttgaaagtct gccctatctg ccaggtgccc atccgcaaaa acctgagtta tggaactagc    4980
ataaaacagc ggctagagga gattgaaatc atcgaggaaa agtatccagg gctcatcagg    5040
ggaaatggca accagccagg aacggcttaa ggccctgctg gagaggaaga gcctcctcca    5100
ccagctgctt cctgaagact tcctgatgtt aaaggagaag ctggcccaga aaatctgtc     5160
agtgaaggac ctgggtctgg ttgagaatta catcagcttc tatgaccacc tggccagcct    5220
gtgggattcc ctgaaaaaga tgcatgtctt agaagagaaa agagtgagga ctcgactaga    5280
acaggtccat gagtggctgg ccaagaagcg cttgagcttc actagccagg aactaagtga    5340
cctccgaagt gaaatccaga ggctcacata cctggtgaac cttctgaccc gctacaaagat   5400
agcagagaag aaggtgaaag atagcatagc agtagaggtc tatagtgtcc agaatatcct    5460
tgagaaaaca tgtaagttca cccaagagga tgaacaactt gtgcaggaaa agatggaagc    5520
tctgaaagcc acccttccct gctctggcct gggcatctca gaggaagagc gagtgcagat    5580
tgtcagtgcc ataggttatc ctcgtggtca ctggttcaag tgccgcaatg gccatatcta    5640
tgtgattggc gattgtgggg gagccatgga gaggggcacg tgtcctgact gtaaggaagt    5700
gattggtggc acaaatcata ctctggaaag aagcaaccag cttgcttctg aaatggatgg    5760
agcccagcat gctgcctggt ctgacacggc caacaacctg atgaactttg aggagatcca    5820
ggggatgatg taggaagatg gtacacccct gccttttgcc ctcgccactg aatgcctggg    5880
gccagctccc taatgaagga actgaagttt gttttttatt atcatccttt tta           5933
```

```
        <210> 33
        <211> 2607
        <212> DNA
        <213> Homo sapiens


        <400> 33
        ggaattcgcc ggtcgcgcgc ccgccagcct gccgcctggg ctgggggtca cgaaaggaaa      60
        ccttacagaa acatgaagcc ctcaaccatc tgctactcag ttattcgggg ctgacggcgg     120
        cttctagaac atccaggtgt tctgcagatg cgagaactca tcctgtagtc accagatgga     180
        gtcccaaaca gccaagcaga tgtaaggcct gtgctgtggc tctgaggccc tgaatacaga     240
        agggtcactt tcttagtggc caaagagcag ttgttgacat tgatgtctaa ttattgaaca     300
        cgaccagtca tttttactgag ctgcggtgag gaaacactga cccatataag atcaagccca     360
        atgagggatt ggcaattttcc ctgattcttt tgaattaaga ttccagatgg gggcctcatt     420
        tctacagccc ccaacattcc tatagccgtt atcactgcca tcaccactgc caccagcatc     480
        ttcttgcaga ttccacccct gctccccaga gacttcctgc tttgaaagtg agcagaaagg     540
        aagctctcag aaaaatctct agtggtggct gccgtcgctc caggacaatc ggaatcctgc     600
        cttcaccacc atgggctggc ttttttctaaa ggttttggtg gcgggagaga gtttctcagg     660
        acttctttat cctcttgtgg attttttgcat cagcgggaaa acaagaggac agaagccaaa     720
        ctttgtgatt atttttggccg atgacatggg gtgggggtgac ctgggagcaa actgggcaga     780
        aacaaaggac actgccaacc ttgataatat ggcttcggag ggaatgaggt ttgtggattt     840
        ccatgcagct gcctccacct gctcaccctc ccgggcttcc ttgctcaccg gccggcttgg     900
        ccttcgcaat ggagtcacac gcaactttgc agtcacttct gtgggaggcc ttccgctcaa     960
        cgagaccacc ttggcagagg tgctgcagca ggcgggttac gtcactggga taataggcaa    1020
        atggcatctt ggacaccacg gctcttatca gccccgcgtt ccgtggtctt gattactact    1080
        ttggaatccc atatagccat gatatgggct gtactgatac tccaggctgc aaccaccctc    1140
        cttgtccagc gtgtccacag ggtgatggac catcaaggaa ccttcaaaga gactgttaca    1200
        ctgacgtggc cctccctctt tatgaaaacc tcaacattgt ggagcagccg gtgaacttga    1260
        gcagccttgc ccagaagtat gctgagaaag caacccagtt catccagcgt gcaagcacca    1320
        gcgggaggcc cttcctgctc tatgtggctc tggcccacat gcacgtgccc ttacctgtga    1380
        ctcaactacc agcagcgcca cggggcagaa aagcctgtat ggtgcagggc tctgggagat    1440
        ggacagtctg gtgggccaga tcaaggacaa agttgaccac acagtgaagg aaaacacatt    1500
        cctctggttt acaggagaca atggcccgtg ggctcagaag tgtgagctag cgggcagtgt    1560
        gggtcccttc actggatttt ggcaaactcg tcaagggtga agttcagcca agcagacgac    1620
        ctgggaagga gggcaccggg tcccagcact ggcttactgg cctggcagag ttccagttaa    1680
        tgtcaccagc actgccttgt taagcgtgct ggacattttt ccgactgtgg tagccctggc    1740
        ccaggccagc ttacctcaag gacggcgctt tgatggtgtg gacgtctccg aggtgctctt    1800
        tggccggtca cagcctgggc acaggtgct gttccacccc aacagcgggg cagctggaga    1860
        gtttggagcc ctgcagactg tccgcctgga gcgttacaag gccttctaca ttaccggtgg    1920
        agccagggcg tgtgatggga gcacggggcc tgagctgcag cataagtttc tctgatttt     1980
        caacctggaa gacgataccg cagaagctgt gcccctagaa agaggtggtg cggagtacca    2040
        ggctgtgctg cccgaggtca gaaaggttct tgcagacgtc ctccaagaca ttgccaacga    2100
        caacatctcc agcgcagatt acactcagga cccttcagta actccctgct gtaatcccta    2160
        ccaaattgcc tgccgctgtc aagccgcata acagaccaat ttttattcca cgaggaggag    2220
```

```
tacctggaaa ttaggcaagt ttgcttccaa atttcatttt taccctcttt acaaacacac      2280
gctttagttt agtcttggag tttagttttg gagttagcct tgcatatccc ttctgtatcc      2340
tgtccctcct ccacgccgac ccgagagcag ctgagctgcg ctggctctgg gcagggagtg      2400
tgccttaatg ggaagcacac gggctttgga gtcaggcaca ggtgccagct ccagcttttg      2460
aacttgggca attgtttaac ctaacctgca agttgatttt gagggttaaa taaaggcata      2520
catgaaaatg cctggcaaat tacctgacac agagcagaca ttcaatacat tttagtttcc      2580
ttgtttctct ggttcccagt ttctctg                                         2607
```

```
        <210> 34
        <211> 1120
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 34
cccgttgcta cgacgatttc gcagcccctg agtctggagg ctgacatgtg gagcataggc       60
gtcatcacct acatcctctt aagtggagca tcccctttcc tgggagacac gaagcaggaa      120
acactggcaa atatcacagc agtgagttac gactttgatg aggaattctt cagcgcagac      180
gagcgagctg gcccaggact ttattcggaa gcttctgggt taagagaccc ggaaacgggt      240
cacaatccaa gaggctctca gacacccctg gatcacgtca aaaggagaag gcagagcccc      300
tgaacagcgg aagacagagc ccacccagct gaagaccaag cacctgagag agtacactct      360
caaatgccac tcaagcatgc ctcccaacaa ctgctatgtc aacttcgagc gttttgcctg      420
tgtggtggaa gacgtggctc gggtcgacct gggatgccgt gccctggtgg aggcccacga      480
taccatccag gacgatgtgg aggccctggt ctccatcttc aatgagaagg aagcttggta      540
ccgagaggag aatgagagcg cccggcatga cctgtcccag ctcaggtatg agttccgcaa      600
ggtggagtca ttgaagaagc tgctgcgaga agacatccag gccacgggat gtagcctcgg      660
aagcatggcc aggaaactgg accatctgca agcccagttt gagattctga ggcaggagct      720
ctccgcagac ctgcagtgga ttcaggagct ggtgggcagc ttccagctgg agagtgggag      780
ctctgagggc ctgggctcca cattctacca ggacaccagt gaatccctgt cagagctgct      840
cagcagatca tgcactgagg aatttctggc aggctggaag ctctaatcgc cagaatccag      900
tcagtgatgc atcccaagag gtttgcagaa gcatgttctc atccaccctg ctgcggcctc      960
cagctagaat tatcctgcag gggtgtgtgt ctgtagtata gccttccagc ccctccacag     1020
aatccagaat tgctgaggtg ccagttaatt cttcattctg cacctcccct caccaatctg     1080
gtttctggg agggctctgg cagggcagcc aaactgtatt                            1120
```

```
        <210> 35
        <211> 264
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 35
cttttggaat tctatttgca aagggtgtgg aggagaaagt gtagggtggt gttgctatct       60
tgagagcatg ggaaataccc ttgaactgct gaaagcaggt acctatggtg ccagttttca      120
gtgtggagaa ggatggagag gagctcggta gcttcaggcc acgctgggcc gattggctga      180
ctggattact ggagtggggtt tcagtagaga gcctttctat ctattgcatt tctcaacctg      240
tttatatgtg ggtggaataa ggct                                            264
```

```
        <210> 36
        <211> 836
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 36
gagccctccg tggcagtgct tgggtgtccg ggctccgaga ctccggcctg acctctccat       60
ggggtcgaaa ggacggtctc tggatgccag gagtcgcgga gggcggacca gcatgaggaa      120
accattggcg gaaaatggca gaagcagtgc ggcatcccag cctcaactgc cgggacggtg      180
```

```
ttcaagagac attggtgggg taaacataca aaaatgtgat tgcctcactc aaccaagagc   240
cttagccata attaaaagat gttcagatgg agctgtacag gaatgtgatg ctggagaact   300
agagcaacag agccacatta gcacaagcag gcccaccgcg gtctcacaca cactcgagcc   360
ttcctttgcc cagtctcaca tgcatgactg ggatcgcgga tttcgtcccc ttccgactcc   420
ccatgctggt tcggtcccag acgctcaggt gccacattgg ggtgcgctct cccggctcct   480
ccacacgcta cgcagctgcc cgcctcaaga gcgtctgcgt gcttccagcg ttaagtggaa   540
ttccaagcag cctccggggc acagttagtc tggtcactgc ggccagactg ccgcctcagg   600
acccagagaa cgcagcacac tttagttggg cccatctatc cccggcgagg cttggactac   660
gtttcccagg agaccctgcg gtccaaagag tggctccccg gggtggggag atgatttgga   720
cccctgtggg ttggagccag ccccccactt ctccgaggct tcaggaacta caagcaaaac   780
aaaggacgtg gggccccgca gcccaagcgg agccacagag tgaggagcat cagaag        836
```

```
        <210> 37
        <211> 2834
        <212> DNA
        <213> Homo sapiens


        <400> 37
atgatcagcg ccctgacgt agtggccttc accaaagagg aagagtatga agaagagcct   60
tacaatgagc cggccctgcc tgaggagtac tcggtgccgc tcttcccctt cgccaagtca   120
aggtgctaac ccctggtcaa aaactgtccc gggccaagtt ttcgaaggac ttcattctta   180
attccgaagt ctctgaacaa ggggggaacc ccaccccttac tgaccaatcc caatggacac   240
ccaaagtttt gggcactttt gaatctcaat taacttcttc cttggcgtat catgtctgtg   300
gattaccagg cttccttcgt gggccatcct cctggatctg cctaccccaa gctgaacttc   360
gtggaggact ccaaggtggt gctgggagat tctaaggagg cgcctttgc atacgtgcac   420
caccttaccc tatacgacct ggaggcccgt ggcttcgtga ggccgttttg catggcttat   480
atctctgcag accagcataa aatcatgcag cagttccagg agctttcagc cgaattttcc   540
agagcttctg agtgcttgaa gactggcaac aggaaggcat ttgctgggga acttgaaaaa   600
aagctgaaag acttggatta caccaggaca gtgctacaca cagaaacgga gatccagaag   660
aaagccaacg acaaaggctt ttactcatct caggcaattg agaaagccaa tgaactggcc   720
agtgtggaga agtccatcat tgaacatcaa gacctgctga agcagatccg ctcataccct   780
catcggaagt tgaaggggca tgatttgtgt cctggtgaga tggagcacat ccaggatcag   840
gccagccagg catccactac ctctaaccct gatgagtctg ccgacacaga ccttttacacc   900
tgcagaccag cctacacccc aaaaacttatc aaagcaaagt ccaccaagtg ttttgacaag   960
aagttgaaga ccttggagga gctctgtgac actgaatatt tcacccagac cctggctcag   1020
ctcagccaca ttgaacacat gttcagagga gacctgtgtt acctcctgac cagtcagatt   1080
gatagagcac ttctaaaaca acagcatata acaaactttc tctttgaaga ctttgtggag   1140
gtcgatgaca ggatggtgga gaaacaagaa agcataccct ctaagcccag tcaagacagg   1200
ccgccttcca gttctctaga agaatgccca attcctaaag tgttaattag tgttggttct   1260
tacaagtcca gtgtgagtc tgtgttgatc aagatggagc aggaactggg agatgaggag   1320
tacaaggaag tggaagtgac tgagttgagc agtttcgacc cccaggaaaa cttggactac   1380
ctggatatgg atatgaaagg gagtatcagc agtggtgaaa gtattgaagt tttgggcacg   1440
gagaaatcca cctccgtgct ttctaaatct gacagccagg caagcctcac agtaccattg   1500
agcccccagg tggtccggag caaagcagtc agccacagga ccatcagcga ggacagtatt   1560
gaagtcctca gtacctagcc cctctgaggc cctcatccat gatgactta aggccagcta   1620
cccaagtgcc attaatgaag aagaatcata tccagatggc aatgaacgag ccatccactt   1680
ccaggcaagc atcagtcctc cagaactggg tgagacagag gaaggcagca tagaatacac   1740
cccatcacaa atagactcct gctgctgtat tgggaaggag agcgatggtc agttggtgct   1800
gccctccact ccagcccaca cacactctga cgaggatggt gtggtgagca gccccccaca   1860
gcgccacagg cagaacgacc aggggttccg tgtagacttt tcagtggaaa atgccaaccc   1920
ttcttcccga gacaacagtt gtgaagggtt tcccgcttat gagctggacc cgagccacct   1980
gctggctagc cgggacatca gtaagaccag cctggacaac tactcagaca ccaccagcta   2040
cgtgagcagt gtagcgtcca ccagctcaga caggatcccc tctgcttatc ctgctggcct   2100
gtcttccgat aggcataaaa agagggctgg ccagaacgcc ttaaaattca tccgccagta   2160
cccctttgcc cacccagcca tctactccct gctcagtggg aggacacttg tggtcctggg   2220
ggaagatgag gccatagtca ggaaactcgt gactgcactg gctatctttg tccccagcta   2280
tggctgctac gctaagcccg tgaaacattg ggcctcctcc cctttgcaca ttatggattt   2340
tcagaagtgg aagcttattg gcttgcagag agtggcctcc cctgccggtg ccggtaccct   2400
ccatgccctg agccgctaca gccgctacac gagcatcctg gaccttgaca caaaaaccct   2460
gcgctgcccc ctttacagag gcacccggt gccccgcctg gcagaccacc gcacacagat   2520
caagcggggc agcacctact acctgcatgt ccagagcatg ctcacccagc tctgctccaa   2580
```

```
ggccttcctc tacaccttct gccaccacct gcacctgcct acccacgaca aggagacaga      2640
ggagctggta gccagccgcc agatgagctt cctaaagctg accctgggtc tggtgaatga      2700
ggatgttagg gtggtccagt acctggctga gctgctgaag ctgcactaca tgcaggaatc      2760
tccagggacc agccacccca tgctcaggtt tgactatgtc cccagctttt tgtataaaat      2820
ctgaggtcgg tccc                                                       2834
```

```
        <210> 38
        <211> 909
        <212> DNA
        <213> Homo sapiens


        <400> 38
gctaattgaa caagccccaa ttcaaatggg agaagaggca gtgaggtggg caaaactggt       60
cataccttta gtggttcatt cagcacaaaa ggtacatttg cggggagcaa ctgctctgga      120
gatgggaatg ccattattgc ttcagaaaca gcaagaaata gcatctatta cggagcagct      180
tatgactact accttgcatc gaagtgggag tttcatcaat tctctcttgc aactagaaga      240
acttggattt cgtagtggag cacccatgat taaaaagata gcttttattg cttggaagag      300
tttaatagat aattttgctt taaatccaga tatactatgt agtgcaaaaa gactcaagtt      360
gttaatgcag cctttgagtt ccatccatgt gagaacagaa actctagcat taacaaaact      420
agaagtctgg tggtatttac tgatgagact tggacctcat cttcctgcta attttgaaca      480
gggttgtgtg cctctgattc aaagtacaat aggcattgat tctaatgcct aacctcaggg      540
caattcgtgt catgtagcta catctccagg tttaaatcct atgactcctg tacacaaagg      600
tgcttcctcc ccgtacggag ccccgggaac tccccgaatg aacctgagtt cgaatttagg      660
tggaatggcc acaatcccat ccattcaact tttgggactt gaaatgttgc ttcatttctt      720
gttgggtcca gaagccttga gttttgctaa gcaaataaaa cttgtgctga gcttagagcc      780
attggaacat ccgttaatca gcagcccttc ctttttttcc aaacatgcaa atacacttat      840
cactgctgtt catgatagct ttgttgcagt tggaaaagat gcccccggta agagaatttg      900
atttattat                                                             909
```

```
        <210> 39
        <211> 1468
        <212> DNA
        <213> Homo sapiens


        <400> 39
aggaagaaat cagaaaaatt cgagatctct caaatcagga agaacagtac aatcgattca       60
tgaaattggt tggtggcaag aggagatcaa gaagtaaatc ttcagatcct gacctgaggc      120
gatccttaga taagcaacct actgatagtg gaggaggcat ttatcagtat gataactatg      180
aagaagttgc tatggataca gatagtgaaa ccagttctcc agctccttca ccagtgcaac      240
cgccattttt ctctgaatgt tcattggggt attttttctcc agcaccatct ctttctttgc      300
ctccaccacc tcaggtttct tctctgccac ctttgagcca gccttatgtg gaaggcttgt      360
gtgtttctct tgaacctcta cctcctctac caccattacc acctctccca cctgaagatc      420
cagaacagcc tccaaaacca ccttttgcag atgaggaaga ggaggaagaa atgctgcttc      480
gagaagaact acttaaatct ctagcaaata aagagctttt aagccagag cttccaaagc      540
ataaatcagt ggttgtaaca ctaaatgatt cagatgatag tgaatctgat ggagaggctt      600
ccaagtcaac aaatagtgtt tttggtggat tagagtccat gattaaagaa gcaagacgaa      660
ctgctgagca agcttcaaaa ccgaaagtac ctccaaaatc tgaaaaagaa aatgatcctc      720
tgcgaacacc ggaggctttg cctgaagaaa agaagattga atatagattg ttaaaaggaa      780
gagattgcca atttaagttt attcttgggt gtaatgcata tatcctttta gataatttta      840
gccgtgagaa acagcgtttg attaaatcag atcagctgaa gacaagttca tcatccccag      900
caaactctga tgtggaaatt gatggtattg gcaggatagc aatggttact aagcaggtta      960
cagatgcaga atcaaaactg aaaaaacata ggattctctt gatgaaagat gaatctgttt     1020
taaagaattt agtgcaacaa gaagctaaga agaaagaatc tgttagaaat gctgaagcaa     1080
agattacaaa acttacagaa cagcttcaag caactgaaaa aattcttaat gttaacagaa     1140
tgtttttgaa gaagcttcag gaacaaattc acagagttca acagcgtgtt acaattaaga     1200
aagctttgac tctaaaatat ggagaagagc ttgctcgggc aaaggcagtg gccagtaaag     1260
aaataggaaa acgtaaactg gaacaagatc gctttggggt gagggtttta tagaaatatt     1320
ttactttttgg aaagcagaaa gtttttatga tagtttttaag ggtaagatgt atatataaag     1380
```

28

```
taactctttg ctgtaaattc caagagatta agattaaagc tttgtttta aatgacatcc    1440
acatttttgg atgtctactt tattaaaa                                      1468
```

```
        <210> 40
        <211> 602
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 40
gtcttctcct tcctgccacc ttgtgaagaa gataaaaata aaaatgaagt caccagccct    60
caggggtctg tcaaggcaac acacaaaatc tccagttacc ttctggtgga tgacgtttgg   120
agacacatcg cgtccgtcac aggacacact tccgatggat ttacagcaac tcctgggggt   180
cacgaaggtg tgttccaagg ccacatctcc aacctcacag agaggacagg aagtgatcag   240
taccccaact agcaagagtg gcccgttcat tggccgaggt tcttgaggat agagtgggag   300
gtgggagcgt ccctcgtgct gccttcattt ttcctaccct cagctcaggg gtctgtgcta   360
gaggaagaca cacgaaggct actgtgcccc caccacaaga gagggaaaca gggagacgcg   420
tgggtctgga gccaagcgta tctctctgta cccatcgcac acgaatttga atcatctgct   480
ctttggaatc gcctacaccc tgctgcaccc acgatgtggc tgtaactcca ttaaagaatt   540
gaatatcatc ttccacggaa tctctgtctg cacaaaaggg gcacatttaa ttttctgttt   600
tt                                                                 602
```

```
        <210> 41
        <211> 789
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 41
tttttttttt ttagctgggg aaagggtgat caccttatat tgataataag acgtccttgg    60
gcggctacag ggagaaggaa gagacagatt aaaccttttt gaatgttaat ttggaaggcg   120
ttgatcctgg agtgaaggtc caagatccct ccagggatgg ggcccttcc gaccgtcatc   180
tcggtggtca ggagcacccg ataaagtcct tcccaggtta gctgagtttt tcctctttcc   240
aacttctgac aaggaggtga tccccaggct ggtgtcggtg aattccttga cgaacgcttc   300
ggccgtgcgt agactggtca gcttccgggg tgacttagag cagggctgtg gtcactttca   360
ctggcatctg ggtcctgtcc gtaggatcag ccggtttgga tggtctgggt cttgctggca   420
tggtccactt gtcctgggct gctgggtttc aagccgactg tggagatcga aggcacagtt   480
ccgtggtcgc ccgcgggaac ttcaagggtc cttcctaccc gcgttgctga gagtctgggt   540
ttacgcgtca cctcgggcgg gacccgatcc tccgctcctg aggcccccac aatgaagcag   600
tcggacgcgt ctccccaaga aaggtacccg ccagcctctc ctgaaacaga atgggatcca   660
aatgggatat ttgggggcgg cgagtcggtc ccgcaaagag aaaccagcac ttagaaaatt   720
tctcagcgag accactttac ttgtacgcaa ggcggctgcc tgcgtgggat gcaatctcca   780
gagcacacg                                                         789
```

```
        <210> 42
        <211> 806
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 42
cgccgcggaa ttcccgggtg gaccatctat gaccttgttt acgtgcagcc ctaaaaagaa    60
tcccctatag tagagttgct ttaatggcca tgtgcaggac cgccgttctg aatgagccca   120
ccagcggggt ggacccttgc tcccgtcata gcctgtggga cattctgctg aagtaccgag   180
aaggtcgtac gatcatattc acatcccgcc atctgcatta ctctgatccg ctgagtgacc   240
gcgtgcccgt gctccagcat gtgaggctca cgcgctgcgt gcctcccttg tgcctgaagg   300
aggcatatgg ccagggactc cgcctgacac tcacgaggca gccttctgtt ctgtaggccc   360
atgagctgaa cgacatggct tgtgtgacat ccctgatgaa gagctatatt ccacacgcat   420
```

```
tgctcaaaga cagcagtgga agtgatctga cctacaccat tccaaaggac acagacaagg    480
cctgcttgaa agggctcttc caggccctgg atgagaacct gcatcagctg cacctgacgg    540
gctatgggat ctcagacacc accttagaag aggcagaagg gaggaccgca gcacctgagc    600
ctcccatgct ggaggacggc cacgcggtca ctcagcgctt cagcttcatc caggtggtgg    660
gttgtgaaga tgatcgtacg acctgggtcc aagcacaggg tgcatcagca ccaggaggac    720
aaaggcccca ggaggacctt ccctcctttc ctcaggatgg tagatccagg gcacaattta    780
aagatcctca ccaattttca aactga                                         806
```


```
        <210> 43
        <211> 1597
        <212> DNA
        <213> Homo sapiens


        <400> 43
atggcttctc atgcttatga taaaaatcaa aatgccaatg tcttagtcca cttgtgcttc     60
tataacagaa tacccaagac tggagcatat tacctagatt ctaggagtgt gagcatcagt    120
tatttgattg gccatcatat agacatgggt cttgagacag ccacttccaa aaatgaattc    180
attttcgata gtgcaagtac actgctgggg atgcttttta ggaaaccctc ccaacactct    240
ctctcccttt ttagcaagaa attccaggag aatctgatat acctggaatc tgatgactgc    300
ttgccacctc ctccccctcc accttggtct gagccaccgt catttctcac ctggactatc    360
gtcacagttt tccagtgggt ctccctgctt ctgtccttgc ccaacataca ggtcattctt    420
tacagagcag ttggagtagt accttcacaa cctaagtcag acaacctgaa aggatgggga    480
tcggggagag tcgttaaaga gaagctcaga tcagagatac ctgactggaa gattaaaagt    540
attcacatac tggagaggac tgcttcctct agcaccgagc cctctgtaag tcggcaattg    600
ctagaaccgg agccagtccc cctctccaag gaagctgaca gctgggaaat tatagaaggg    660
ctgaaaatag gccaaaccaa tgtccagaaa ccagacaaac atgagggctt tatgctgaag    720
aaaagaaaat ggcctttaaa aggctggcac aagattcaga aggaaaggt ccatgggagc    780
atagatgtgg gactctcagt catgtcaatt aaaaagaaag ctcgaagaat agaccttgac    840
accgaagagc acatctatca tttgaaggtg aaatcagttt tcaacagttt ctctgccatt    900
atcaggggaa acgatttgcc tacaccagtg gtgaaatccc aggactggtt tgatgcatgg    960
gtctccaaac tgcgacatca tcggttgtat cgtcagaatg aaattgtgag atcaccaaga   1020
gatgctagtt ttcacatatt tccttcaacg tccacagctg aatcctcacc agctgctaat   1080
gtttctgtaa tggatggaaa gatgcaacca aacagctttc cgtggcagtc cccttttacca   1140
tgcagcaata gcctccctgc aacgtgcaca actggccaga gtaaagtggc agcctggtta   1200
caggactcgg aagagatgga caggtgtgca gaagatcttg cacattgcca gtcaaacctt   1260
gtggaactta gcaaactcct gcaaaatttg gaaatacttc agagaactca gtcggcacct   1320
aactttactg acatgcaggc taactgtgta gatatttcaa agaaagacaa gcgggtcaca   1380
agacgatgga gaacaaaaag tgtcagcaaa gatacaaaaa tacaactgca ggttcctttc   1440
agtgctacca tgtcaccagt tcgcttgcat tcctccaacc ccaacctttg tgcagatatt   1500
gaatttcaga ctccccctag ccacctcact gaccctctgg aaagttcaac agattataca   1560
aagctgcaag aagaattttg tctaatcgca cagaaag                            1597
```


```
        <210> 44
        <211> 1827
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(1827)
        <223> n = a,t,c or g


        <400> 44
agctgttcag gtgttcgtgc tgaccaggta ccaggtcaaa gcttccagag aggaccgtca     60
ggggccagtc tttttaagat tgtggctgat aaaactccat accttactat ggaagaaatc    120
acaaggacca ttcatattgg accaagtaga ctaggcatc cttgcttcta tcatcagaag     180
gatataaaac tagagaacct catcataaag cagggtgagc aaatcatgct caactcagtt    240
gaagagattg atggagaaat aatggtgagc tgtgcagtag caaggaatca tcaaactcac    300
```

```
tcatttaatt tgcctttgtc acaagaagga gaattctacg agtgtgaaga tgaacgtatt      360
tacactctaa aggagattgt tgaatggaag attcctaaga acagaacaag aactgtaaac      420
cttacagatt tttcaaataa gtgggactca acgaatccat ttcctaaaga cttttatggt      480
accctgattc tcaagcctgt ttatgaaatt caaggtgtga tgaaatttcg aaaagatata      540
atccgcatcc tccccagtct agaatgtcaa gtcaaagaca tcactgattc ttacgatgct      600
aactggtttc ttcagctgtt atcaacagaa gatctttttg aaatgactag taaagagttc      660
ccgcataggg actgaagtca tagaaccacc tgaaggaaac cacctgcccc aaagcatttt      720
acagcctggg aaaaccattg tgatccacaa aaagcaccag gcatcaagaa tcttaacttc      780
agaaattaga agcaattttc ctaaaagatca cttcttgatc cccactagct ataaaggcaa      840
gttcaagcgg cgaccgaggg agttcccaac ggcctatgac ctagagatcg ctaagagtga      900
aaaggagcct cttcacgtgg tggccaccaa acgcgtttcat tcccctcatg acaagctgtc      960
atccgtatct gttggggacc agtttctggt gcatcagtca gagacgactg aagtcctctg     1020
tgagggaata aaaaaagtgg tgaatgttct ggcctgtgaa aaaatcctca aaaagtccta     1080
tgaggctgcg ctgctccctt tgtacatgga aggaggtttt gtagaggtga ttcatgataa     1140
gaaacagtac ccgatttctg agctctgtaa acagttccgt ttgcccttca atgtgaaggt     1200
gtctgtcagg gatctttcca ttgaagagga cgtgttggct gccacaccag gactgcagtt     1260
ggaggaggac attacagact cttacctact cataagtgac tttgccaacc ccacggagtg     1320
ctgggaaatt cctgtgggcc gcttgaatat gactgttcag ttagttagta atttctctag     1380
ggatgcagaa ccatttctag tcaggactct ggtagaagag atcactgaag agcaatatta     1440
catgatgcgg agatatgaaa gctcagcctc acatccccca cctcgccctc cgaaacaccc     1500
ctcagtagag gaaacaaagt taaccctgct aaccttagca gaagaaagga cggtagacct     1560
gcccaagtct cccaagcgtc atcacgtaga cataaccaag aaacttcacc caaatcaagc     1620
tggcctggnn nnnnnnnnnn nnnnnnnnnn nnnnnnngat ttggtggatg aagagaaaga     1680
taggagcaac cgtggggcca cagcattagc agaaacattc aacaatgata aacatcataa     1740
atatcaagat gtgacagaag ccacttaggc agcatacata aatgttgcag tgaaaaaaga     1800
tgctagcctt ctagctgaca aacgagg                                         1827
```

<210> 45
<211> 2435
<212> DNA
<213> Homo sapiens

<400> 45
```
atgtttgcgt ttgaacctct tggcggggtgc cggccatggc ggctctcgct cccgggacct       60
gggagccggc tttttccgcac atatggggct gcggacggca ggagacagcg gcggccgggc      120
cgggaagccg cgcagtggtt cccgccgcag gaccggaggc gtttcttcaa cagcagcggc      180
agcagcgacg ccagcatcgg cgacccctcg cagtccgacg atcctgacga tcccgacgac      240
cccgacttcc ccggcagccc ggtgaggcgg cggcgaaggt gtcccggcgg ccgagtgccc      300
aaggaccggc ccagcctgac cgtgaccccca aagcgctgga agctgcgagc tcgcccaagc      360
ctaaccgtga ccccaagacg cctggggctg cgagctcggc ccccgcagaa gtgcagcaca      420
ccctgtggcc cgctccgact tccgcccttc cccagccgcg actccggccg cctcagcccg      480
gacctcagcg tgtgcggcca gcccagggac ggcgacgagc tgggcatcag tgcctccctg      540
ttcagctctc tggcctcgcc ctgccccggg tccccaacgc caagggacag tgtcatctcg      600
atcggcacct ccgcctgtct ggttgcagcc tcagccgtcc cgagcggcct ccacctccca      660
gaagtctccc tggaccgagc atctctcccc tgctcccagg aggaagcgac aggaggagcc      720
aaggacacca ggatggtcca ccaaacccgc gccagcctca ggtcagttct ctttggcctt      780
atgaactcag gaacccctga ggattctgag tttcgggcag atgggaagaa tatgagagag      840
tcctgctgta aaaggaaact ggtggtggga aatggaccag agggtccagg tctgtcaagc      900
acaggcaaga ggagggccac aggccaggac tcttgtcaag agagagggct tcaagaggcc      960
gtccggagag agcatcagga ggccagtgtt cccaagggcc gcattgtgcc aaggggaata     1020
gacaggctgg agagaactag atcaagccgg aagagcaaac atcaggaggc aacggaaacc     1080
tctctcctcc attcccaccg ctttaaaaag ggccaaaagc tgggaaaaga ttcgttcccc     1140
acccaggacc tgactccttt acagaatgcc tgcttttgga ccaaaaccag ggcttccttc     1200
agtttccaca agaagaaaat tgtgactgat gtgtcagagg tctgcagcat ctataccact     1260
gccacttctc tctctggatc cctcctatca gaatgttcaa accggcctgt catgaacaga     1320
acaagtggtg ctccgtcctc ttggcactcc tcctctatgt atttgctaag cccccttaaac     1380
actctaagta tttcaaacaa aaaggcatct gatgctgaaa aggtttatgg ggaatgcagt     1440
cagaagggtc ctgtcccctt tagccattgc cttcccacag aaaaactgca acgctgtgag     1500
aagattgggg aaggggtgtt tggcggaagt gtttcaaaca attgctgatc acacacccgt     1560
agccataaaa atcattgcta ttgaggacc agatttagtc aatggatccc atcagaaaac     1620
ctttgaggaa atcctgccag agatcatcat ctccaaagag ttgagcctct tatccggtga     1680
```

```
agtgtgcaac cgcacagaag gctttatcgg gctgaactca gtgcactgtg tccagggatc    1740
ttaccctccc ttgctcctca aagcctggga tcactataat tcaaccaaag gctctgcaaa    1800
tgaccggcct gattttttta aagacgacca gctcttcatt gtgctggaat ttgagtttgg    1860
agggattgac ttagagcaaa tgcgaaccaa gttgtcttcc ttggctactg caaagagcat    1920
tctacaccag ctcacagcct ccctcgcagt ggcagaggca tcactgcgct ttgagcaccg    1980
agacttacac tgggggaacg tgctcttaaa gaaaaccagc ctcaaaaaaa ctccactaca    2040
ccctcaatgg gaagagcagc actatcccca gctgtggggtt gcaagtgagc atcattgact    2100
acaccctgtc gcgcttggaa cgggatggga ttgtggtttt ctgtgacgtt tccatggatg    2160
aggacctgtt taccggctacc ggtgactacc agtttgacat ctacaggctc atgaagaagg    2220
agaataacaa ccgctggggt gaatatcacc cttatagtaa tgtgctctgg ttacattacc    2280
tgacagacaa gatgctgaaa caaatgacct tcaagactaa atgtaacact cctgccatga    2340
agcaaattaa gagaaaaatc caggagttcc acaggacaat gctgaacttc agctctgcca    2400
ctgacttgct ctgccagcac agtctgtttta agtaa                              2435
```

```
        <210> 46
        <211> 786
        <212> DNA
        <213> Homo sapiens


        <400> 46
ctcggctgac tccaaggaag tccagggcaa cgtgattgtc catggccact tgtgttggtg      60
cattccgaac aaacagtctg ctgcctggct gcacaggtct gaccagtgtg gtcatgggtg     120
ggtgacgatg taacaaggtg cattctggct gctgtttttcc agccccagat ccttcttcct     180
cctctcggtc ccaggtggct tccagagtca tcccgctggc tcctcctgca tggcaagtcc     240
cagttagctg tacagaatct gcagaaggtg gctgcaatga acgggaggaa ggaggaaggg     300
gaaaggctga ccaaggaggt gatgagctcc tacatccaaa gcgagtttgc aagtgtctgc     360
acctccaact caatcttgga cctcttccga accccggcca tccgcaaggt cacatgctgt     420
ctcatggtga tttggagaat ggccccacct gcaggcagag agctccggat agctgccgag     480
tcactttctc agcaaaaacg ggcttttgct gtttccagaa ggatccaaga gaggactttc     540
agctctggaa ttttgaactc aggatctgtt tctccctcgc ggaaagagga aggtggacga     600
agggcaagcc caggccggca ggggctaccg caggaagacg cccattcctg gactcgggtt     660
cgcaggagcc cccttgctcc ccagagccgg aactgcgctg cctgccacgc tcggctgact     720
ccaaggaagt ccagggcaac gtgattgtcc atggccactt gtgttggtgc attccgaaca     780
aacagt                                                              786
```

```
        <210> 47
        <211> 749
        <212> DNA
        <213> Homo sapiens


        <400> 47
ggggagaatc gatgacatta ggccactgga ggccattagc gagtgagctg agctgcgcgg      60
cgcggcgcgg cgcggcacgg cacggtggga gtgtctccgg ctggcctgca gggagaacac     120
cgactgagac ctctaaccct ggctccagtg gcatgtgata accagtcgtt ctgctcagtg     180
gtgggggtgg tatttgccga gccagaatgt gtgtgctgtt ttaggaatcc gtcaccttttg     240
aggatgtggc cgtggagttc atccaggagt gggcattgct ggacagcgca cggaggagcc     300
tgtgcaaata caggatgctt gaccagtgca ggaccctggc ctccagggga actccaccat     360
gcaaacccag ttgtgtctcc cagctggggc aaagagcaga gccaaaggca acagaacgag     420
ggattctccg tgccacatgt gttgctggg aatctcaact aaacccgaa gagttgcctt     480
ctatgcagga tcttttggaa gaagcatcct ccaggacat gcaaatgggg ccggggctgt     540
tcctgaggat gcagctggtg ccctccatag aagagaggga gacaccattg actcgagagg     600
accggccagc tctccaggag ccgccttggt ctctgggatg cacgggactg aaggccgcta     660
tgcagattca gaggtggtg ataccagtgc ctactctggg ccaccgcaac ccatgggtgg     720
ccagggattc tggtgccatt ggaaatggg                                       749
```

```
        <210> 48
```

```
<211> 1622
<212> DNA
<213> Homo sapiens


<400> 48
tttcgtaaag aacaagacag aactatctct gtttctggct ccactgcctg ccagtgaagg      60
agttttcatt cagactttcc gaagagaggt ggagaaatct aaagactgag gagaagagat     120
cctttgagcc agatggggca ttagttcttc tgcttttctc agcatggata aaccatttcc     180
tcaaggattt tctcatgtgc cctgaaatcc atgtaactac aagggctcct ctttatcacc     240
ataagtgcca ccctgactta aaaccactca gagctaaaaa atcaaggcaa aatggatgct     300
gcggtgacag atgattttca acaaattctg cctattgaac agctgcgctc tactcatgct     360
agcaatgact acgtggaacg gcctccagcc ccctgtaaac aggccctctc cagcccttcc     420
cttattgtgc aaacccacaa gtctgattgg tctctggcta ccatgcctac ttctcttccc     480
cgcagtctca gccagtgcca tcaactgcag cccttgcctc agcatctgag ccaatctagc     540
attgccagct caatgtccca tagcaccact gcctctgatc aaaggctctt ggccagcatt     600
acaccctcac cttcaggcca atccatcatc cgaacccaac ctggagcagg ggtccaccca     660
aaggctgatg gtgctctgaa gggagaagct gagcaatctg cagggcaccc tagtgagcac     720
ctcttcatct gtgaggaatg tgggcgctgc aagtgcgtcc cctgcacagc agctcgccct     780
ctcccctcct gctggctgtg caaccagcgc tgcctttgct ctgctgagag cctcctcgat.     840
tatggcactt gtctctgctg tgtcaagggc ctcttctacc actgctccac tgatgatgaa     900
gacaactgtg ctgatgagcc ctgctcttgt gggcctagtt cttgctttgt ccgctgggca     960
gccatgagcc tcatctccct cttcctaccc tgcctgtgct gctacctgcc tacccgtgga    1020
tgcctccatc tgtgccaaca gggctatgat agcctccggc gaccaggctg ccgctgcaag    1080
aggcacacca acactgtgtg cagaaagatc tcttctggta gtgcaccctt ccccaaggcc    1140
caggaaaagt ctgtatgacc ttccaacaag gtggatccag agctttttctc cttctagtcc    1200
ccaacagcaa agcataggcc tcatctttgg agaggggggag gagtgataaa ctagccaaag    1260
ttagggcctc tcttttgttc ctgcagtgtc aggggaatga ccaagtacat cctggtgcag    1320
gatgccttgt tctttctcac agtatctatc ccactcctct tcagtcttta caccctgcca    1380
gctcagccct ttatggttgt catgcaaaat tcaggtgata tatgggtatg aggtttgaac    1440
actgaggact gacagggcca gcaacgtgga ggtttagggg ctccccaatg taatacctct    1500
cgatgcaggc tctgatcgtc actctgtttt ctgctgtgcc tttggaagct ttcttctaag    1560
atggttttca caggtacatg tggaacagcg ttcaaccttc cagggaatac gacccctgaa    1620
tt                                                                    1622
```

```
<210> 49
<211> 1219
<212> DNA
<213> Homo sapiens


<400> 49
gcgttaccgc gccgcgaatg cccgggtcga cgatttcgtg ccacccgaac agggagtaaa      60
tagtgctttg tatctttaag gaagcccttt tttaaattta aaaaaaaagt cttaattata     120
agactcttta aatgcccaac tgcatacttg gagctttggg actgaatttg gaactttcct     180
gtcaagcgac ctcccacgac tttactgctg agcctgtgca cgtgtgtgta aggggagaaa     240
tccaggcatc tagatgcaga cttgtaccca gttacttggg gtcgcgtgcg ctcacctggg     300
acctgggctc gtgcgcttag tccggagccc tgatctgcga acaggatatt aaaactttta     360
gtacaattga ttggactact tgaaccatcg ggatttgggg aggaactcca gattttttcat     420
ttttaaactc taaatgtatg aggaatttac agaatggaga acgaaaagga aaatctcttt     480
tgtgagccac ataaaagggg actaatgaaa acacctctga aagaatccac cacagcaaat     540
atcgtgttgg cagagatcca gcctgacttt ggccctttaa ccacacctac caagcccaag     600
gaaggctctc agggagagcc gtggacaccg acagccaacc tgaaaatgct catcagtgct     660
gtgagccctg agatccgcaa cagagatcag aaaaggggtt tgtttgacaa cagaagtgga     720
ttacctgagg ccaaagactg tatacacgaa cacttatctg gagatgaatt tgagaaatcc     780
caaccaagtc gaaaagagaa aagtttagga ttattgtgtc ataagttctt agcacgatat     840
cctaattatc ccaaccctgc tgtgaataat gacatctgcc ttgacgaagt ggcagaggaa     900
cttaatgttg aacgtcgacg catttacgat atcgtgaacg tcctagagag tttacatatg     960
gtgagccgcc tcgccaaaaa caggtacact tggcacgggc gacacaatct caacaaaacc    1020
cttggcacct tgaagagcat cggggaggag aataagtacg ccgagcagat tatgatgatc    1080
aaaagaaag aatatgagca agagtttgac tttattaaga gttacagtat agaggatcat    1140
atcatcaaat caaacactgg cccaaatgga cacccagaca tgtgtttttgt ggaactccct    1200
```

ggagtggaat ttcgggcag   1219

        <210> 50
        <211> 1241
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(1241)
        <223> n = a,t,c or g

        <400> 50
gcaccgtccc gcaattcccg ggtcgacgat ttcgtaggaa agaatagggc acaggtgggg   60
atggatggtt ggttggatat gtcacttttc ttatggtaaa caattaaatc ccatattctc   120
tctgccttaa aagaagaaat taatgttttg tagtcctagg taattgatgt tttgcccatg   180
atttcccaaa cttgtgtcag tcccacgtta cacgcaaact aaattttagg tttgaaattt   240
gtccctagtt aattggtctg cttgacaatt ttgtgagtct tattaacccc aatcaataga   300
gttgagagac tatggcttta aaaaattaat gcaaacctgg gctttagctg taataacacc   360
cacctaggaa taaattaata ttaccataag gaaaatgtga tactttctga tcttgttttt   420
aaagttgaaa tgcaacaaac ttttcttgc tgtatataaa tattctggca tagtattaat   480
aaggcatagc ttttcaggaa attgtccaca aaagggtttt attctctttg gcttgtggac   540
tatttttcat tgaagcatgc gcttacctat gctgattctt actaaaagca taggctgggg   600
tatttattgg cgaaaggaaa tgtgtagtgt gggctggact gttggtggag gctggctttt   660
tagcccactt gctatacatg ctgccaatgg atttaagacc tgaaaatggt gaaagttgag   720
tgggattatt tccctcctga cacacttaat ttacagtact cctctctacc ccttaggttg   780
ggctctgcct cagaggagtg agtttttttt tttttctat aaagtttaca ttgtcttact   840
atttattgag ttgaattttt ggtcatggcc tatgcaaata taagaaatcg ggctttaaat   900
attagtcagt tttcatggct atgactagat tgttttcttg tataactaaa tacctgtata   960
aaatgaacta atgttttttc tcccctccct aacccttcc ttatgaacaa tgctttaggt   1020
gtattgaaat ctttaagacc agtagagctg aagttagaac tcattatgtt ccaccgcgaa   1080
agcttatggc catgcagcgg ccgggtcccc atcacagcct tggaaatggt cgaggctatt   1140
ngagctttgg cagaggaaat gatattaaaa agatgagggt tgncgcggcc gcgaattcca   1200
gatctgtgtc ctcgtagatn ctaaaaacgc cagtattttg t   1241

        <210> 51
        <211> 811
        <212> DNA
        <213> Homo sapiens

        <400> 51
ggagcctggg gccagagggc cagacagcca cagagctcct ggcgtgggca aggctggcca   60
aggatggcga cgcccagggg cctgtttggc cctgctcctg ctcctcctgc tcccgacctc   120
aggtcaggaa aagcccaccg aagggccaag aaacacctgc ctggggagca acaacatgta   180
cgacatcttc aacttgaatg acaaggcttt gtgcttcacc aagtgcaggc agtcgggcag   240
cgactcctgc aatgtggaaa acttgcagag atactggcta aactacgagg cccatctgat   300
gaaggaaggt ttgacgcaga aggtgaacac gcctttcctg aaggctttgg tccagaacct   360
cagcaccaac actgcagaag acttctatct ctctctggag ccctctcagg ttccgaggca   420
cgtgatgaag gacgaggaca gccccctga cagagtgcga cttcccaaga gcctttttcg   480
atccctgcca ggcaacaggt ctgtggtccg cttggccgtc accattctgg acattggtcc   540
agggactctc ttcaagggcc cccggctcgg cctgggagat ggcagcggcg tgttgaacaa   600
tcgcctggtg ggtttgagtg tgggacaaat gcatgtcacc aagctggctg agcctctgga   660
gatcgtcttc tctcaccagc gaccgccccc taagcccaca atgcattccg agatcactag   720
ctctatattc aaccgcatca gcatgacgtg tactacgtac tactactctt ccaccaggta   780
taagtacaac aacattattc ataaagattg a   811

                                        34

```
<210> 52
<211> 688
<212> DNA
<213> Homo sapiens


<400> 52
ccttcaaagc ccaaactcag cctcctctgg ggtgacttcc tgactggtca ctgccatggg      60
acccacctcc tctatccagt cattcagcta atacccaagg agcacctact gcataaggac     120
ctgggttacc tgcagcagtg gctgaaggcc tttgtaggtg ccttcaagaa gagcatctca     180
ctgtcctctc tggagccacg aaggccagag gaggcaggtg cagaggtccc gctgctacca     240
ctggatgagc tgcatgtgct ggccgaacat gctgaaccat ggtgaactgg agcaagccct     300
cctgctgctc aagctcttga tcatgctctg cacgaacctg gagagcatac aggcgggacg     360
gcgccaagtg ctagagcacc gagtgctgtc gctgtggacc agatacctgg cggagctgaa     420
aggatgccca ccaccccagg gccgaggcac gcagttggag aatgtggccc tacatgctct     480
gcttctctgc gagggcctct ttgacccctta ccaaacctgg cggcgccagc gcagtgggga     540
agtcatcagc tccaaggaga agagcaaata caagttccct cctgctgctt tgccccagga     600
attcagcgcc ttcttccaag gtcaggcccc gcccctgccc ccacttggct ccacccccaa     660
acctaggccc cttcctgtcg ttccttga                                        688



<210> 53
<211> 323
<212> DNA
<213> Homo sapiens


<400> 53
gtgcgattca tctttctgtc tctaggtctt agcatgtgca cggcacagag caggcgctca      60
gagtgccttc agtgaaggaa taaatgacca taccaccagg cacagagtga ggcctttaga     120
aaccctgagc atcatcgggt gcgcccacca cttctgtatg tgactcaaag taagtgtaag     180
gaaatccagt tctgtttttgt ttctgaaata ctagatgtca ggaagggtgt ttaggtgtca     240
ggctttggtg gcctacactg tgctttcgga attattcact gaggcgaaag aacagagatt     300
agctactgat gaaggacaaa aag                                             323



<210> 54
<211> 339
<212> DNA
<213> Homo sapiens


<400> 54
gtgcgattca tctttctgtc tctagttctt agcatgtgca cggcacagag caggcgctca      60
gagtgccttc agtgaaggaa taaatgacca taccaccagg cacagagtga ggcctttaga     120
aaccctgagc atcatcgggt gcgcccacca cttctgtatg tgactcaaag taagtgtaag     180
gaaatccagt tctgttttgt ttctgaaata ctagatgtca ggaagggtgt ttaggtgtca     240
ggctttggtg gcctacactg tgctttcgga attattcact gaggcgaaag aacagagatt     300
agctactgat gaaggacaaa aagaattttc tgctgaatc                            339



<210> 55
<211> 1187
<212> DNA
<213> Homo sapiens


<400> 55
ggaggcaggg ggccgggcag taacacttgc ttgcccactg ctcacgtctg atgggtgccc      60
ccattcgtca cgaggctatg gaccagtacc catctgcagc ccagggttgg ggaccccac     120
catacatgct ctgaaaataa gtgtctttaa gttgtgtttt tctgtgtgac atcatctctg     180
```

```
aacttgaaca tgttcattac ggcaagattg taatcctgct gtattcctcg ccctccgtat    240
tctatccctt taaaaactag atatttaaac attttatcct aatgtgtttc atcagaacac    300
tttgcacact ttcttactaa aacggtatgt gggtggtccg agacagaatg gtacctacag    360
tgcaggctat gtttctgtgg gaatggaaaa gaggacttta gaaagtgaac ctgaagaact    420
cttatttcta agggaatcca gtcaagcttg agaaaatgaa atattcttgt gtgtagtgat    480
tcagtctcag gatattgaag tcctttttaa acgtccagtg ttctcctgta agaatacaat    540
ataaattaat ggcaagcttg cgccaggtgc ctgcccctcc taagcacttt acacgcacag    600
ctcattcaac ctcacgtgtc gggagcatca gggagctcac cagtctcttg aggatcacag    660
gccaattgct tgtccttccc gacccaagcc ccacccaca gtgacttgct ctcttctgat    720
tttacaggtt ttttggcagt aatacacatg ggagtgaaat tgaaaacctc cctattattt    780
tccctctttt cctggaaagc tgttttttgc cctcacaatc attcattact tctctaacta    840
gggggaagta ctacaagctg tcctcaggta ctgcccctac gtgtgtttcc ctgggatggg    900
gccttgctag aggtgattct gctgccccag cattgggaag caggaccagt gcatgtgccc    960
catgcagcca cggtacatgg aagctgtcac ttgagccatc agaccggctc agcccatgtg    1020
accggagctc tgaagaggca cacacgcatg ccccgcacag gctgttagca cttgtcgcct    1080
cgctgccctg gtccagacta cccttgcttg cgtcagtcaa aactgttgta actactttga    1140
gtctttctg catgattgct ctttgagaga actttacaag ggtgttt                   1187
```

```
        <210> 56
        <211> 327
        <212> DNA
        <213> Homo sapiens


        <400> 56
ccctgccggc ttcgtgacct ggaggagtca cagaactacc ctgagcctca ggtgagaaaa    60
ctggggctca ggaaggcagt gagaaactgg aagtcagcca cgtgtcagga caggagcctg    120
gatttagccc acatctttgg ctttggtttt gcacacagct gctgctggga ctggggcca    180
gggcaggcag aaataatcct gggctctgca gagcctgttt caggctcatg tctacccta    240
ccccgccccc atttccggca aaaccaggct gagggctggg ctgctagcga agctgacagc    300
aagagtgaca gccctgtcct gtcgctg                                        327
```

```
        <210> 57
        <211> 1471
        <212> DNA
        <213> Homo sapiens


        <400> 57
gaaaggccac gtggttgact tattcctaga ccctccactc aaagtactca gctaggaagt    60
tagaatttga agagaaatcc aggtccacag aaactgcctt ctcattggcc actgttgtct    120
cttccctttc aggtgctcct cgcctgcttg cagatatcag accccagctc atctcagacc    180
tcagcccctg aggccaagca aacatacatc atcatggagg ctgcagacgt agctcaccgt    240
gcccacatgt cccagaaggc agggggcttt cgcaacattg caatccaaac ttccccagt    300
ctcaggaagc atttcccagt tttcaaaagg aagagactca cagccagtaa gtccctggtg    360
gaaatgccaa cagcctccca aagtgccatc caggtcaacg gtaacctctc tgaacaggac    420
attgtgtctt ctgaccttgc ctacttaagg ttggctcagc atcttgagga tgggcctcga    480
agggtcaagg tgtcccatgc attcctccca agggtcccca aggtgcaaag caatggtcct    540
gttagcatat gcttggaagc aggaacttgg aggtccttag agaaagccac agctgccatt    600
caggttccag atgatattta tcacagtcct tcctgggaag ctagagagtc tgctctcagc    660
ccagacaggt cagctgaagt aagtaactcc atacacctt tggatgacac acgtccaggt    720
gatgggagaa gggtgactcc actagattca gaaaaatcca cctcctgctt aaatgccacc    780
agcgttgcca gccacacacc aggcacagag gaacttaaac ctgaattgct tttgcccaaa    840
gacaactcag atgacaaaga ccttggctca ctgtcatctc agtcaaagga aacgtgtgtt    900
ccttcatctc cacggactca cagttccccc tcacaaggct cccacagcca gccagcccac    960
ccaggaagag cctcagactg tccttcatca agtaacaatc accagaatct ggtgtcactc    1020
aaaactaaca gtgcatcgaa atctgcccct gggtgtcagg agcagacggc aaacaacccc    1080
accgagtcag acacactgga gtttccaaat tgtccaggaa gtaatcatct cccatcctct    1140
ctttcaagga gtgagaccaa acttcagagc aacagggaga ttagtgacat taatcaaatt    1200
cacctggcac ggggtgaact ctgcgacctc caaggccgac tgcaatctgt ggaggaatct    1260
```

```
ctgcactcga accaagagaa aattaaagtc cttttgaatg taattcaaga cttggagaaa   1320
gctcgagctc tcactgaagg cctccttggc tctcctctta ccattgaaca cttggataca   1380
tcctatctca ccaagagcac agacccaaca ccaatgccta gagattctat ccatggctct   1440
caggagcttg cagggatttc cgtacataaa g                                  1471
```

```
        <210> 58
        <211> 811
        <212> DNA
        <213> Homo sapiens


        <400> 58
atggacagtc aagaagtaga gaaatacccc aacacttctg tagcttgtga ggaaatcccc   60
ttttcaggaa tccatgttgc tggtgggaaa tcaggagcat tagaacatgg aaaggatgac   120
cttgatgaac ccattgaaaa tcccctcttt tgtttctcaa gctttagcaa tgcacttgca   180
atattgcttc caaaagtgtt ccttaagaat attcatatac tgcaattcat ctacaggagt   240
tttcaccttt tgacaatggc aaaagcaaag tttgaaggtg ctgagtctgt ggagccagtg   300
tcaccttcac agcccaaaag gccatcctat gtccccctag aagagctatg acgaggtta   360
acaaaaggga acagcaggcc tcagcagagg gacaggagaa agggaggatg gatgaaggga   420
gtgcagcaag gccatcaagg agtaggaaag caggaggaag gttcagagaa catcaaagaa   480
aaagctggta actggggaga tgggcggagg tggggaagaa atcagcaggt tttgattaat   540
aagattactt ttaagcaaac tagcttgaat tatacatcca acttagtctt tcctgaagaa   600
agctatttta gcaatgcgta ttccttgagt tggactcata ttgtcctaca tcattgtgaa   660
attcatttac ggaaggttaa gattggatgc cttcttaggg aaacgaacct aaaagtccgc   720
catgcactat cagttacttc agaacttgga gcagatatca gcagacttgc agggtttgat   780
gaggcatata aacttacaag tattggctct g                                  811
```

```
        <210> 59
        <211> 593
        <212> DNA
        <213> Homo sapiens


        <400> 59
attcccgggt cgacgatttc gtctccttcc cccttccgga agctatagac acttccgaga   60
gagcgcgaac ttgcggagca ctttgcatgc gcgccgcggg taggactgga cggtcggatt   120
tgtaggcaat tctgacaccg agctcccggg ctcggttggc agaagatcgc tttgggaatc   180
ctcctactct acgaggacca gaaaccaagg acgccaagcc atacaaattc agcacagctg   240
actcagagag gtggaaagga aatcaggaca aaaagccaca atgtcttctg gaggaggata   300
ttgccagcca gaataactgt gagagatgta ggcaagcata gtcctggaaa caaacagcac   360
aattccttta aagccctaaa ggatgaagat cttcctgtag agaagtattt aatggaaagg   420
cagcctgtag gtgagccagc tgccgaccag gtagctatgg atgtgatgca cagccccatc   480
ctccaactgg aaaggaaaca caaagtctca agtgacagca accagacaga gactactgca   540
gagaagttgc cagaggactc tttcctaaaa aacaagcaaa aacaggttta tat           593
```

```
        <210> 60
        <211> 538
        <212> DNA
        <213> Homo sapiens


        <400> 60
atgaccattg tcagaaatgg tgtcagagac aaggatatca ctgcagacat caaacggata   60
ataagagaat actatgaaca attccatata cataagttta caaagattgg aaatgcttat   120
gctgttttaa gtaatccaga aaagcgaaaa cagtatgacc tcacgggcaa tgaagaacaa   180
gcatgtaacc accaaaacaa tggcagattt aatttccata gaggttttgt gaagttgata   240
taactccaga agacttgttt aatatatttt ttggggggtgg atttccttca ggtagtatac   300
attcttttc aaatggaaga gctggttata gccaacaaca tcagcattga catagtggac   360
```

```
atgaaagaga   agaggaaaga   ggagatggag   gtttttctgt   gtttatccag   ctgatgccca      420
taattgtatt   gatcctcgtg   tcattattaa   gccagttgat   ggtctgtaat   cctccttatt      480
ccttctatcc   cagatctgga   acagggcaaa   ctattaaaac   gcagacagaa   aacttggg        538
```

```
<210> 61
<211> 816
<212> DNA
<213> Homo sapiens


<400> 61
atgcctaaga   aagatgatag   caactggggc   tatgcgttca   cagatgggga   gcaactagga       60
gggccaagtg   caaaaggtaa   gatcaagtgg   cagcccacca   tttgcacttg   gcccactttt      120
gcaaaggaga   gtgggcgctc   ccttctctt    cctggaagat   cagtcccacc   ccccatttct      180
acatctcctt   gggtatacca   gcctacttat   agttactcta   gtaaaccaac   cgatggacta      240
gagaaagcaa   acaagagacc   aactccttgg   gaagcagcag   caaagtctcc   tctcggtcta      300
gtggatgatg   ctttccaacc   cagaaacatc   caggaatcca   ttgtggcaaa   tgtggtttca      360
gcagctcgga   ggaaggtgct   tccagggcct   ccagaggatt   ggaatgaaag   actgtcctat      420
attcctcaaa   cccagaaggc   ctatatgggc   tcatgtggaa   ggcaagagta   taatgtcaca      480
gccaataata   atatgtccac   cacctcccaa   tatggttcac   agttgccata   tgcatattat      540
aggcaggctt   caagaaatga   ttctgcaatc   atgtccatgg   aaaccaggtc   tgattactgt      600
cttccagtag   ctgattacaa   ctacaaccca   cacccaaggg   gatggagacg   ccaaacatga      660
aagttagaag   aacggatcat   gtgccaactg   tagttttta   aaaaaaacgc   tcctttgtag      720
ggtttttaaac  ttttctaata   gatttagatt   cactttggt    cttggcttgt   tctcataagt      780
catttatcta   agtttgtgtt   tctgtgtgtg   tgagtg                                    816
```

```
<210> 62
<211> 646
<212> DNA
<213> Homo sapiens


<400> 62
gatgggggca   aaagcagatt   ccttagcctg   cttttctgat   gagagatcgc   gggggagcca       60
aaggcagttt   gcaaaagagg   accagtctct   gcgcaggagt   tttggtggta   aacatgctgt      120
atcggctgtg   ggtgggagtg   cgtatcagca   ccacccccgt   ggaaggctac   ttgatgcgga      180
taagttccat   ccactggcaa   acccaaaagc   tacacatgtc   tacatgggaa   gggctgtgcg      240
gcacaggtgc   acagcagatc   tcagcgctct   tcccctgatg   tttctgctct   tcccatgcac      300
taaggagctg   agcaaacagc   aagtcagaag   gcagggccat   ggagggtccc   gacctgcgga      360
taaagaccta   gaggaagggg   gaggccttga   ggcggagtcc   cccaagcaga   gccccaactt      420
gtgtgtgatc   ctgcgccaca   acttggccag   ccggcctgga   cagctggctc   tggttactgt      480
gggaacaatg   caaggaaggc   cgttgtcaca   ttcctctgag   gtcaaaggca   caaccttcgt      540
cacacactca   gtccctgctg   gcaaagagaa   agacgaggag   cgtggaatcg   gagacctgga      600
gcatgcgagg   gacttgagaa   attcaccaac   tcccttgttt   tactga                       646
```

```
<210> 63
<211> 590
<212> DNA
<213> Homo sapiens


<400> 63
agatatagaa   tgattagaga   aatttgaaag   attttcagag   tcttttttt    ccaattcatg       60
gtatgaggtc   agatggttgc   ttgtaagtgt   tttcaaactg   ctaaggagcc   ttctgttgga      120
gcttgggagt   cagaaacctg   ggtctcacct   ggctctgtga   agtactcaca   tggcctttga      180
ccttggccaa   ctcacttaac   cttgttgagt   gaatgagagt   accatggagt   aagtgcttga      240
gtgcaggcat   gcctttgcct   tctcagaggt   tatggttaag   tgaattaata   tatctgaagt      300
tcttagcatc   aggtctgttt   aatggttatc   ccaatccaga   aaatttttcc   tggacagaat      360
```

38

```
acctggaagc tactcaaacc aatgcagttc ctgccaaagt ttttaaaatg gacagtgatg    420
ttggggagaa cagaaagatt ctccgggatg aaagacctaa ttacagtcag tatactccat    480
ttagtagatg tgataatgca tcttacaaag aaaatgtgtt tctacaaaag ctggagagaa    540
acacaccaga tattgcagaa agatttgact gtttattact gacatattag                590
```

```
        <210> 64
        <211> 386
        <212> DNA
        <213> Homo sapiens


        <400> 64
agttaatgtg taagagctgg cagtgctctg taaatgcaca gctgcagcca catcttgggt    60
tgctgggaag cctttgggtc atgctacctt ccctggttca gttagctata gctaggagaa    120
aagtgtggcc ctttggtcca gaacctggcc acctgatctc tgaatttggg catttttgaag   180
ggactgtcct tgacaaacca tcctgggtca cgtgcagaat tcttggagga ggtagactgc    240
aggggatggg ctggttgacg attgactttt ctcctcaagc atctaaacgt gccctaacgt    300
cttccattat ggagctgggg ccaggtgtca gcaaactggt tcagtggcag ctggagaacc    360
taaaaaggca ttgtgggcct ctgtag                                          386
```

```
        <210> 65
        <211> 615
        <212> DNA
        <213> Homo sapiens


        <400> 65
ctgaggggtt ttaaggcgta ggagtccttc tgtttgtttg gttttgttcc cctgtagcca    60
tttctgctgc tgtgaagaaa tgagcaggga ggtggcaagt gtgtgggtga taatgacaac    120
taatgttttt gagcagtgag tctgagtcag gccttatgcg atgcaaggtc catgcaccgt    180
cttattcaaa ccttccacac ctgtaagggg ttctctttaa tcaacccatt gtacaaatga    240
gaaaaccaag acttgtgaag attttgcagg ttgcccaagt tccccataga ttaagagata    300
aagcaagact tcaaatccag gccagtgtga ccctggagtg tgtggactca cccctgcagt    360
acactacctc tcaccatcct tgtaaaaaga aaaagtaagt tgtcagggca agagcactga    420
tgcaggagtc aggaactctg agagctggtc ccagctttgc cactcacttg ttacatgacc    480
tttagcaaaa ttgcttcaag gggaaaggag ttagcattgt gtgtgcacct actatgtgtc    540
agttgctggg ctatgggctt agaatacaat tgattatgaa atcctcaccc cattaccaca    600
agggaaatgg gatgg                                                      615
```

```
        <210> 66
        <211> 613
        <212> DNA
        <213> Homo sapiens


        <400> 66
cttggtccca cagtgagaac gctttgctat cacatgggca ggctctgaga gccctgccgg    60
cctggccttc tcaaagaaga cctgagagct tgggacccaa gcagagagga agaacagggc    120
tcagggtgct tgctccatgc tcgctccaca cctggggctc aaccctggct ttccccggct    180
ccctgtgtga cttcagggca ggtcccttgg gccctctggg ccttatcatc ttcatctgta    240
acagggcgat gcctctgccg tgtctggtgg tgttgaggag ttcctgtttg tgtaagcagc    300
tagttcagtg ccagcacgag atgggaggcc catgaagtta gcagtgcaca aaaaatagag    360
caaagactgg atgcatttcc tgagaacaac catcactgta aagcacttta caaatccaaa    420
gacaacccccc ggcaaaaact caaaatgaaa ctccctctcg cagagcacaa ttccaattcg    480
ctctaaaaac attacaagtt agttcatgtc atgccagata gctgaaggca gcttcacaag    540
ttcttaaggc caggaatgcc atgtgtctgc tatgcacagc tgggccctgg cccttgagcc    600
ctgatgacag cac                                                        613
```

<210> 67
<211> 930
<212> DNA
<213> Homo sapiens

<400> 67

```
tttcgtcccg cgtgctgcgg tggcgatcag cgcggacacg gagcctggct ccacccgtcc    60
gcccagcctt ggggttctgc cagagcgccg ggcgcagagc aagcgggtct gagctccagc   120
acctttggca gctcccggcc ccggggtgcg aacggcggcc gtggctcacc gcttcaggag   180
caggcgacca ggacactagg aagagaagcc cggaccaggg ctagtttgtt tccccaactc   240
ctctggccag ctcaggttct taaacccgcc gtgcaacaga cgcaggtacc ggctcagaaa   300
gctcagtcag tggtgcagga agcctgggtc gcggtgcatc gtgtttaaaa ataaacacac   360
acttcccttg gggccagtgg catttattct atttaaatta catagaatcg ttccattcct   420
ttgtgtctga aagattaagg ctgaagtctg ctttcccagc tatttgcatg tatttgttta   480
gggatggagt cgccctgcaa cacgggctgc tcctatggca actgctacaa aacaagatca   540
ggcttcacca gggtcgggag aagaaacctc ccaagaaagc caggcgctgg agtcatgggt   600
gtggatgtcc ttttagggcc taggaaagta gggtctgatg aggaggcatt gaagaaaagc   660
cagtatgacg acgatgcttt catggtgaag ttttgtgcat cttctactga acattttta    720
aacaaccccc aaacagatgc agttttgggc cagcgttatg gaagagaaag caaatccccc   780
aaatgtctga atcacaaaca cagagacctc accccgtga cagtggaaac aaatgccctg   840
gcctctgacc cctacagatc cgcgttcctg cccctaaacg gtgcagtgag gggagagctg   900
ggctgcagaa caggtggaga gaagaacgtg                                      930
```


<210> 68
<211> 239
<212> DNA
<213> Homo sapiens

<400> 68

```
tcctgatcag ggatgagtcc gtgctgttgg gtttattcat ttactttagc catcttggag    60
ccgtgtcagc tgcagagact ggagtccggg gcatgatggg gatgtacctg aaacctagtg   120
agagtcatcc tgactctggg gaagagccgc tcaaagatga gaaagataaa ggggtaacca   180
gaggtggtgg tgtggtccac tgtgactcgt cagctgttgc tctgtgtgtt catttttga    239
```


<210> 69
<211> 336
<212> DNA
<213> Homo sapiens

<400> 69

```
cacaaaatgc aaccactgag aatttattgc attacaggaa cttggaaatt caccttctaa    60
atatctggta agggtatgtc taactgctga atttcaccat aattcttaca tactagccaa   120
tttctatttc atgctgttta atagggcttg ctgtgaatcc gtgctacctt tgaatttttc   180
agcacagtaa atgtaagact tctagacatc tgcaagaagc atataagtaa aagagctcca   240
ctgtaatgcg aatggcatta gactcatgca tgcaacttta ttcagtcttt cctttgtgtc   300
acctcaacac atcaatggtt tgacaagtga aaaagt                               336
```


<210> 70
<211> 489
<212> DNA
<213> Homo sapiens

```
    <400> 70
cggaattccc ggatcgacgc tttcgtacgg cctgcacctt cgcagccagc cttgcctttg       60
attttgggcg gcacatgggc cgggtgcgtg ggcttggttt ggatggggac ggggttttgc      120
ggcgcgcctg agttttgaca ctccaacccc accgaaagtc cggaggagcc gggtgtgctg      180
ctcgcgtctt tgaaaggtgg aggcaggaga agtagggcaa ctggtgtggc tgcatgctga      240
ggcacatgat ttaaaaattt caactgctga tattctttcc gaggcgcgga gctctgctgc      300
tgtttcaggc tgtgtccaga cccaggaatg tggtgtgacg atcaccaatt cctccaacct      360
ggcagcaaca tttgctgctc ctttggaatg gctggggtg gggcacgggc ggaaaaaaac      420
tctgtgtcct ggctacatca aaatctgttg gggtggatct tggactcagc acccagggat      480
tctgataag                                                               489
```

```
    <210> 71
    <211> 362
    <212> DNA
    <213> Homo sapiens
```

```
    <400> 71
gaaaagagtt gttgactttc agggagccca aacctagggc ctccccaagc cagggttgtg       60
agacctttga ggctctatgg ttcctagcat ttccaagctt ctgggcacaa ctgcattacc      120
cggtacccat agtggaagcc acttgcagta tgcctggtcc agctgcagcc tcacacagag      180
ctagcaccta tgttagcact tggagttgcc cacctcacca cagctggcat gcctggcagt      240
gcacagtggc cagacctcac ttgcagacct ctcattgctg cacatctggc ttgcccttgg      300
cagacatgga atccaggctg gttgcttcac caagtgagtg gaacaagctc acttgggccc      360
ag                                                                      362
```

```
    <210> 72
    <211> 265
    <212> DNA
    <213> Homo sapiens
```

```
    <400> 72
aatgagccta tagaaaaaca cacacacaca ctgaagataa tcagggtcac tgaattgaat       60
gtgattttg gtgagattga aattgtgcaa gtccaggcct atcagtggca agtaggagga      120
ggagatgatc agcagtgctt tcctcctcct aacccttatc cggtcttatc tgctgctgcg      180
gtatcaaaac accacatcga tgacagaatt ggaccacgc aggctgcact gcaccatctg      240
gatggaagtg tagaggcctg caaag                                            265
```

```
    <210> 73
    <211> 390
    <212> DNA
    <213> Homo sapiens
```

```
    <400> 73
tttcgtgtga caaaagggaa ggacaagtga gtggctgcat gaggataaaa atgccctttg       60
gcaacagctg tattcagtga gcctcttccc cagaggatac gccctccctg cttcctggtc      120
agagccgggg cttgaggtca gctggtggga agatgagcag ggccccggg atcctggctt      180
cttggagaag agcccctcc ctttctgtgc agaagggcag ccagactgct agacacacct      240
gccacccaga ggttccgctg gaaactgct tcttacctgt ctacaaggcc agtcccctca      300
cagttacccg tctttgggct gaaaggtaag aggggagggt ggtgacggac tctgctggtc      360
acttggctct tccactgagc aactcacacc                                       390
```

```
    <210> 74
    <211> 362
```

41

```
        <212> DNA
        <213> Homo sapiens


        <400> 74
cccatgtggt gaactgctgc ccatcctcaa aaaaaaccag ttaaacatcc ttctcttgca        60
accagtggac acagagactt tggaagggcc tccaggcctt ggcctggatg cagagggccc       120
tgagaagaga cacaggtggc agtcagtctg actatcctct cgccctgtcc tcatttccca       180
cagctggatc ctcctgccct gccctgggat tgaccacacc tctggcttgg aggttatgtc       240
tgatctttat cacaggaagg gaaactcgct ccatccccaa ggaaagagaa ccaaggatgc       300
cagaaaggaa agcttccccc agaagatggg acaatttccc ttacaaagtc tggcagtcat       360
ct                                                                      362



        <210> 75
        <211> 340
        <212> DNA
        <213> Homo sapiens


        <400> 75
atgcttcttg ctgacaaaga ggcctctgaa gcaggcctca ccaatgttcc caacgatgca        60
aactatccaa gatacagtcc agcagagtgc ttaatggcca taggctttgg tgtccggaag       120
tctaggttgg agcacttgca tctgcaacag tgtgcaggtg attttctctc tgcaagcctc       180
agcccaacta accagatatc agtatctgtg tgggcacata tccataagct ggcccgtggt       240
aattcttaag tacgctgcga gcgtctatgg tatttctcta gcagaccgta agcgacaata       300
tgacagatac tttcgatatg aacgtttacg caccataaag                             340



        <210> 76
        <211> 390
        <212> DNA
        <213> Homo sapiens


        <400> 76
tttcgtggga gacgcaagcc aggaggccag ggctcctctt cggctgcccg ctgctgagat        60
gggcgcggca gccaaggggt cgttgtgggc ctcccctttc tctcgttcag tgctgcccct       120
ttgtcttggg tccagtctct gactcctcgt agctgctcgc ttggaccagg ctggccgtgg       180
tgacagcact gtgtcgtccc cgctcctagg cagtgggcct tccgggtagt agcggtcgag       240
tcccgcctag gctctcagga ctccacagcc cctgagtatt tgactcaaat caccagtcca       300
atatccctcc cgttaccagt gaggaacctg gggcccagag aagaggacgg agtcttgccc       360
aagtgactca agaccctctt aggaacttct                                        390



        <210> 77
        <211> 614
        <212> DNA
        <213> Homo sapiens


        <400> 77
tttcgtaaga aatgaagcca gagagttggc ctgggggcag accatggatc tctttggaca        60
tgccaacaag tttgggtttt attctgattg aggagggtca tatattgtgt catttattct       120
tcacagccac ccatgaggct aatttttattc ctatttatag atgaagtgcc tgaagcttag       180
aggggcctta gttaaggtca cataactggt aagtgatagg ctggggttt gaccacctgc        240
tctggatgcc aggatctgtc cttttcagct acagctgctc cttggaagct gccagtagaa       300
aatctgctgg atgctttca gtgattctgg tgtaaaactt caaaggatgc tttgggtgtt        360
tgtgagagca gatttgaaag atggtggtgg taacaaattg ggtccaacta tataggtcct       420
gtgagttcag ggtaaaggat gaggtgcttt tgctatagag aaccctggat ccaaaggaga       480
ggaccgtgc agagtctgag gggaactgct ggtagttaga gtcagaaagc atgttccaca        540
```

                                   42

```
tgggtgaaga gggtagacca caggtaaata ggggttgtag atggaggtaa ctgttggaaa     600
tccgggaaaa tggg                                                       614
```

```
        <210> 78
        <211> 627
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 78
cgctccattt ttcttttccc caaatacatc taagataaaa ttgtggatat cagaaggttc      60
atagggggtcc cccttccacc agcctgccaa ggagaattct gcagtccctg gcccagcttt     120
cccgcctcat ccctggagag ggatgcctgt ggaaggcttg gtgattggga ctcagagaaa     180
caggaaggga gaaaaggttt cccctccacg aattcagtca ttctacataa aaaaagaaca     240
aaaaggagtg tgttgggagg ggacaagttt tggcaaaaaa aatctccaga aagtccacaa     300
ggggacttcc aggacagtag gagcctcagg tccacagtga agtttcccac gtccacaagg     360
aagttgcaag gggaagtgga aaagagcagt gttgccagaa attatggatt tgatcctctt     420
taatgcctgt gaagatacac aaaaacatga aatttctttt caatattttt gggctgaacc     480
acttgggtgg tggctgaaat gagaccatac atacagcaca atgcatgtct gttatattgc     540
aaagtgtatt acctaggtct catacatccc cctagtcatc agcattaatg catgttggga     600
ccccgaccca cacaagcaga agtaatg                                         627
```

```
        <210> 79
        <211> 255
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 79
cacagcccga ggtccgtggc aggaggagat gacaagcagg gagaacacca acggaataaa      60
ctctgcagtt tccttcagat catccctgca taggtgtttc tcgaaactca tgttcagtga     120
gaacagcaga catagactca ggacaaaccc tccgtctcct ttcaggttag gttggcccat     180
gggctggagc gtctgcgtct tggtcggccc ggcagtgtac atgtcaagca gcgcgcaaag     240
actccacagc cattc                                                      255
```

```
        <210> 80
        <211> 231
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 80
aaacaacttc agttccatct gatgtagctg acttttttgat gagactaaaa ctgtgtagtt      60
catcatctcc atccaagttc agatctcaag tctatgatct tgactacctt aatgtatggc     120
tattattatc ttgatgatca cattggcttt gctttcggca caccccgatc tctctccctt     180
tcttctgatt ttctccactc aaaacaagag gggtattttt ctccgacatt g             231
```

```
        <210> 81
        <211> 415
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 81
tttcgttgga tagtcacttt tcaaaggtca catgtccctt gcttggaccc catcacacac      60
aacctgctgg tagtgtctgc ctcctgacag gtgccactgg ccatgggctg tgggagccca     120
```

```
gaggcttcga aggacccctt cagcatttca tgcgataggc tccattcatt gtactgctcg       180
gggctgtgag tggctgcgtc tgatcgtctc ttaatgtcca gtgtagggag cactgaggca       240
ggcaggtctg agcaggctga aagggggatt ggtgtatcag agagagtagg agtccaggct       300
caggatcgga cagagctgag tgcagattgc aacactgtga ctcccaaggt caaggcttcg       360
tgatcttggg aggttattta aaagaggccc tatggtgtcg tggtaagagc atggg           415
```


        <210> 82
        <211> 291
        <212> DNA
        <213> Homo sapiens

        <400> 82
```
gtcaagtgct acccgttgca ggcgcagggg ccacgcgggt ctggttggga gatcgagcct        60
ggtcgatccg tttgggcgg aagagtagga tttattcctg aaagtgtgga ggcgcgagcg       120
tttgggtccg aagttgagtt gcagggagat gtgtggcctg tggaccatgg ctctttact        180
gcaaagttct tttgcttatt tctgaaactt acattgttta ttcgctactg ggctggagaa       240
gccaattgta cagaatttaa accgtctctc agatgtgtac agtagaactc a                291
```


        <210> 83
        <211> 426
        <212> DNA
        <213> Homo sapiens

        <400> 83
```
aaatcaaaag ctctaacagc actccaggtt gcttttacaa gccagcctgt gaagctctaa        60
cgttctctag cgaaaccagc gaatcgccaa cttccgagaa gaaatgatgc gaaaatccct       120
cccgcactga cacctcagta agtgaaagag acttcttttc tctctccgta acctccctcc       180
tcctcactgc cgaatagtgc ggtgcttctt aactgagacg acgctaaact accagaagat       240
ccttagtgtc cgtccaggaa ccaaactcgc gaccgcctcg cacgtgtcag gcctaggact       300
acagacacca ccttcggcc ttgctcagca cctcatccgc ccccacgcct tccttgcgcc       360
caaagacccc ctcacctcct ttacagagag aaattcaaga agcgacgaaa tcgtcgaccc       420
gggaat                                                                   426
```


        <210> 84
        <211> 58
        <212> DNA
        <213> Homo sapiens

        <400> 84
```
ttttttttt ttaaagtata aaatttttt ggaaaaaaag gaaaaaaatc tatataaa           58
```


        <210> 85
        <211> 101
        <212> PRT
        <213> Homo sapiens

        <400> 85
```
Met His Cys Gln Lys Lys His Pro Tyr Trp Tyr Gln Gln Lys Ser Gly
1               5                   10                  15
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly
                20                  25                  30
Ile Pro Glu Arg Phe Ser Gly Ser Asn Leu Gly Ile Met Ala Thr Leu
```

```
                35                     40                     45
Ile Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr Tyr Cys Tyr
    50                     55                     60
Ser Thr Asp Ser Ser Gly Asn His Arg Glu Val Phe Gly Gly Gly Thr
65                     70                     75                     80
Arg Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Phe Gly His Ser
                85                     90                     95
Val Pro Ala Leu Leu
                100
```

```
        <210> 86
        <211> 57
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 86
Met Arg Lys Glu Gln Glu Val Thr Lys Lys His Ile Cys Glu Leu Leu
1                   5                   10                     15
Thr Glu Thr Val Thr Ser Ala Glu Thr Pro Asp Ala Leu Ala Lys Ser
                20                     25                     30
Arg Tyr Arg Ser Lys Leu Ala Asn Gln Met His Phe Leu Gly Leu Lys
        35                     40                     45
Tyr Arg Trp Val Leu Ile Phe Arg Met
    50                     55
```

```
        <210> 87
        <211> 99
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 87
Met Ala Leu Val Ala Ser Pro Ser Met Gly Arg Asn Leu Lys Asp Glu
1                   5                   10                     15
Lys Leu His Pro Lys Ala Tyr Gly Ser Trp His Leu Val Pro Trp Gln
                20                     25                     30
Met Leu Asp Pro Asn Thr Asn Gly Ser Pro Val Phe Pro Ser Ala Leu
        35                     40                     45
Pro Lys Thr Gly Val Val Gly Trp Gln Ser Met Trp Cys Phe Gly Lys
    50                     55                     60
Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg Leu Trp Val
65                     70                     75                     80
Pro Gly Met Ala Arg Pro Ala Arg Arg Ser Pro Met Leu Thr Val Asp
                85                     90                     95
Asn Ser Lys
```

```
        <210> 88
        <211> 144
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 88
Met His Glu Val Asn Ala Lys Ser Cys Cys Arg Val Pro Cys Gly Lys
1                   5                   10                     15
Arg Val Ala Arg Lys Leu Arg Glu Asn Gln Gln Ala Leu Trp Arg Pro
```

```
                        20                           25                           30
    Lys Ala Pro Glu Asp Val Arg Pro Gly Asn Gly Leu Glu His Arg Pro
            35                           40                           45
    Gly Gly Asp Pro Gly Ala Ala Glu Pro Asp Ala Val Cys Ala Ser Arg
        50                           55                           60
    Pro Ser Thr Glu Gln Arg His Gly Arg Ser His Gly Ala Arg Thr Pro
    65                           70                           75                           80
    Gly Lys Thr Thr Arg Gly Ala Phe Ser Pro Arg Pro Pro Ala Pro Ala
                        85                           90                           95
    Phe Ser Ser Arg Leu Val Gly Leu Asn Pro Thr Pro Ala Phe Ser Leu
                100                          105                          110
    His Phe Met Ser Phe Pro Gln Lys Tyr Ile Gln Lys Met Pro Phe Phe
                115                          120                          125
    Pro Leu Val Thr Leu Ile Pro Gly Phe Ser Pro Phe Ser Gly Ser Leu
        130                          135                          140
```

```
        <210> 89
        <211> 59
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 89
    Met Cys Asn Gly His Val Trp Leu His Asp Arg Tyr Trp Asp Ser Gly
    1                   5                            10                           15
    Ala Pro Arg Trp Gly Glu Glu Phe Ser Leu Ser Lys His Pro Gln Gly
                    20                           25                           30
    Thr Glu Val Lys Ala Ile Thr Tyr Ser Ala Met Gln Val Tyr Asn Glu
            35                           40                           45
    Glu Asn Pro Glu Val Phe Val Ile Ile Asp Ile
        50                           55
```

```
        <210> 90
        <211> 78
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 90
    Met Gly Gly Gly Gly Leu Arg Arg Gly Pro Glu Gly Glu Leu Gly Glu
    1                   5                            10                           15
    Gly Arg Lys Arg Lys Ser Ser Ala Arg Val Val Glu Lys Lys Ser Pro
                    20                           25                           30
    Pro Pro Ser Ala Tyr Thr Glu Ala Ala Thr Arg Leu Phe Ala Ser Pro
            35                           40                           45
    Thr Pro Pro Ser Phe Ser Gly Arg Gly Leu Leu His Pro Trp Ala Gly
        50                           55                           60
    Thr Arg Tyr Phe Ser Pro Ser Ser Ser Leu His Pro Arg Ile
    65                           70                           75
```

```
        <210> 91
        <211> 1089
        <212> PRT
        <213> Homo sapiens
```

<400> 91

```
Met Asn Leu His Ser Thr Leu Gln Val Ile Ser Leu Gln Val Asn Asn
1                   5                   10                  15
Leu Asp Ile Ile Val Ile Pro Glu Thr Ser Val Glu Leu Ser Gly Phe
            20                  25                  30
Leu Gln Lys Ser Phe Pro Lys Glu Lys Asp Asp Leu Ser Pro Gln Pro
        35                  40                  45
Leu Met Thr Val Cys Glu Arg Ser Phe Arg Glu Gln Gly Ser Phe Gln
    50                  55                  60
Ser Thr Tyr Glu Arg Ile Thr Glu Val Ala Val Glu Ile His Arg Met
65                  70                  75                  80
Asn Leu Val Leu Leu Arg Thr Val Gly Met Ala Asn Arg Glu Lys Tyr
                85                  90                  95
Gly Arg Lys Ile Ala Thr Ala Ser Ile Gly Gly Thr Lys Val Asn Val
            100                 105                 110
Ser Met Gly Ser Thr Phe Asp Met Asn Gly Ser Leu Gly Cys Leu Gln
        115                 120                 125
Leu Met Asp Leu Thr Gln Asp Asn Val Lys Asn Gln Tyr Val Val Ser
    130                 135                 140
Ile Gly Asn Ser Val Gly Tyr Glu Asn Ile Ile Ser Asp Ile Gly Tyr
145                 150                 155                 160
Phe Glu Ser Val Phe Val Arg Met Glu Asp Ala Ala Leu Thr Glu Ala
            165                 170                 175
Leu Ser Phe Thr Phe Val Glu Arg Ser Lys Gln Glu Cys Phe Leu Asn
            180                 185                 190
Leu Lys Met Ala Ser Leu His Tyr Asn His Ser Ala Lys Phe Leu Lys
        195                 200                 205
Glu Leu Thr Leu Ser Met Asp Glu Leu Glu Glu Asn Phe Arg Gly Met
    210                 215                 220
Leu Lys Ser Ala Ala Thr Lys Val Thr Thr Val Leu Ala Thr Lys Thr
225                 230                 235                 240
Ala Glu Tyr Ser Glu Met Val Ser Leu Phe Glu Thr Pro Arg Lys Thr
            245                 250                 255
Arg Glu Pro Phe Ile Leu Glu Glu Asn Glu Ile Tyr Gly Phe Asp Leu
            260                 265                 270
Ala Ser Ser His Leu Asp Thr Val Lys Leu Ile Leu Asn Ile Asn Ile
        275                 280                 285
Glu Ser Pro Val Val Ser Ile Pro Arg Lys Pro Gly Ser Pro Glu Leu
    290                 295                 300
Leu Val Gly His Leu Gly Gln Ile Phe Ile Gln Asn Phe Val Ala Gly
305                 310                 315                 320
Asp Asp Glu Ser Arg Ser Asp Arg Leu Gln Val Glu Ile Lys Asp Ile
            325                 330                 335
Lys Leu Tyr Ser Leu Asn Cys Thr Gln Leu Ala Gly Arg Glu Ala Val
            340                 345                 350
Gly Ser Glu Gly Ser Arg Met Phe Cys Pro Pro Ser Gly Ser Gly Ser
        355                 360                 365
Ala Asn Ser Gln Glu Glu Ala His Phe Thr Arg His Asp Phe Phe Glu
    370                 375                 380
Ser Leu His Arg Gly Gln Ala Phe His Ile Leu Asn Asn Thr Thr Ile
385                 390                 395                 400
Gln Phe Lys Leu Glu Lys Ile Pro Ile Glu Arg Glu Ser Glu Leu Thr
            405                 410                 415
Phe Ser Leu Ser Pro Asp Asp Leu Gly Thr Ser Ser Ile Met Lys Ile
            420                 425                 430
Glu Gly Lys Phe Val Asn Pro Val Gln Val Val Leu Ala Lys His Val
        435                 440                 445
Tyr Glu Gln Val Leu Gln Thr Leu Asp Asn Leu Val Tyr Ser Glu Asp
    450                 455                 460
Leu Asn Lys Tyr Pro Ala Ser Ala Thr Ser Ser Pro Cys Pro Asp Ser
465                 470                 475                 480
Pro Leu Pro Pro Leu Ser Thr Cys Gly Glu Ser Ser Val Glu Arg Lys
            485                 490                 495
Glu Asn Gly Leu Phe Ser His Ser Ser Leu Ser Asn Thr Ser Gln Lys
```

47

```
                    500                     505                     510
Ser Leu Ser Val Lys Glu Val Lys Ser Phe Thr Gln Ile Gln Ala Thr
        515                     520                     525
Phe Cys Ile Ser Glu Leu Gln Val Gln Leu Ser Gly Asp Leu Thr Leu
        530                     535                     540
Gly Ala Gln Gly Leu Val Ser Leu Lys Phe Gln Asp Phe Glu Val Glu
545                     550                     555                     560
Phe Ser Lys Asp His Pro Gln Thr Leu Ser Ile Gln Ile Ala Leu His
                565                     570                     575
Ser Leu Leu Met Glu Asp Leu Leu Glu Lys Asn Pro Asp Ser Lys Tyr
                580                     585                     590
Lys Asn Leu Met Val Ser Arg Gly Ala Pro Lys Pro Ser Ser Leu Ala
        595                     600                     605
Gln Lys Glu Tyr Leu Ser Gln Ser Cys Pro Ser Val Ser Asn Val Glu
        610                     615                     620
Tyr Pro Asp Met Pro Arg Ser Leu Pro Ser His Met Glu Glu Ala Pro
625                     630                     635                     640
Asn Val Phe Gln Leu Tyr Gln Arg Pro Thr Ser Ala Ser Arg Lys Lys
                645                     650                     655
Gln Lys Glu Val Gln Asp Lys Asp Tyr Pro Leu Thr Pro Pro Pro Ser
                660                     665                     670
Pro Thr Val Asp Glu Pro Lys Ile Leu Val Gly Lys Ser Lys Phe Asp
        675                     680                     685
Asp Ser Leu Val His Ile Asn Ile Phe Leu Val Asp Lys Lys His Pro
        690                     695                     700
Glu Phe Ser Ser Ser Tyr Asn Arg Val Asn Arg Ser Ile Asp Val Asp
705                     710                     715                     720
Phe Asn Cys Leu Asp Val Leu Ile Thr Leu Gln Thr Trp Val Val Ile
                725                     730                     735
Leu Asp Phe Phe Gly Ile Gly Ser Thr Ala Asp Asn His Ala Met Arg
                740                     745                     750
Leu Pro Pro Glu Gly Ile Leu His Asn Val Lys Leu Glu Pro His Ala
                755                     760                     765
Ser Met Glu Ser Gly Leu Gln Asp Pro Val Asn Thr Lys Leu Asp Leu
        770                     775                     780
Lys Val His Ser Leu Ser Leu Val Leu Asn Lys Thr Thr Ser Glu Leu
785                     790                     795                     800
Ala Lys Ala Asn Val Ser Lys Leu Val Ala His Leu Glu Met Ile Glu
                805                     810                     815
Gly Asp Leu Ala Leu Gln Gly Ser Ile Gly Ser Leu Ser Leu Ser Asp
        820                     825                     830
Leu Thr Cys His Gly Glu Phe Tyr Arg Glu Arg Phe Thr Thr Ser Gly
        835                     840                     845
Glu Glu Ala Leu Ile Phe Gln Thr Phe Lys Tyr Gly Arg Pro Asp Pro
850                     855                     860
Leu Leu Arg Arg Glu His Asp Ile Arg Val Ser Leu Arg Met Ala Ser
865                     870                     875                     880
Val Gln Tyr Val His Thr Gln Arg Phe Gln Ala Glu Val Val Ala Phe
                885                     890                     895
Ile Gln His Phe Thr Gln Leu Gln Asp Val Leu Gly Arg Gln Arg Ala
        900                     905                     910
Ala Ile Glu Gly Gln Thr Val Arg Asp Gln Ala Gln Arg Cys Ser Arg
        915                     920                     925
Val Leu Leu Asp Ile Glu Ala Gly Ala Pro Val Leu Leu Ile Pro Glu
        930                     935                     940
Ser Ser Arg Ser Asn Asn Leu Ile Val Ala Asn Leu Gly Lys Leu Lys
945                     950                     955                     960
Val Lys Asn Lys Phe Leu Phe Ala Gly Phe Pro Gly Thr Phe Ser Leu
                965                     970                     975
Gln Asp Lys Glu Ser Val Pro Ser Ala Ser Pro Thr Gly Ile Pro Lys
        980                     985                     990
His Ser Leu Arg Lys Thr Thr Ser Thr Glu Glu Pro Arg Gly Thr His
        995                     1000                    1005
Ser Gln Gly Gln Phe Thr Met Pro Leu Ala Gly Met Ser Leu Gly Ser
```

                                      48

```
        1010                   1015                   1020
Leu Lys Ser Glu Phe Val Pro Ser Thr Ser Thr Lys Gln Gln Gly Pro
1025                   1030                   1035                   1040
Gln Pro Thr Leu Ser Val Gly Gln Glu Ser Ser Ser Pro Glu Asp His
                1045                   1050                   1055
Val Cys Leu Leu Asp Cys Val Val Val Asp Leu Gln Asp His Gly Pro
                1060                   1065                   1070
Ser Leu Leu Arg Arg Asp Ile Arg Arg Asp Tyr Ser Lys Gly Thr Arg
          1075                   1080                   1085
Gly
```

```
        <210> 92
        <211> 182
        <212> PRT
        <213> Homo sapiens


        <400> 92
Met Ser Asn Glu Thr Val Leu Leu Ala Lys His Asn Ile Phe Thr Leu
1                   5                   10                  15
Ala Leu Met Ile Val Asn Leu Phe Asn Met Phe Ile Thr Tyr Gly Asp
                20                  25                  30
Thr Phe Leu Pro Thr Pro Ser Ser Tyr Asp Glu Leu Tyr Tyr Glu Ile
          35                  40                  45
Ile Arg Met His Gln Ser Phe Asp Asn Leu Tyr Ser Met Gly Leu Arg
          50                  55                  60
Leu Ser Thr Asn Ala Gly Gln Trp Lys Glu Ala Ala Ser Lys Val Thr
65                  70                  75                  80
His Ala Leu Val Asn Ile Arg Ala Ile Ile Asn His Phe Asn Pro Lys
                85                  90                  95
Ile Glu Ser Tyr Ala Ala Val Asn His Ile Ser Gln Leu Ser Glu Glu
          100                 105                 110
Gln Val Leu Glu Gly Val Arg Ala Asn Tyr Asp Thr Leu Thr Leu Lys
          115                 120                 125
Leu Gln Asp Gly Leu Asp Gln Tyr Glu Arg Tyr Ser Glu Gln His Lys
          130                 135                 140
Glu Ala Ala Phe Phe Lys Glu Leu Val Arg Ser Ile Ser Thr Asn Val
145                 150                 155                 160
Arg Arg Asn Leu Ala Phe His Thr Leu Ser Gln Glu Val Leu Leu Lys
                165                 170                 175
Glu Phe Ser Thr Ile Ser
                180
```

```
        <210> 93
        <211> 255
        <212> PRT
        <213> Homo sapiens


        <400> 93
Met Ser Arg Asn Ser Arg Lys Thr Ile Gly Lys Gly Arg Val Asp Tyr
1                   5                   10                  15
Ile Ile Ile Lys Pro Leu Pro Gly Tyr Ser Cys Asp Met Lys Ser Ser
                20                  25                  30
Phe Ser Lys Tyr Trp Lys Pro Arg Ile Pro Leu Asp Val Gly His Arg
          35                  40                  45
Gly Ala Gly Asn Ser Thr Thr Ala Gln Leu Ala Lys Val Gln Glu
          50                  55                  60
Asn Thr Ile Ala Ser Leu Arg Asn Ala Ala Ser His Gly Ala Ala Phe
```

49

```
        65                          70                          75                          80
Val Glu Phe Asp Val His Leu Ser Lys Asp Phe Val Pro Val Val Tyr
                        85                          90                          95
His Asp Leu Thr Cys Cys Leu Thr Met Lys Lys Lys Phe Asp Ala Asp
                100                         105                         110
Pro Val Glu Leu Phe Glu Ile Pro Val Lys Glu Leu Thr Phe Asp Gln
            115                         120                         125
Leu Gln Leu Leu Lys Leu Thr His Val Thr Ala Leu Lys Ser Lys Asp
        130                         135                         140
Arg Lys Glu Ser Val Val Gln Glu Glu Asn Ser Phe Ser Glu Asn Gln
145                         150                         155                         160
Pro Phe Pro Ser Leu Lys Met Val Leu Glu Ser Leu Pro Glu Asp Val
                        165                         170                         175
Gly Phe Asn Ile Glu Ile Lys Trp Ile Cys Gln Gln Arg Asp Gly Met
                180                         185                         190
Trp Asp Gly Asn Leu Ser Thr Tyr Phe Asp Met Asn Leu Phe Leu Asp
            195                         200                         205
Ile Ile Leu Lys Thr Val Leu Glu Asn Ser Gly Lys Arg Arg Ile Val
        210                         215                         220
Phe Ser Ser Phe Asp Ala Asp Ile Cys Thr Met Val Arg Gln Lys Gln
225                         230                         235                         240
Asn Lys Tyr Pro Ile Leu Phe Leu Thr Gln Gly Lys Cys Val Asp
                245                         250                         255
```

```
        <210> 94
        <211> 49
        <212> PRT
        <213> Homo sapiens


        <400> 94
Met Arg Gly Asn Tyr Glu Thr Leu Val Ser Leu Asp Tyr Ala Ile Ser
1                       5                       10                      15
Lys Pro Glu Val Leu Ser Gln Ile Glu Gln Gly Lys Glu Pro Cys Asn
                20                          25                          30
Trp Arg Arg Pro Gly Pro Lys Ile Pro Asp Val Pro Val Asp Pro Ser
        35                          40                          45
Pro


        <210> 95
        <211> 308
        <212> PRT
        <213> Homo sapiens


        <400> 95
Met Gly Ser Ser Gly Leu Gly Lys Ala Ala Thr Leu Asp Glu Leu Leu
1                       5                       10                      15
Cys Thr Cys Ile Glu Met Phe Asp Asp Asn Gly Glu Leu Asp Asn Ser
                20                          25                          30
Tyr Leu Pro Arg Ile Val Leu Leu Met His Arg Trp Tyr Leu Ser Ser
        35                          40                          45
Thr Glu Leu Ala Glu Lys Leu Leu Cys Met Tyr Arg Asn Ala Thr Gly
    50                          55                          60
Glu Ser Cys Asn Glu Phe Arg Leu Lys Ile Cys Tyr Phe Met Arg Tyr
65                          70                          75                          80
Trp Ile Leu Lys Phe Pro Ala Glu Phe Asn Leu Asp Leu Gly Leu Ile
                        85                          90                          95
Arg Met Thr Glu Glu Phe Arg Glu Val Ala Ser Gln Leu Gly Tyr Glu
```

```
                 100                    105                    110
Lys His Val Ser Leu Ile Asp Ile Ser Ser Ile Pro Ser Tyr Asp Trp
        115                    120                    125
Met Arg Arg Val Thr Gln Arg Lys Lys Val Ser Lys Lys Gly Lys Ala
    130                    135                    140
Cys Leu Leu Phe Asp His Leu Glu Pro Ile Glu Leu Ala Glu His Leu
145                    150                    155                    160
Thr Phe Leu Glu His Lys Ser Phe Arg Arg Ile Ser Phe Thr Asp Tyr
                165                    170                    175
Gln Ser Tyr Val Ile His Gly Cys Leu Glu Asn Asn Pro Thr Leu Glu
            180                    185                    190
Arg Ser Ile Ala Leu Phe Asn Gly Ile Ser Lys Trp Val Gln Leu Met
        195                    200                    205
Val Leu Ser Lys Pro Thr Pro Gln Gln Arg Ala Glu Val Ile Thr Lys
    210                    215                    220
Phe Ile Asn Val Ala Lys Lys Leu Leu Gln Leu Lys Asn Phe Asn Asn
225                    230                    235                    240
Leu Ile Ala Ile Ala Gly Ser Pro Gln Val Ile Gly Pro Phe Gln Ala
                245                    250                    255
Ser Lys Gly Pro Ile Pro His Leu Ser Ser Glu Val Tyr Lys Glu Leu
            260                    265                    270
Glu Cys Glu Met Thr Glu Val Gly Leu Leu Gln Arg Ala Ile Thr Ala
        275                    280                    285
Ile Thr Ala Ser Pro Leu Pro Thr Ala Met Ala Ser Lys Ser Pro Ser
    290                    295                    300
Leu Glu Tyr Thr
305
```

```
        <210> 96
        <211> 217
        <212> PRT
        <213> Homo sapiens


        <400> 96
Met Gly Val Pro Val Thr Ser Gln Glu Ser Gly Gln Lys Leu Val Ser
  1           5                    10                    15
Pro Leu Cys Leu Ala Pro Tyr Phe Arg Leu Leu Lys Leu Cys Val Glu
                20                    25                    30
Arg Gln His Asn Gly Asn Leu Glu Glu Ile Asp Gly Leu Leu Asn Cys
        35                    40                    45
Pro Ile Phe Leu Thr Asp Leu Glu Pro Gly Glu Lys Leu Glu Ser Met
    50                    55                    60
Ser Ala Lys Glu Arg Ser Phe Met Cys Ser Leu Ile Phe Leu Thr Leu
65                    70                    75                    80
Asn Trp Phe Arg Glu Ile Val Asn Ala Phe Cys Gln Glu Thr Ser Pro
                85                    90                    95
Glu Met Lys Gly Lys Val Leu Thr Arg Leu Lys His Ile Val Glu Leu
            100                    105                    110
Gln Ile Ile Leu Glu Lys Tyr Leu Ala Val Thr Pro Asp Tyr Val Pro
        115                    120                    125
Pro Leu Gly Asn Phe Asp Val Glu Thr Leu Asp Ile Thr Pro His Thr
    130                    135                    140
Val Thr Ala Ile Ser Ala Lys Ile Arg Lys Lys Gly Lys Ile Val Tyr
145                    150                    155                    160
Thr Leu Lys Glu Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro
                165                    170                    175
Glu Asn Tyr Arg Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu
            180                    185                    190
Glu Asp His Pro Asn Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu
        195                    200                    205
Arg Ile Ala His Gln Arg Met Gly Asp
```

210   215

<210> 97
<211> 265
<212> PRT
<213> Homo sapiens

<400> 97
Met Pro Ala Pro Arg Ala Arg Glu Gln Pro Arg Val Pro Gly Glu Arg
1   5   10   15
Gln Pro Leu Leu Pro Arg Gly Ala Arg Gly Pro Arg Arg Trp Arg Arg
            20   25   30
Ala Ala Gly Ala Ala Val Leu Leu Val Glu Met Leu Glu Arg Ala Ala
        35   40   45
Phe Phe Gly Val Thr Ala Asn Leu Val Leu Tyr Leu Asn Ser Thr Asn
    50   . 55   60
Phe Asn Trp Thr Gly Glu Gln Ala Thr Arg Ala Ala Leu Val Phe Leu
65   70   75   80
Gly Ala Ser Tyr Leu Leu Ala Pro Val Gly Gly Trp Leu Ala Asp Val
            85   90   95
Tyr Leu Gly Arg Tyr Arg Ala Val Ala Leu Ser Leu Leu Leu Tyr Leu
            100   105   110
Ala Ala Ser Gly Leu Leu Pro Ala Thr Ala Phe Pro Asp Gly Arg Ser
        115   120   125
Ser Phe Cys Gly Glu Met Pro Ala Ser Pro Leu Gly Pro Ala Cys Pro
    130   135   140
Ser Ala Gly Cys Pro Arg Ser Ser Pro Ser Pro Tyr Cys Ala Pro Val
145   150   155   160
Leu Tyr Ala Gly Leu Leu Leu Leu Gly Leu Ala Ala Ser Ser Val Arg
            165   170   175
Ser Asn Leu Thr Ser Phe Gly Ala Asp Ala Gly Asp Gly Ser Arg Pro
            180   185   190
Arg Arg His Pro Pro Leu Leu Gln Leu Val Leu Leu Glu His Gln Pro
        195   200   205
Gly Cys Cys Ala Val Ala Ala Gly Gly Gly Val Tyr Ser Ala Glu His
    210   215   220
Gln Leu Pro Ala Gly Leu Gln His Pro Cys Gly Leu Cys Gly Pro Gly
225   230   235   240
Ile Phe His Leu Pro Leu Cys His Pro Arg Leu His His Gln Ala Pro
            245   250   255
Asp Gly Gln Pro Ser Val Leu Tyr Ala
            260   265

<210> 98
<211> 111
<212> PRT
<213> Homo sapiens

<400> 98
Met Ile Lys Tyr Asn Glu Gly Arg Ala Glu Gly Leu Ser Leu Ala Val
1   5   10   15
Pro Gly Cys Cys Gly Gly Gly Arg Leu Ala Thr Gln Thr Val Ala Ala
            20   25   30
Ala Ala Ala Ser Trp Trp Pro Pro Cys Trp Arg Gly Ser Leu Ala Phe
        35   40   45
Ser Val Ala Ala Ser Ala Val Ser Phe Ala Phe Ser Leu Ala Ser Leu
    50   55   60
Ala Val Ser Thr Gly Gly Leu Glu Gly Ala Ser Pro Cys Ser Leu Ala

```
    65                      70                      75                      80
Lys Ile Tyr Ser Lys Pro Phe Ile Gly Leu Gly His Val Ala Phe Glu
                    85                      90                      95
Pro Gly Lys Thr Lys Phe Leu Gly Gln Leu Leu Glu Thr Pro Asn
            100                     105                     110


        <210> 99
        <211> 421
        <212> PRT
        <213> Homo sapiens


        <400> 99
Met Ala Met Ala Thr Cys Gly Gly Lys Gly Lys Gln Ala Ala Pro Lys
1               5                   10                      15
Gly Arg Glu Ala Phe Arg Ser Gln Arg Arg Glu Ser Glu Gly Ser Val
                20                  25                  30
Asp Cys Pro Thr Leu Glu Phe Glu Tyr Gly Asp Ala Asp Gly His Ala
            35                  40                  45
Ala Glu Leu Ser Glu Leu Tyr Ser Tyr Thr Glu Asn Leu Glu Phe Thr
        50                  55                  60
Asn Asn Arg Arg Cys Phe Glu Glu Asp Phe Lys Thr Gln Val Gln Gly
65                  70                      75                      80
Lys Glu Trp Leu Glu Leu Glu Glu Asp Ala Gln Lys Ala Tyr Ile Met
                85                      90                      95
Gly Leu Leu Asp Arg Leu Glu Val Val Ser Arg Glu Arg Arg Leu Lys
            100                     105                     110
Ala Ala Arg Ala Val Leu Tyr Leu Ala Gln Gly Thr Phe Gly Glu Cys
        115                     120                     125
Asp Ser Glu Val Asp Val Leu His Trp Ser Arg Tyr Asn Cys Phe Leu
    130                     135                     140
Leu Tyr Gln Met Gly Thr Phe Ser Thr Phe Leu Glu Leu Leu His Met
145                     150                     155                     160
Glu Ile Asp Asn Ser Gln Ala Cys Ser Ala Leu Arg Lys Pro Ala
                165                     170                     175
Val Ser Ile Ala Asp Ser Thr Glu Leu Arg Val Leu Leu Ser Val Met
                180                     185                     190
Tyr Leu Met Val Glu Asn Ile Arg Leu Glu Arg Glu Thr Asp Pro Cys
            195                     200                     205
Gly Trp Arg Thr Ala Arg Glu Thr Phe Arg Thr Glu Leu Ser Phe Ser
        210                     215                     220
Met His Asn Glu Glu Pro Phe Ala Leu Leu Leu Phe Ser Met Val Thr
225                     230                     235                     240
Lys Phe Cys Ser Gly Leu Ala Pro His Phe Pro Ile Lys Lys Val Leu
                245                     250                     255
Leu Leu Leu Trp Lys Val Val Met Phe Thr Leu Gly Gly Phe Glu His
            260                     265                     270
Leu Gln Thr Leu Lys Val Gln Lys Arg Ala Glu Leu Gly Leu Pro Pro
        275                     280                     285
Leu Ala Glu Asp Ser Ile Gln Val Val Lys Ser Met Arg Ala Ala Ser
    290                     295                     300
Pro Pro Ser Tyr Thr Leu Asp Leu Gly Glu Ser Gln Leu Ala Pro Pro
305                     310                     315                     320
Pro Ser Lys Leu Arg Gly Arg Arg Gly Ser Arg Arg Gln Leu Leu Thr
                325                     330                     335
Lys Gln Asp Ser Leu Asp Ile Tyr Asn Glu Arg Asp Leu Phe Lys Thr
            340                     345                     350
Glu Glu Pro Ala Thr Glu Glu Glu Glu Ser Ala Gly Asp Gly Glu
        355                     360                     365
Arg Thr Leu Asp Gly Glu Leu Asp Leu Leu Glu Gln Asp Pro Leu Val
    370                     375                     380
Pro Pro Pro Pro Ser Gln Ala Pro Leu Ser Ala Glu Arg Val Ala Phe
```

```
385                      390                      395                      400
Pro Lys Gly Leu Pro Trp Ala Pro Lys Val Arg Gln Lys Gly Thr Leu
                405                      410                      415
Ser Thr Ser Trp Arg
                420
```

```
        <210> 100
        <211> 290
        <212> PRT
        <213> Homo sapiens


        <400> 100
Met Pro Phe Asp Phe Arg Arg Phe Asp Ile Tyr Arg Lys Val Pro Lys
  1               5                  10                  15
Asp Leu Thr Gln Pro Thr Tyr Thr Gly Ala Ile Ile Ser Ile Cys Cys
                20                  25                  30
Cys Leu Phe Ile Leu Phe Leu Phe Leu Ser Glu Leu Thr Gly Phe Ile
                35                  40                  45
Thr Thr Glu Val Val Asn Glu Leu Tyr Val Asp Asp Pro Asp Lys Asp
        50                  55                  60
Ser Gly Gly Lys Ile Asp Val Ser Leu Asn Ile Ser Leu Pro Asn Leu
 65                  70                  75                  80
His Cys Glu Leu Val Gly Leu Asp Ile Gln Asp Glu Met Gly Arg His
                85                  90                  95
Glu Val Gly His Ile Asp Asn Ser Met Lys Ile Pro Leu Asn Asn Gly
                100                 105                 110
Ala Gly Cys Arg Phe Glu Gly Gln Phe Ser Ile Asn Lys Val Pro Gly
        115                 120                 125
Asn Phe His Val Ser Thr His Ser Ala Thr Ala Gln Pro Gln Asn Pro
        130                 135                 140
Asp Met Thr His Val Ile His Lys Leu Ser Phe Gly Asp Thr Leu Gln
145                 150                 155                 160
Val Gln Asn Ile His Gly Ala Phe Asn Ala Leu Gly Gly Ala Asp Arg
                165                 170                 175
Leu Thr Ser Asn Pro Leu Ala Ser His Asp Tyr Ile Leu Lys Ile Val
                180                 185                 190
Pro Thr Val Tyr Glu Asp Lys Ser Gly Lys Gln Arg Tyr Ser Tyr Gln
        195                 200                 205
Tyr Thr Val Ala Asn Lys Glu Tyr Val Ala Tyr Ser His Thr Gly Arg
        210                 215                 220
Ile Ile Pro Ala Ile Trp Phe Arg Tyr Asp Leu Ser Pro Ile Thr Val
225                 230                 235                 240
Lys Tyr Thr Glu Arg Arg Gln Pro Leu Tyr Arg Phe Ile Thr Thr Ile
                245                 250                 255
Cys Ala Ile Ile Gly Gly Thr Phe Thr Val Ala Gly Ile Leu Asp Ser
                260                 265                 270
Cys Ile Phe Thr Ala Ser Glu Ala Trp Lys Lys Ile Gln Leu Gly Lys
        275                 280                 285
Met His
    290


        <210> 101
        <211> 133
        <212> PRT
        <213> Homo sapiens


        <400> 101
Met Pro Pro Arg Asn Leu Pro Gly His Cys Thr Ser Pro Pro Ala Ile
```

54

```
1                   5                    10                    15
Arg Val Pro Pro Val Ile Pro Leu Gly Ser Arg Glu Leu Phe Cys Ser
            20                    25                    30
Lys Leu Arg Arg Ala Ala Val Phe Pro Pro Ala His Gln Gln Arg Thr
        35                    40                    45
Leu Arg Pro Cys His Asn Tyr Cys Lys Gly Arg Arg Cys Leu Leu Thr
    50                    55                    60
His Cys Gly Cys Asp Ala Pro His Leu Pro Arg Ala Pro Pro Pro Leu
65                    70                    75                    80
Arg Thr Asp Val Gly Asp Ser Thr Pro Phe Arg Glu Lys Pro Val Ser
                85                    90                    95
Ala Ala Glu Asp Ala Asn Ala Ser Glu Ser Pro Leu Thr Leu Asn His
            100                   105                   110
Ser Leu Glu Met Gly Val Val Tyr Leu Thr Thr Gly Ala Val Ser Gly
        115                   120                   125
Asn Ala Asn Tyr His
        130
```

```
        <210> 102
        <211> 38
        <212> PRT
        <213> Homo sapiens


        <400> 102
Met His Arg Ile Trp Ile Glu Asp Thr Thr Trp Lys Phe Ser Asn Phe
1                   5                    10                    15
Thr Ile Ile Ser Gly Leu Tyr Gly Leu Thr Thr Phe Asn Phe Leu Leu
            20                    25                    30
Arg Tyr Lys Tyr Phe Pro
        35
```

```
        <210> 103
        <211> 1130
        <212> PRT
        <213> Homo sapiens


        <400> 103
Met Ser Ala Gly Ile Gly Pro Met Ala Trp Trp Pro Ser Thr Thr Gly
1                   5                    10                    15
Pro Cys Met Met Ser Thr Val Ser Thr Met Ala Lys Pro His Arg Glu
            20                    25                    30
Cys Pro Gly Cys Phe Val Pro Phe Ala Val Cys Val Val Ser Arg Phe
        35                    40                    45
Pro Tyr Tyr Asn Ser Leu Lys Asp Cys Leu Ser Cys Leu Leu Ala Leu
    50                    55                    60
Leu Lys Pro Cys Lys Asp Phe Glu Val Asp Asn His Ile Lys Asp Phe
65                    70                    75                    80
Ala Ala Lys Leu Ser Leu Ile Pro Ser Pro Pro Gly Pro Leu His
                85                    90                    95
Leu Val Phe Asn Met Lys Ser Leu Gln Ile Val Leu Pro Ala Arg Ala
            100                   105                   110
Asp Pro Glu Ser Pro Ile Leu Asp Leu Asp Leu His Leu Pro Leu Leu
        115                   120                   125
Cys Phe Arg Pro Glu Lys Val Leu Gln Ile Leu Thr Cys Ile Leu Thr
        130                   135                   140
Glu Gln Arg Ile Val Phe Phe Ser Ser Asp Trp Ala Leu Leu Thr Leu
145                   150                   155                   160
Val Thr Glu Cys Phe Met Ala Tyr Leu Tyr Pro Leu Gln Trp Gln His
```

```
                         165                      170                      175
Pro Phe Val Pro Ile Leu Ser Asp Gln Met Leu Asp Phe Val Met Gly
             180                      185                      190
Pro Thr Ser Phe Leu Met Gly Cys His Leu Asp His Phe Glu Glu Val
             195                      200                      205
Ser Lys Glu Ala Asp Gly Leu Val Leu Ile Asn Ile Asp His Gly Ser
             210                      215                      220
Ile Thr Tyr Ser Lys Ser Thr Asp Asp Asn Val Asp Ile Pro Asp Val
225                      230                      235                      240
Pro Leu Leu Ala Ala Gln Thr Phe Ile Gln Arg Val Gln Ser Leu Gln
                         245                      250                      255
Leu His His Glu Leu His Ala Ala His Leu Leu Ser Ser Thr Asp Leu
             260                      265                      270
Lys Glu Gly Arg Ala His Arg Arg Ser Trp Gln Gln Lys Leu Asn Cys
             275                      280                      285
Gln Ile Gln Gln Thr Thr Leu Gln Leu Leu Val Ser Ile Phe Arg Asp
             290                      295                      300
Val Lys Asn His Leu Asn Tyr Glu His Arg Val Phe Asn Ser Glu Glu
305                      310                      315                      320
Phe Leu Lys Thr Arg Ala Pro Gly Asp His Gln Phe Tyr Lys Gln Val
                         325                      330                      335
Leu Asp Thr Tyr Met Phe His Ser Phe Leu Lys Ala Arg Leu Asn Arg
             340                      345                      350
Arg Met Asp Ala Phe Ala Gln Met Asp Leu Asp Thr Gln Ser Glu Glu
             355                      360                      365
Asp Arg Ile Asn Gly Met Leu Leu Ser Pro Arg Arg Pro Thr Val Glu
             370                      375                      380
Lys Arg Ala Ser Arg Lys Ser Ser His Leu His Val Thr His Arg Arg
385                      390                      395                      400
Met Val Val Ser Met Pro Asn Leu Gln Asp Ile Ala Met Pro Glu Leu
                         405                      410                      415
Ala Pro Arg Asn Ser Ser Leu Arg Leu Thr Asp Thr Ala Gly Cys Arg
             420                      425                      430
Gly Ser Ser Ala Val Leu Asn Val Thr Pro Lys Ser Pro Tyr Thr Phe
             435                      440                      445
Lys Ile Pro Glu Ile His Phe Pro Leu Glu Ser Lys Cys Val Gln Ala
             450                      455                      460
Tyr His Ala His Phe Val Ser Met Leu Ser Glu Ala Met Cys Phe Leu
465                      470                      475                      480
Ala Pro Asp Asn Ser Leu Leu Leu Ala Arg Tyr Leu Tyr Leu Arg Gly
                         485                      490                      495
Leu Val Tyr Leu Met Gln Gly Gln Leu Leu Asn Ala Leu Leu Asp Phe
             500                      505                      510
Gln Asn Leu Tyr Lys Thr Asp Ile Arg Ile Phe Pro Thr Asp Leu Val
             515                      520                      525
Lys Arg Thr Val Glu Ser Met Ser Ala Pro Glu Trp Glu Gly Ala Glu
             530                      535                      540
Gln Ala Pro Glu Leu Met Arg Leu Ile Ser Glu Ile Leu Asp Lys Pro
545                      550                      555                      560
His Glu Ala Ser Lys Leu Asp Asp His Val Lys Lys Phe Lys Leu Pro
                         565                      570                      575
Lys Lys His Met Gln Leu Gly Asp Phe Met Lys Arg Val Gln Glu Ser
             580                      585                      590
Gly Ile Val Lys Asp Ala Ser Ile Ile His Arg Leu Phe Glu Ala Leu
             595                      600                      605
Thr Val Gly Gln Glu Lys Gln Ile Asp Pro Glu Thr Phe Lys Asp Phe
             610                      615                      620
Tyr Asn Cys Trp Lys Glu Thr Glu Ala Glu Ala Gln Glu Val Ser Leu
625                      630                      635                      640
Pro Trp Leu Val Met Glu His Leu Asp Lys Asn Glu Cys Val Cys Lys
                         645                      650                      655
Leu Ser Ser Ser Val Lys Thr Asn Leu Gly Val Gly Lys Ile Ala Met
             660                      665                      670
Thr Gln Lys Arg Leu Phe Leu Leu Thr Glu Gly Arg Pro Gly Tyr Leu
```

56

```
              675                    680                 . 685
Glu Ile Ser Thr Phe Arg Asn Ile Glu Glu Val Arg Arg Thr Thr Thr
     690                    695                 700
Thr Phe Leu Leu Arg Arg Ile Pro Thr Leu Lys Ile Arg Val Ala Ser
705                    710                 715                 720
Lys Lys Glu Val Phe Glu Ala Asn Leu Lys Thr Glu Cys Asp Leu Trp
                725                 730                 735
His Leu Met Val Lys Glu Met Trp Ala Gly Lys Lys Leu Ala Asp Asp
            740                 745                 750
His Lys Asp Pro His Tyr Val Gln Gln Ala Leu Thr Asn Val Leu Leu
         755                 760                 765
Met Asp Ala Val Val Gly Thr Leu Gln Ser Pro Gly Ala Ile Tyr Ala
     770                 775                 780
Ala Ser Lys Leu Ser Tyr Phe Asp Lys Met Ser Asn Glu Met Pro Met
785                 790                 795                 800
Thr Leu Pro Glu Thr Thr Leu Glu Thr Leu Lys His Lys Ile Asn Pro
                805                 810                 815
Ser Ala Gly Glu Ala Phe Pro Gln Ala Val Asp Val Leu Leu Tyr Thr
            820                 825                 830
Pro Gly His Leu Asp Pro Ala Glu Lys Val Glu Asp Ala His Pro Lys
         835                 840                 845
Leu Trp Cys Ala Leu Ser Glu Gly Lys Val Thr Val Phe Asn Ala Ser
     850                 855                 860
Ser Trp Thr Ile His Gln His Ser Phe Lys Val Gly Thr Ala Lys Val
865                 870                 875                 880
Asn Cys Met Val Met Ala Asp Gln Asn Gln Val Trp Val Gly Ser Glu
                885                 890                 895
Asp Ser Val Ile Tyr Ile Ile Asn Val His Ser Met Ser Cys Asn Lys
            900                 905                 910
Gln Leu Thr Ala His Cys Ser Ser Val Thr Asp Leu Ile Val Gln Asp
         915                 920                 925
Gly Gln Glu Ala Pro Ser Asn Val Tyr Ser Cys Ser Met Asp Gly Met
     930                 935                 940
Val Leu Val Trp Asn Val Ser Thr Leu Gln Val Thr Ser Arg Phe Gln
945                 950                 955                 960
Leu Pro Arg Gly Gly Leu Thr Ser Ile Arg Leu His Gly Gly Arg Leu
                965                 970                 975
Trp Cys Cys Thr Gly Asn Ser Ile Met Val Met Lys Met Asn Gly Ser
            980                 985                 990
Leu His Gln Glu Leu Lys Ile Glu Glu Asn Phe Lys Asp Thr Ser Thr
         995                 1000                 1005
Ser Phe Leu Ala Phe Gln Leu Leu Pro Glu Glu Glu Gln Leu Trp Ala
     1010                 1015                 1020
Ala Cys Ala Gly Arg Ser Glu Val Tyr Ile Trp Ser Leu Lys Asp Leu
1025                 1030                 1035                 1040
Ala Gln Pro Pro Gln Arg Val Pro Leu Glu Asp Cys Ser Glu Ile Asn
                1045                 1050                 1055
Cys Met Ile Arg Val Lys Lys Gln Val Trp Val Gly Ser Arg Gly Leu
            1060                 1065                 1070
Gly Gln Gly Thr Pro Lys Gly Lys Ile Tyr Val Ile Asp Ala Glu Arg
         1075                 1080                 1085
Lys Thr Val Glu Lys Glu Leu Val Ala His Met Asp Thr Val Arg Thr
     1090                 1095                 1100
Leu Cys Ser Ala Glu Asp Arg Tyr Val Leu Ser Gly Ser Gly Arg Glu
1105                 1110                 1115                 1120
Glu Gly Lys Val Ala Ile Trp Lys Gly Glu
                1125                 1130
```

```
<210> 104
<211> 140
<212> PRT
<213> Homo sapiens
```

```
        <400> 104
Met Gly Gln Ala Gln Ser Lys Pro Thr Pro Leu Gly Thr Val Leu Lys
1                   5                   10                  15
Asn Phe Lys Lys Gly Ser Asn Gly Asp Tyr Gly Ile Ala Met Thr Pro
            20                  25                  30
Gly Lys Leu Lys Ala Leu Cys Glu Ile Asp Trp Pro Ala Leu Glu Val
        35                  40                  45
Gly Trp Pro Ser Glu Gly Ser Leu Asp Lys Ser Leu Val Ser Lys Val
    50                  55                  60
Trp His Lys Val Thr Glu Phe Pro Val Asn Gln His Gln Leu Glu Asp
65                  70                  75                  80
His Ile Leu Ile Lys Gly Trp Lys Glu Arg Lys Leu Glu Pro Ala Trp
                85                  90                  95
Glu Gly Pro Tyr Pro Val Leu Leu Thr Thr Lys Thr Ala Val Arg Thr
            100                 105                 110
Ala Lys Lys Lys Lys Lys Lys Lys Asp Gly Leu Ile Thr Pro Lys
            115                 120                 125
Ser Arg Lys Cys His Pro Leu Gln Ser Arg Gly Pro
    130                 135                 140


        <210> 105
        <211> 562
        <212> PRT
        <213> Homo sapiens


        <400> 105
Met Arg Arg Gly Gly Trp Arg Lys Arg Ala Glu Asn Asp Gly Trp Glu
1                   5                   10                  15
Thr Trp Gly Gly Tyr Met Ala Ala Lys Val Gln Lys Leu Glu Glu Gln
            20                  25                  30
Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
        35                  40                  45
Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
    50                  55                  60
Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
65                  70                  75                  80
Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
                85                  90                  95
Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
            100                 105                 110
Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
        115                 120                 125
Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
    130                 135                 140
Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
145                 150                 155                 160
Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
            165                 170                 175
Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
            180                 185                 190
Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
            195                 200                 205
Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
    210                 215                 220
Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
225                 230                 235                 240
Cys Leu Val Pro Met Val Asn Ser Val Ala Ser Arg Leu Ser Pro Ala
            245                 250                 255
Phe Ser Gln Glu Glu Asp Lys Ala Glu Lys Ser Ser Thr Asp Phe Arg
```

```
                  260                      265                      270
Asp Cys Thr Leu Gln Gln Leu Gln Gln Ser Thr Arg Asn Thr Asp Ala
        275                      280                      285
Leu Arg Asn Pro His Arg Thr Asn Ser Phe Ser Leu Ser Pro Leu His
    290                      295                      300
Ser Asn Thr Lys Ile Asn Gly Ala His His Ser Thr Val Gln Gly Pro
305                      310                      315                      320
Ser Ser Thr Lys Ser Thr Ser Ser Val Ser Thr Phe Ser Lys Ala Ala
                325                      330                      335
Pro Ser Val Pro Ser Lys Pro Ser Asp Cys Asn Phe Ile Ser Asn Phe
            340                      345                      350
Tyr Ser His Ser Arg Leu His His Ile Ser Met Trp Lys Cys Glu Leu
        355                      360                      365
Thr Glu Phe Val Asn Thr Leu Gln Arg Gln Ser Asn Gly Ile Phe Pro
    370                      375                      380
Gly Arg Glu Lys Leu Lys Lys Met Lys Thr Gly Arg Ser Ala Leu Val
385                      390                      395                      400
Val Thr Asp Thr Gly Asp Met Ser Val Leu Asn Ser Pro Arg His Gln
                405                      410                      415
Ser Cys Ile Met His Val Asp Met Asp Cys Phe Phe Val Ser Val Gly
            420                      425                      430
Ile Arg Asn Arg Pro Asp Leu Lys Gly Lys Pro Val Ala Val Thr Ser
        435                      440                      445
Asn Arg Gly Thr Gly Arg Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln
    450                      455                      460
Leu Glu Trp Gln Tyr Tyr Gln Asn Lys Ile Leu Lys Gly Lys Ala Ala
465                      470                      475                      480
Asp Ile Pro Asp Ser Ser Leu Trp Glu Asn Pro Asp Ser Ala Gln Ala
                485                      490                      495
Asn Gly Ile Asp Ser Val Leu Ser Arg Ala Glu Ile Ala Ser Cys Ser
            500                      505                      510
Tyr Glu Ala Arg Gln Leu Gly Ile Lys Asn Gly Met Phe Phe Gly His
        515                      520                      525
Ala Lys Gln Leu Cys Pro Asn Leu Gln Ala Val Pro Tyr Asp Phe His
    530                      535                      540
Ala Tyr Lys Glu Val Ala Gln Thr Leu Tyr Glu Thr Leu Ala Ser Leu
545                      550                      555                      560
His Ser
```

```
        <210> 106
        <211> 72
        <212> PRT
        <213> Homo sapiens


        <400> 106
Met Glu Lys Ser Ser Gly Pro Trp Asn Lys Thr Ala Pro Val Gln Ala
1                   5                   10                      15
Pro Pro Ala Pro Val Ile Val Thr Glu Thr Pro Glu Pro Ala Met Thr
            20                      25                      30
Ser Gly Val Tyr Arg Pro Pro Gly Ala Arg Leu Thr Thr Thr Arg Lys
        35                      40                      45
Thr Pro Gln Gly Pro Pro Glu Ile Tyr Ser Asp Thr Gln Phe Pro Ser
    50                      55                      60
Leu Gln Ser Thr Ala Lys His Val
65                      70


        <210> 107
        <211> 320
```

```
       <212> PRT
       <213> Homo sapiens


       <400> 107
Met His Ser Ala Glu Trp Lys Lys Asp Gln Gln Ile Gly Gly Glu Asn
1               5                   10                  15
Gly Ala Glu Ile Gln Ile Gln Gly Lys Arg Asn Leu Arg Glu Val Gly
                20                  25                  30
Gly Glu Asp Gly Val Lys Thr Trp Ala Pro Gly Lys Glu Thr Gln Ser
            35                  40                  45
Gln Phe Arg Ser Asp Leu Gly Arg Lys Ile Leu Leu Ser Glu Trp Lys
        50                  55                  60
Ser Gln Lys Gln Met Gly Ser Glu Asn Gly Thr Glu Ile Gln Ala Pro
65                  70                  75                  80
Val Glu Arg Asn Gln Arg Glu Pro Gly Gly Glu Asp Gly Val Lys Thr
                85                  90                  95
Gln Arg Pro Lys Arg Glu Asn Glu Asp Gln Leu Asp Ser Glu Ile Gly
            100                 105                 110
Gly Ser His Ser Pro Gly Arg Arg Asn Trp Glu Leu Ile Gly Lys Asp
        115                 120                 125
Val Ala Glu Asn Gln Ala Ser Glu Lys Arg Asn Gln Arg Glu Val Gly
        130                 135                 140
Asn Glu Asp Glu Trp Lys Asn Gln Glu Gln Gly Gly Gly Gly Asn Asp
145                 150                 155                 160
Glu Glu Ile Gln Ile Gln Gly Lys Arg Asn Leu Arg Gly Thr Thr Ala
                165                 170                 175
Asp Asp Gly Thr Glu Thr Gln Ala Pro Ala Gly Asp Asp Gln Gly Gln
            180                 185                 190
Leu Arg Val Glu Ile Ala Glu Glu Ile Gln Val Gln Gly Gln Gly Asn
        195                 200                 205
Lys Asn Asp Gly Gly Val Glu Asp Val Ala Glu Leu Gln Asp Ile Gly
        210                 215                 220
Ser Gln Arg Lys Cys Thr Asp Glu Asp Val Gly Glu Pro Arg Ala Pro
225                 230                 235                 240
Arg Gly Gly Asn Lys Asp Leu Val Arg Gly Glu Asp Ala Val Arg Asp
                245                 250                 255
Ser Leu Gln Val Asp Cys Ser Gly Ser Glu Arg Pro Thr Gly Arg Lys
            260                 265                 270
His Ser Leu Pro Trp Pro Pro Ala Phe Thr Gly Tyr Gly Cys Gly Thr
        275                 280                 285
Arg Glu Gln Glu Gln Ala Val Ala Val Asn Gly Phe Ile Ser Ala Pro
    290                 295                 300
Cys Pro Glu Met Asn Pro Val Pro His Trp Gly Glu Val Phe Leu Leu
305                 310                 315                 320



       <210> 108
       <211> 295
       <212> PRT
       <213> Homo sapiens


       <400> 108
Met Ser Lys Leu Lys Val Ile Pro Glu Lys Ser Leu Thr Asn Asn Ser
1               5                   10                  15
Arg Ile Val Gly Leu Leu Ala Gln Leu Glu Lys Ile Asn Ala Glu Pro
                20                  25                  30
Ser Glu Ser Asp Thr Ala Arg Tyr Val Thr Ser Lys Ile Leu His Leu
            35                  40                  45
Ala Gln Ser Gln Glu Lys Thr Arg Arg Glu Met Thr Ala Lys Gly Ser
```

```
        50                      55                      60
Thr Gly Met Glu Ile Leu Leu Ser Thr Leu Glu Asn Thr Lys Asp Leu
 65                      70                      75                      80
Gln Thr Thr Leu Asn Ile Leu Ser Ile Leu Val Glu Leu Val Ser Ala
                85                      90                      95
Gly Gly Gly Arg Arg Val Ser Phe Leu Val Thr Lys Gly Gly Ser Gln
               100                     105                     110
Ile Leu Leu Gln Leu Leu Met Asn Ala Ser Lys Glu Ser Pro Pro His
           115                     120                     125
Glu Asp Leu Met Val Gln Ile His Ser Ile Leu Ala Lys Ile Gly Pro
       130                     135                     140
Lys Asp Lys Lys Phe Gly Val Lys Ala Arg Ile Asn Gly Ala Leu Asn
145                     150                     155                     160
Ile Thr Leu Asn Leu Val Lys Gln Asn Leu Gln Asn His Arg Leu Val
               165                     170                     175
Leu Pro Cys Leu Gln Leu Leu Arg Val Tyr Ser Ala Asn Ser Val Asn
               180                     185                     190
Ser Val Ser Leu Gly Lys Asn Gly Val Val Glu Leu Met Phe Lys Ile
           195                     200                     205
Ile Gly Pro Phe Ser Lys Lys Asn Ser Ser Leu Ile Lys Val Ala Leu
       210                     215                     220
Asp Thr Leu Ala Ala Leu Leu Lys Ser Lys Thr Asn Ala Arg Arg Ala
225                     230                     235                     240
Val Asp Arg Gly Tyr Val Gln Val Leu Leu Thr Ile Tyr Val Asp Trp
               245                     250                     255
His Arg His Asp Asn Arg His Arg Asn Met Leu Ile Arg Lys Gly Ile
           260                     265                     270
Leu Arg Ser Leu Asn Lys Arg Leu Gln Thr Ser Cys Trp Glu Glu Lys
       275                     280                     285
His Leu Leu Met Pro Met Gly
       290                     295
```

```
        <210> 109
        <211> 1125
        <212> PRT
        <213> Homo sapiens


        <400> 109
Met Asp Pro Phe Thr Glu Lys Leu Leu Glu Arg Thr Arg Ala Arg Arg
 1               5                      10                      15
Glu Asn Leu Gln Arg Lys Met Ala Glu Arg Pro Thr Ala Ala Pro Arg
                20                      25                      30
Ser Met Thr His Ala Lys Arg Ala Arg Gln Pro Leu Ser Glu Ala Ser
            35                      40                      45
Asn Gln Gln Pro Phe Ser Gly Gly Glu Glu Lys Ser Cys Ser Lys Pro
        50                      55                      60
Ser Pro Ser Lys Lys Arg Cys Ser Asp Asn Thr Glu Val Glu Val Ser
 65                      70                      75                      80
Asn Leu Glu Asn Lys Gln Pro Val Glu Ser Thr Ser Ala Lys Ser Cys
                85                      90                      95
Ser Pro Ser Pro Val Ser Pro Gln Val Gln Pro Gln Ala Ala Asp Thr
               100                     105                     110
Ile Ser Asp Ser Val Ala Val Pro Ala Ser Leu Leu Gly Met Arg Arg
           115                     120                     125
Gly Leu Asn Ser Arg Leu Glu Ala Thr Ala Ala Ser Ser Val Lys Thr
       130                     135                     140
Arg Met Gln Lys Leu Ala Glu Gln Arg Arg Arg Trp Asp Asn Asp Asp
145                     150                     155                     160
Met Thr Asp Asp Ile Pro Glu Ser Ser Leu Phe Ser Pro Met Pro Ser
               165                     170                     175
Glu Glu Lys Ala Ala Ser Pro Pro Lys Pro Leu Leu Ser Asn Ala Ser
```

```
                      180                    185                    190
Ala Thr Pro Val Gly Arg Arg Gly Arg Leu Ala Asn Leu Ala Ala Thr
         195                    200                    205
Ile Cys Ser Trp Glu Asp Asp Val Asn His Ser Phe Ala Lys Gln Asn
         210                    215                    220
Ser Val Gln Glu Gln Pro Gly Thr Ala Cys Leu Ser Lys Phe Ser Ser
225                    230                    235                    240
Ala Ser Gly Ala Ser Ala Arg Ile Asn Ser Ser Ser Val Lys Gln Glu
                 245                    250                    255
Ala Thr Phe Cys Ser Gln Arg Asp Gly Asp Ala Ser Leu Asn Lys Ala
                 260                    265                    270
Leu Ser Ser Ser Ala Asp Asp Ala Ser Leu Val Asn Ala Ser Ile Ser
         275                    280                    285
Ser Ser Val Lys Ala Thr Ser Ser Pro Val Lys Ser Thr Thr Ser Ile
         290                    295                    300
Thr Asp Ala Lys Ser Cys Glu Gly Gln Asn Pro Glu Leu Leu Pro Lys
305                    310                    315                    320
Thr Pro Ile Ser Pro Leu Lys Thr Gly Val Ser Lys Pro Ile Val Lys
                 325                    330                    335
Ser Thr Leu Ser Gln Thr Val Pro Ser Lys Gly Glu Leu Ser Arg Glu
                 340                    345                    350
Ile Cys Leu Gln Ser Gln Ser Lys Asp Lys Ser Thr Thr Pro Gly Gly
         355                    360                    365
Thr Gly Ile Lys Pro Phe Leu Glu Arg Phe Gly Glu Arg Cys Gln Glu
         370                    375                    380
His Ser Lys Glu Ser Pro Ala Arg Ser Thr Pro His Arg Thr Pro Ile
385                    390                    395                    400
Ile Thr Pro Asn Thr Lys Ala Ile Gln Glu Arg Leu Phe Lys Gln Asp
                . 405                    410                    415
Thr Ser Ser Ser Thr Thr His Leu Ala Gln Gln Leu Lys Gln Glu Arg
                 420                    425                    430
Gln Lys Glu Leu Ala Cys Leu Arg Gly Arg Phe Asp Lys Gly Asn Ile
         435                    440                    445
Trp Ser Ala Glu Lys Gly Gly Asn Ser Lys Ser Lys Gln Leu Glu Thr
         450                    455                    460
Lys Gln Glu Thr His Cys Gln Ser Thr Pro Leu Lys Lys His Gln Gly
465                    470                    475                    480
Val Ser Lys Thr Gln Ser Leu Pro Val Thr Glu Lys Val Thr Glu Asn
                 485                    490                    495
Gln Ile Pro Ala Lys Asn Ser Ser Thr Glu Pro Lys Gly Phe Thr Glu
         500                    505                    510
Cys Glu Met Thr Lys Ser Ser Pro Leu Lys Ile Thr Leu Phe Leu Glu
         515                    520                    525
Glu Asp Lys Ser Leu Lys Val Thr Ser Asp Pro Lys Val Glu Gln Lys
         530                    535                    540
Ile Glu Val Ile Arg Glu Ile Glu Met Ser Val Asp Asp Asp Ile
545                    550                    555                    560
Asn Ser Ser Lys Val Ile Asn Asp Leu Phe Ser Asp Val Leu Glu Glu
                 565                    570                    575
Gly Glu Leu Asp Met Glu Lys Ser Gln Glu Glu Met Asp Gln Ala Leu
                 580                    585                    590
Ala Glu Ser Ser Glu Glu Gln Glu Asp Ala Leu Asn Ile Ser Ser Met
         595                    600                    605
Ser Leu Leu Ala Pro Leu Ala Gln Thr Val Gly Val Val Ser Pro Glu
         610                    615                    620
Ser Leu Val Ser Thr Pro Arg Leu Glu Leu Lys Asp Thr Ser Arg Ser
625                    630                    635                    640
Asp Glu Ser Pro Lys Pro Gly Lys Phe Gln Arg Thr Arg Val Pro Arg
                 645                    650                    655
Ala Glu Ser Gly Asp Ser Leu Gly Ser Glu Asp Arg Asp Leu Leu Tyr
         660                    665                    670
Ser Ile Asp Ala Tyr Arg Ser Gln Arg Phe Lys Glu Thr Glu Arg Pro
         675                    680                    685
Ser Ile Lys Gln Val Ile Val Arg Lys Glu Asp Val Thr Ser Lys Leu
```

```
           690                      695                  700
Asp Glu Lys Asn Asn Ala Phe Pro Cys Gln Val Asn Ile Lys Gln Lys
705                      710                  715                  720
Met Gln Glu Leu Asn Asn Glu Ile Asn Met Gln Gln Thr Val Ile Tyr
                    725                  730                  735
Gln Ala Ser Gln Ala Leu Asn Cys Cys Val Asp Glu Glu His Gly Lys
                    740                  745                  750
Gly Ser Leu Glu Glu Ala Glu Ala Glu Arg Leu Leu Leu Ile Ala Thr
                    755                  760                  765
Gly Lys Arg Thr Leu Leu Ile Asp Glu Leu Asn Lys Leu Lys Asn Glu
            770                  775                  780
Gly Pro Gln Arg Lys Asn Lys Ala Ser Pro Gln Ser Glu Phe Met Pro
785                      790                  795                  800
Ser Lys Gly Ser Val Thr Leu Ser Glu Ile Arg Leu Pro Leu Lys Ala
                    805                  810                  815
Asp Phe Val Cys Ser Thr Val Gln Lys Pro Asp Ala Ala Asn Tyr Tyr
                    820                  825                  830
Tyr Leu Ile Ile Leu Lys Ala Gly Ala Glu Asn Met Val Ala Thr Pro
                    835                  840                  845
Leu Ala Ser Thr Ser Asn Ser Leu Asn Gly Asp Ala Leu Thr Phe Thr
            850                  855                  860
Thr Thr Phe Thr Leu Gln Asp Val Ser Asn Asp Phe Glu Ile Asn Ile
865                      870                  875            ·     880
Glu Val Tyr Ser Leu Val Gln Lys Lys Asp Pro Ser Gly Leu Asp Lys
                    885                  890                  895
Lys Lys Lys Thr Ser Lys Ser Lys Ala Ile Thr Pro Lys Arg Leu Leu
                    900                  905                  910
Thr Ser Ile Thr Thr Lys Ser Asn Ile His Ser Ser Val Met Ala Ser
            915                  920                  925
Pro Gly Gly Leu Ser Ala Val Arg Thr Ser Asn Phe Ala Leu Val Gly
            930                  935                  940
Ser Tyr Thr Leu Ser Leu Ser Ser Val Gly Asn Thr Lys Phe Val Leu
945                      950                  955                  960
Asp Lys Val Pro Phe Leu Ser Ser Leu Glu Gly His Ile Tyr Leu Lys
                    965                  970                  975
Ile Lys Cys Gln Val Asn Ser Ser Val Glu Glu Arg Gly Phe Leu Thr
                    980                  985                  990
Ile Phe Glu Asp Val Ser Gly Phe Gly Ala Trp His Arg Arg Trp Cys
            995                  1000                 1005
Val Leu Ser Gly Asn Cys Ile Ser Tyr Trp Thr Tyr Pro Asp Asp Glu
    1010                     1015                 1020
Lys Arg Lys Asn Pro Ile Gly Arg Ile Asn Leu Ala Asn Cys Thr Ser
1025                     1030                 1035                 1040
Arg Gln Ile Glu Pro Ala Asn Arg Glu Phe Cys Ala Arg Arg Asn Thr
                    1045                 1050                 1055
Phe Glu Leu Ile Thr Val Arg Pro Gln Arg Glu Asp Asp Arg Glu Thr
                1060                 1065                 1070
Leu Val Ser Gln Cys Arg Asp Thr Leu Cys Val Thr Lys Asn Trp Leu
            1075                 1080                 1085
Ser Ala Asp Thr Lys Glu Glu Arg Asp Leu Trp Met Gln Lys Leu Asn
    1090                     1095                 1100
Gln Val Leu Val Asp Ile Arg Leu Trp Gln Pro Asp Ala Cys Tyr Lys
1105                     1110                 1115                 1120
Pro Ile Gly Lys Pro
                    1125
```

```
<210> 110
<211> 226
<212> PRT
<213> Homo sapiens
```

```
        <400> 110
Met Cys His Pro Gln Arg Cys Pro Gln Thr Val Ile Pro Glu Gly Glu
1               5                   10                  15
Cys Cys Pro Val Cys Ser Ala Thr Val Ser Tyr Ser Leu Leu Ser Gly
            20                  25                  30
Ile Ala Leu Asn Asp Arg Asn Glu Phe Ser Gly Asp Ser Ser Glu Gln
            35                  40                  45
Arg Glu Pro Thr Asn Leu Leu His Lys Gln Leu Pro Pro Pro Gln Val
    50                  55                  60
Gly Met Asp Arg Ile Val Arg Lys Glu Ala Leu Gln Ser Glu Glu Asp
65                  70                  75                  80
Glu Glu Val Lys Glu Glu Asp Thr Glu Gln Lys Arg Glu Thr Pro Glu
                85                  90                  95
Ser Arg Asn Gln Gly Gln Leu Tyr Ser Glu Gly Asp Ser Arg Gly Gly
                100                 105                 110
Asp Arg Lys Gln Arg Pro Gly Glu Glu Arg Arg Leu Ala His Gln Gln
            115                 120                 125
Gln Arg Gln Gly Arg Glu Glu Glu Glu Asp Glu Glu Glu Glu Gly Glu
        130                 135                 140
Glu Gly Glu Glu Asp Glu Glu Asp Glu Glu Asp Pro Val Arg Gly Asp
145                 150                 155                 160
Met Phe Arg Met Pro Ser Arg Ser Pro Leu Pro Ala Pro Pro Arg Gly
                165                 170                 175
Thr Leu Arg Leu Pro Ser Gly Cys Ser Leu Ser Tyr Arg Thr Ile Ser
            180                 185                 190
Cys Ile Asn Ala Lys Leu Thr Ala Asn Thr Thr Ala Asp Ser Thr Thr
            195                 200                 205
Asp Asn Lys Ser Gly Ser Leu Thr Trp Gln Tyr Pro Ser Ala Ser Ile
    210                 215                 220
Ser Arg
225
```

```
        <210> 111
        <211> 100
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 111
Met Tyr Arg Ala Ser Glu Ser Ala Lys Trp Ser Leu Gly Gly Gly Glu
1               5                   10                  15
Glu Gln Gln Lys Pro Trp Leu Arg Leu Thr His Gln Gly Leu Pro Cys
            20                  25                  30
Pro Pro Glu Glu Val Ser Gly Ile Gln Thr Phe Ser Ser Asp Pro Cys
            35                  40                  45
Leu Pro Gly Gly Leu Glu Ala His Ala Leu Lys Gln Val Ser Ala Ile
    50                  55                  60
Asn Ser Arg Thr Arg Pro Lys Asp Lys Ile Leu Glu Gln Lys His Arg
65                  70                  75                  80
Pro Ser Leu Asp Gln Gly Lys Gln Leu Ser Met Lys Lys Glu Lys Ile
                85                  90                  95
Pro Val Gly Gly
                100
```

```
        <210> 112
        <211> 155
        <212> PRT
        <213> Homo sapiens
```

<400> 112

```
Met Ser Arg Trp Gly Ala Ala Val Gly Gln Gly Ala Leu Arg Glu Glu
1               5                   10                  15
His Phe Ala His Ala His Ile Thr Glu Arg Thr Arg Arg Val Arg Glu
            20                  25                  30
Gly Arg Arg Lys Arg Arg Ser Ser Leu Leu Thr Thr Ser Pro Thr Ser
        35                  40                  45
Ala Asn Ala Gln Ala His Phe Leu Lys Leu Lys Val Ser Ile Asp Lys
    50                  55                  60
Gly Pro Gln Asn Arg Ala Gly Ala Ile Val Pro Trp Phe Ala Lys Met
65                  70                  75                  80
Ser Phe Pro Lys Tyr Lys Pro Cys Glu Pro Ala His Ser Ala Val Arg
                85                  90                  95
Pro Ser Thr Gln Pro Asn Thr Thr Tyr Leu Arg Lys Pro Gly Gly Arg
            100                 105                 110
Lys Pro Glu Arg Leu Ala His Arg Ser Pro Ala Ala Asn Glu Ser Thr
        115                 120                 125
Leu Leu Gln Tyr Asn Asp Pro Asn Thr Pro Arg Ala His Arg Lys Ser
    130                 135                 140
Val Pro Cys Phe Val Gly Pro Met Gln Glu Gln
145                 150                 155
```

<210> 113
<211> 194
<212> PRT
<213> Homo sapiens

<400> 113

```
Met Gln Phe Arg Arg Ala Pro Phe Met Tyr Ser Val Arg Met Glu Leu
1               5                   10                  15
Ala Gly Val Pro Cys Glu Leu Thr Cys Phe Leu Pro Gln Gly Ile Cys
            20                  25                  30
Leu Leu Met Val Pro Ala Val Lys Asn Gln Ala Ser Gly Ser Ala Arg
        35                  40                  45
Gly Ala Thr Lys Val Arg Arg Lys Cys Gln Ala Gly Cys Gln Asn Glu
    50                  55                  60
His Leu Gly Glu Leu Asp Asp Gly Thr Asp Gly Lys Asn Gln Leu Asn
65                  70                  75                  80
Ile Arg Glu Asn Gly Gly Arg Gly Gln Asn Cys Glu Gln Glu Leu Glu
                85                  90                  95
Glu Ser Val Ala Glu Lys Asp Leu Ser Gln Thr Ser Arg Asp Leu Glu
            100                 105                 110
Lys Met Met Ser Lys His Ile Phe Leu Lys Pro Met Leu Ser Ile Ser
        115                 120                 125
Asp Leu Val Asn Phe Leu Met Gln Val Ser Lys Val Leu Val Lys Thr
    130                 135                 140
Ala Glu Gly Ile Val Leu Gln Gln Leu Pro Leu Ala Phe Pro Ala Leu
145                 150                 155                 160
His Phe His Ala Tyr Gly Asn Leu Phe Pro Val Cys Ser Phe Lys His
                165                 170                 175
Tyr Ile Tyr Met Ile Asp His Pro Ile Phe Ile Ser Ile Pro Asp Phe
            180                 185                 190
Leu Thr
```

<210> 114
<211> 814
<212> PRT
<213> Homo sapiens

<400> 114

```
Met Glu Gly Glu Pro Thr Leu Phe Lys Ile Cys Arg Lys His Ser Glu
1               5                   10                  15
Ser Lys Gly Lys Leu Val Ser Lys Tyr Phe Ser Met Glu Cys Leu Ile
            20                  25                  30
Val Glu Val Val Phe Ile Thr Gly Glu Arg Ile Ala Ile Ser Lys Ser
        35                  40                  45
Val Ser Leu His His Glu Asn Ala Glu Tyr Gly Ile Arg Arg Thr Glu
    50                  55                  60
Ser Leu Asp Phe Lys Phe Gly Arg Arg Ser Asn Arg Ala Asp Glu Leu
65                  70                  75                  80
Thr Gly Gly Glu Tyr Ser Val Ala Phe Ser Ser Leu Glu Arg Asn Ala
                85                  90                  95
Ala Thr Ala Gly Asn Arg Gly Leu Ala Phe Pro Ser Arg His Ile Asn
            100                 105                 110
Ile Gly Arg Ser Gln Ser Trp Asp Ala Ala Gly Trp Tyr Glu Gly Pro
            115                 120                 125
Trp Glu Asn Ala Glu Ser Leu Arg Pro Leu Gly Arg Arg Ser Ser Leu
    130                 135                 140
Thr Tyr Gly Thr Ala Glu Gly Thr Trp Phe Glu Pro Asn His Arg Pro
145                 150                 155                 160
Gln Asp Ala Ala Leu Pro Val Ala Ala Glu Pro Tyr Leu Tyr Arg Glu
                165                 170                 175
Ala Val Tyr Asn Ser Val Ala Ala Arg Lys Gly Ser Thr Pro Asp Phe
            180                 185                 190
Thr Phe Tyr Asp Ser Arg Gln Ala Val Met Ser Gly Arg Ser Pro Leu
        195                 200                 205
Leu Pro Arg Glu Tyr Tyr Ser Asp Pro Ser Gly Ala Ala Arg Val Pro
    210                 215                 220
Lys Glu Pro Pro Leu Tyr Arg Asp Pro Gly Val Ser Arg Pro Val Pro
225                 230                 235                 240
Ser Tyr Gly Val Leu Gly Ser Arg Thr Ser Trp Asp Pro Met Gln Gly
                245                 250                 255
Arg Ser Pro Ala Leu Gln Asp Ala Gly His Leu Tyr Arg Asp Pro Gly
            260                 265                 270
Gly Lys Met Ile Pro Gln Gly Arg Gln Thr Gln Ser Arg Ala Ala Ser
            275                 280                 285
Pro Gly Arg Tyr Gly Arg Glu Gln Pro Asp Thr Arg Tyr Gly Ala Glu
    290                 295                 300
Val Pro Ala Tyr Pro Leu Ser Gln Val Phe Ser Asp Ile Ser Glu Arg
305                 310                 315                 320
Pro Ile Asp Pro Ala Pro Ala Arg Gln Val Ala Pro Thr Cys Leu Val
            325                 330                 335
Val Asp Pro Ser Ser Ala Ala Ala Pro Glu Gly Ser Thr Gly Val Ala
            340                 345                 350
Pro Gly Ala Leu Asn Arg Gly Tyr Gly Pro Ala Arg Glu Ser Ile Pro
        355                 360                 365
Ser Lys Met Ala Tyr Glu Thr Tyr Glu Ala Asp Leu Ser Thr Phe Gln
    370                 375                 380
Gly Pro Gly Gly Lys Arg Thr Val Leu Pro Glu Phe Leu Ala Phe Leu
385                 390                 395                 400
Arg Ala Glu Gly Leu Ala Glu Ala Thr Leu Gly Ala Leu Leu Gln Gln
            405                 410                 415
Gly Phe Asp Ser Pro Ala Val Leu Ala Thr Leu Glu Asp Ala Asp Ile
            420                 425                 430
Lys Ser Val Ala Pro Asn Leu Gly Gln Ala Arg Val Leu Ser Arg Leu
        435                 440                 445
Ala Asn Ser Cys Arg Thr Glu Met Gln Leu Arg Arg Gln Asp Arg Gly
    450                 455                 460
Gly Pro Leu Pro Arg Ala Arg Ser Ser Ser Phe Ser His Arg Ser Glu
465                 470                 475                 480
Leu Leu His Gly Asp Leu Ala Ser Leu Gly Ala Ala Ala Pro Leu Gln
```

66

```
                         485                        490                        495
Thr Ala Ser Pro Arg Ala Gly Asp Pro Ala Arg Arg Pro Ser Ser Ala
                500                        505                        510
Pro Ser Gln His Leu Leu Glu Thr Ala Ala Thr Tyr Ser Ala Pro Gly
            515                        520                        525
Val Gly Thr His Ala Pro His Phe Pro Ser Asn Ser Gly Tyr Ser Ser
        530                        535                        540
Pro Thr Pro Cys Ala Leu Thr Ala Arg Leu Ser Pro Thr Tyr Pro Leu
545                        550                        555                        560
Gln Ala Gly Val Ala Leu Thr Asn Pro Gly Pro Ser Asn Pro Leu His
                565                        570                        575
Pro Gly Pro Arg Thr Ala Tyr Ser Thr Ala Tyr Thr Val Pro Met Glu
            580                        585                        590
Leu Leu Lys Arg Glu Arg Asn Val Ala Ala Ser Pro Leu Pro Ser Pro
        595                        600                        605
His Gly Ser Pro Gln Val Leu Arg Lys Pro Gly Ala Pro Leu Gly Pro
    610                        615                        620
Ser Thr Leu Pro Pro Ala Ser Gln Ser Leu His Thr Pro His Ser Pro
625                        630                        635                        640
Tyr Gln Lys Val Ala Arg Arg Thr Gly Ala Pro Ile Ile Val Ser Thr
                645                        650                        655
Met Leu Ala Pro Glu Pro Ile Gln Phe Ala Gly Gln Ala Val Gln Ser
                660                        665                        670
Asp Asn Val Arg Lys Ala Tyr Ala Ala Gly Thr Pro Val Arg Pro Thr
            675                        680                        685
Ser Pro Gly Asp Thr Asp Lys Trp Gly Leu Gln Ala Arg Val Ser Gly
        690                        695                        700
Ser Thr Trp Gln Val Val Gly Ser Ala Val Ala Leu Arg Leu Thr Trp
705                        710                        715                        720
Pro Ala Met Ala Gln Val Ala Glu Pro Ser Gly Gly Gly Cys Glu Pro
                725                        730                        735
Ala Ile Ser Pro Cys His Val Leu Ser Pro Glu Pro Cys Leu His Gln
                740                        745                        750
Met Gln Gln Gly Ser Ser Glu Thr Thr Asn Glu Trp Gly Cys Gly His
            755                        760                        765
Phe His Ile Phe Val Phe Thr Lys Tyr Ser Gln Ala Cys Ser Leu His
        770                        775                        780
Arg Ala Gln Leu Arg Thr His Pro Val Thr Arg Ala Gly His Ser His
785                        790                        795                        800
Gly Phe Phe Ser Cys Gly Leu Gly Phe Gln Gln Leu Glu Val
                805                        810
```

```
        <210> 115
        <211> 241
        <212> PRT
        <213> Homo sapiens


        <400> 115
Met Val Ser Lys Arg Arg Leu Ser Lys Ser Glu Asp Lys Glu Ser Leu
1                   5                       10                      15
Thr Glu Asp Ala Ser Lys Thr Arg Lys Gln Pro Leu Ser Lys Lys Thr
                20                      25                      30
Lys Lys Ser His Ile Ala Asn Glu Val Glu Glu Asn Asp Ser Ile Phe
            35                      40                      45
Val Lys Leu Leu Lys Ile Ser Gly Ile Ile Leu Lys Thr Gly Glu Ser
        50                      55                      60
Gln Asn Gln Leu Ala Val Asp Gln Ile Ala Phe Gln Lys Lys Leu Phe
65                      70                      75                      80
Gln Thr Leu Arg Arg His Pro Ser Tyr Pro Thr Ile Ile Glu Glu Phe
                85                      90                      95
Val Ser Gly Leu Glu Ser Tyr Ile Glu Asp Glu Asp Ser Leu Arg Asn
```

67

```
                  100                      105                     110
Cys Leu Leu Ser Cys Glu Arg Leu Gln Asp Glu Glu Ala Ser Met Gly
        115                     120                     125
Ala Ser Tyr Ser Lys Ser Leu Ile Lys Leu Leu Leu Gly Ile Asp Ile
    130                     135                     140
Leu Gln Pro Ala Ile Ile Lys Thr Leu Phe Glu Lys Leu Pro Glu Tyr
145                     150                     155                     160
Phe Phe Glu Asn Lys Asn Ser Asp Glu Ile Asn Ile Pro Arg Leu Ile
                165                     170                     175
Val Ser Gln Leu Lys Trp Leu Asp Arg Val Val Asp Gly Lys Asp Leu
            180                     185                     190
Thr Thr Lys Ile Met Gln Leu Ile Ser Ile Ala Pro Glu Asn Leu Gln
        195                     200                     205
His Asp Ile Ile Thr Ser Leu Pro Glu Ile Leu Gly Asp Ser Gln His
    210                     215                     220
Ala Asp Val Gly Lys Glu Leu Arg Trp Ile Asn Pro Leu Ser Ser Ser
225                     230                     235                     240
Lys
```

```
        <210> 116
        <211> 396
        <212> PRT
        <213> Homo sapiens


        <400> 116
Met Val Glu Arg Arg Pro Tyr Leu Asp Ala Arg Pro Arg Asn Ser His
1               5                       10                      15
Thr Asn His Arg Gly Pro Val Asp Gly Glu Leu Pro Pro Arg Ala Arg
            20                      25                      30
Asn Gln Ala Asn Asn Pro Pro Ala Asn Ala Leu Arg Gly Gly Ala Ser
        35                      40                      45
His Pro Gly Ser Asp Pro Arg Ala Asn Asn His Pro Ala Ala Tyr Cys
    50                      55                      60
Gln Arg Glu Glu Arg Phe Arg Ala Met Gly Trp Asn Pro His Gln Gly
65                      70                      75                      80
Ser Glu Glu Gln Glu Trp His Val Cys Asp Glu Ala Arg Asp Gln Arg
                85                      90                      95
His Cys Gln Gly Asn Asp Thr Arg Trp Arg Asn Gly Asn Gln Asp Cys
            100                     105                     110
Arg Asn Arg Arg Pro Pro Trp Ser Asn Asp Asn Phe Gln Gln Trp Arg
        115                     120                     125
Thr Pro His Gln Lys Pro Thr Glu Gln Pro Gln Gln Ala Lys Lys Leu
    130                     135                     140
Gly Tyr Lys Phe Leu Glu Ser Leu Leu Gln Lys Asp Pro Ser Glu Val
145                     150                     155                     160
Val Ile Thr Leu Ala Thr Ser Leu Gly Leu Lys Glu Leu Leu Ser His
                165                     170                     175
Ser Ser Met Lys Ser Asn Phe Leu Glu Leu Ile Cys Gln Val Leu Arg
            180                     185                     190
Lys Ala Cys Ser Ser Lys Met Asp Arg Gln Ser Val Leu His Val Leu
        195                     200                     205
Gly Ile Leu Lys Asn Ser Lys Phe Leu Lys Val Cys Leu Pro Ala Tyr
    210                     215                     220
Val Val Gly Met Ile Thr Glu Pro Ile Pro Asp Ile Arg Asn Gln Tyr
225                     230                     235                     240
Pro Glu His Ile Ser Asn Ile Ile Ser Leu Leu Gln Asp Leu Val Ser
                245                     250                     255
Val Phe Pro Ala Ser Ser Val Gln Glu Thr Ser Met Leu Val Ser Leu
            260                     265                     270
Leu Pro Thr Ser Leu Asn Ala Leu Arg Ala Ser Gly Val Asp Ile Glu
```

68

```
          275                    280                    285
Glu Glu Thr Glu Lys Asn Leu Glu Lys Val Gln Thr Ile Ile Glu His
    290                    295                    300
Leu Gln Glu Lys Arg Arg Glu Gly Thr Leu Arg Val Asp Thr Tyr Thr
305                    310                    315                    320
Leu Val Gln Ala Glu Glu Arg Gly Arg Met Leu Arg Ala Thr Leu Thr
              325                    330                    335
Met Pro Arg Tyr Pro Thr Tyr Thr Glu Ala His Leu Gly Glu Glu Ala
              340                    345                    350
Leu Pro Ser Pro Gln Tyr His Phe Trp Lys Ile Arg Gln His Cys Tyr
              355                    360                    365
Leu Ser Gly Tyr Pro Leu Pro Ala Ser Gly Arg Arg Phe Arg Gln Thr
    370                    375                    380
Phe Thr Gly Arg Tyr Phe Gly Thr Ser Pro Lys Leu
385                    390                    395
```

```
          <210> 117
          <211> 153
          <212> PRT
          <213> Homo sapiens
```

```
          <400> 117
Met Gly Trp Leu Phe Leu Lys Val Leu Val Ala Gly Glu Ser Phe Ser
1                   5                   10                   15
Gly Leu Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
              20                   25                   30
Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
              35                   40                   45
Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
    50                   55                   60
Asp Asn Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
65                   70                   75                   80
Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
              85                   90                   95
Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
              100                  105                  110
Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
    115                  120                  125
Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
    130                  135                  140
Ser Tyr Gln Pro Arg Val Pro Trp Ser
145                  150
```

```
          <210> 118
          <211> 169
          <212> PRT
          <213> Homo sapiens
```

```
          <400> 118
Met Pro Pro Asn Asn Cys Tyr Val Asn Phe Glu Arg Phe Ala Cys Val
1                   5                   10                   15
Val Glu Asp Val Ala Arg Val Asp Leu Gly Cys Arg Ala Leu Val Glu
              20                   25                   30
Ala His Asp Thr Ile Gln Asp Asp Val Glu Ala Leu Val Ser Ile Phe
    35                   40                   45
Asn Glu Lys Glu Ala Trp Tyr Arg Glu Glu Asn Glu Ser Ala Arg His
    50                   55                   60
Asp Leu Ser Gln Leu Arg Tyr Glu Phe Arg Lys Val Glu Ser Leu Lys
```

```
     65                      70                      75                      80
Lys Leu Leu Arg Glu Asp Ile Gln Ala Thr Gly Cys Ser Leu Gly Ser
                    85                      90                      95
Met Ala Arg Lys Leu Asp His Leu Gln Ala Gln Phe Glu Ile Leu Arg
            100                     105                     110
Gln Glu Leu Ser Ala Asp Leu Gln Trp Ile Gln Glu Leu Val Gly Ser
            115                     120                     125
Phe Gln Leu Glu Ser Gly Ser Ser Glu Gly Leu Gly Ser Thr Phe Tyr
        130                     135                     140
Gln Asp Thr Ser Glu Ser Leu Ser Glu Leu Leu Ser Arg Ser Cys Thr
145                     150                     155                     160
Glu Glu Phe Leu Ala Gly Trp Lys Leu
                    165
```

```
        <210> 119
        <211> 51
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 119
Met Val Pro Val Phe Ser Val Glu Lys Asp Gly Glu Glu Leu Gly Ser
 1               5                      10                      15
Phe Arg Pro Arg Trp Ala Asp Trp Leu Thr Gly Leu Leu Glu Trp Val
                20                      25                      30
Ser Val Glu Ser Leu Ser Ile Tyr Cys Ile Ser Gln Pro Val Tyr Met
            35                      40                      45
Trp Val Glu
        50
```

```
        <210> 120
        <211> 169
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 120
Met Gly Ser Lys Gly Arg Ser Leu Asp Ala Arg Ser Arg Gly Gly Arg
 1               5                      10                      15
Thr Ser Met Arg Lys Pro Leu Ala Glu Asn Gly Arg Ser Ser Ala Ala
                20                      25                      30
Ser Gln Pro Gln Leu Pro Gly Arg Cys Ser Arg Asp Ile Gly Gly Val
            35                      40                      45
Asn Ile Gln Lys Cys Asp Cys Leu Thr Gln Pro Arg Ala Leu Ala Ile
        50                      55                      60
Ile Lys Arg Cys Ser Asp Gly Ala Val Gln Glu Cys Asp Ala Gly Glu
65                      70                      75                      80
Leu Glu Gln Gln Ser His Ile Ser Thr Ser Arg Pro Thr Ala Val Ser
                85                      90                      95
His Thr Leu Glu Pro Ser Phe Ala Gln Ser His Met His Asp Trp Asp
            100                     105                     110
Arg Gly Phe Arg Pro Leu Pro Thr Pro His Ala Gly Ser Val Pro Asp
            115                     120                     125
Ala Gln Val Pro His Trp Gly Ala Leu Ser Arg Leu Leu His Thr Leu
        130                     135                     140
Arg Ser Cys Pro Pro Gln Glu Arg Leu Arg Ala Ser Ser Val Lys Trp
145                     150                     155                     160
Asn Ser Lys Gln Pro Pro Gly His Ser
                165
```

```
        <210> 121
        <211> 428
        <212> PRT
        <213> Homo sapiens


        <400> 121
Met Ser Val Asp Tyr Gln Ala Ser Phe Val Gly His Pro Pro Gly Ser
1               5                   10                  15
Ala Tyr Pro Lys Leu Asn Phe Val Glu Asp Ser Lys Val Val Leu Gly
            20                  25                  30
Asp Ser Lys Glu Gly Ala Phe Ala Tyr Val His His Leu Thr Leu Tyr
        35                  40                  45
Asp Leu Glu Ala Arg Gly Phe Val Arg Pro Phe Cys Met Ala Tyr Ile
    50                  55                  60
Ser Ala Asp Gln His Lys Ile Met Gln Gln Phe Gln Glu Leu Ser Ala
65                  70                  75                  80
Glu Phe Ser Arg Ala Ser Glu Cys Leu Lys Thr Gly Asn Arg Lys Ala
                85                  90                  95
Phe Ala Gly Glu Leu Glu Lys Lys Leu Lys Asp Leu Asp Tyr Thr Arg
            100                 105                 110
Thr Val Leu His Thr Glu Thr Glu Ile Gln Lys Lys Ala Asn Asp Lys
        115                 120                 125
Gly Phe Tyr Ser Ser Gln Ala Ile Glu Lys Ala Asn Glu Leu Ala Ser
    130                 135                 140
Val Glu Lys Ser Ile Ile Glu His Gln Asp Leu Leu Lys Gln Ile Arg
145                 150                 155                 160
Ser Tyr Pro His Arg Lys Leu Lys Gly His Asp Leu Cys Pro Gly Glu
                165                 170                 175
Met Glu His Ile Gln Asp Gln Ala Ser Gln Ala Ser Thr Thr Ser Asn
            180                 185                 190
Pro Asp Glu Ser Ala Asp Thr Asp Leu Tyr Thr Cys Arg Pro Ala Tyr
        195                 200                 205
Thr Pro Lys Leu Ile Lys Ala Lys Ser Thr Lys Cys Phe Asp Lys Lys
    210                 215                 220
Leu Lys Thr Leu Glu Glu Leu Cys Asp Thr Glu Tyr Phe Thr Gln Thr
225                 230                 235                 240
Leu Ala Gln Leu Ser His Ile Glu His Met Phe Arg Gly Asp Leu Cys
                245                 250                 255
Tyr Leu Leu Thr Ser Gln Ile Asp Arg Ala Leu Leu Lys Gln Gln His
            260                 265                 270
Ile Thr Asn Phe Leu Phe Glu Asp Phe Val Glu Val Asp Asp Arg Met
        275                 280                 285
Val Glu Lys Gln Glu Ser Ile Pro Ser Lys Pro Ser Gln Asp Arg Pro
    290                 295                 300
Pro Ser Ser Ser Leu Glu Glu Cys Pro Ile Pro Lys Val Leu Ile Ser
305                 310                 315                 320
Val Gly Ser Tyr Lys Ser Ser Val Glu Ser Val Leu Ile Lys Met Glu
                325                 330                 335
Gln Glu Leu Gly Asp Glu Glu Tyr Lys Glu Val Glu Val Thr Glu Leu
            340                 345                 350
Ser Ser Phe Asp Pro Gln Glu Asn Leu Asp Tyr Leu Asp Met Asp Met
        355                 360                 365
Lys Gly Ser Ile Ser Ser Gly Glu Ser Ile Glu Val Leu Gly Thr Glu
    370                 375                 380
Lys Ser Thr Ser Val Leu Ser Lys Ser Asp Ser Gln Ala Ser Leu Thr
385                 390                 395                 400
Val Pro Leu Ser Pro Gln Val Val Arg Ser Lys Ala Val Ser His Arg
                405                 410                 415
Thr Ile Ser Glu Asp Ser Ile Glu Val Leu Ser Thr
            420                 425
```

71

```
        <210> 122
        <211> 168
        <212> PRT
        <213> Homo sapiens


        <400> 122
Met Gly Glu Glu Ala Val Arg Trp Ala Lys Leu Val Ile Pro Leu Val
1               5                   10                  15
Val His Ser Ala Gln Lys Val His Leu Arg Gly Ala Thr Ala Leu Glu
            20                  25                  30
Met Gly Met Pro Leu Leu Leu Gln Lys Gln Gln Glu Ile Ala Ser Ile
        35                  40                  45
Thr Glu Gln Leu Met Thr Thr Thr Leu His Arg Ser Gly Ser Phe Ile
    50                  55                  60
Asn Ser Leu Leu Gln Leu Glu Glu Leu Gly Phe Arg Ser Gly Ala Pro
65                  70                  75                  80
Met Ile Lys Lys Ile Ala Phe Ile Ala Trp Lys Ser Leu Ile Asp Asn
                85                  90                  95
Phe Ala Leu Asn Pro Asp Ile Leu Cys Ser Ala Lys Arg Leu Lys·Leu
            100                 105                 110
Leu Met Gln Pro Leu Ser Ser Ile His Val Arg Thr Glu Thr Leu Ala
        115                 120                 125
Leu Thr Lys Leu Glu Val Trp Trp Tyr Leu Leu Met Arg Leu Gly Pro
    130                 135                 140
His Leu Pro Ala Asn Phe Glu Gln Gly Cys Val Pro Leu Ile Gln Ser
145                 150
???????????????????????????????????????????????????????????????????
??????????????????????????????????????????????????                 55
60
Ser Leu Asp Phe Lys Phe Gly Arg Arg Ser Asn Arg Ala Asp Glu Leu
65
???????????????????????????????????????????????????????????????????
?????????????????????????????????????????????????                 85
90                  95
Ala Thr Ala Gly Asn Arg Gly Leu Ala Phe Pro Ser Arg His Ile AsnVal Ala Met
Asp Thr Asp
            35                  40                  45
Ser Glu Thr Ser Ser Pro Ala Pro Ser Pro Val Gln Pro Pro Phe Phe
    50                  55                  60
Ser Glu Cys Ser Leu Gly Tyr Phe Ser Pro Ala Pro Ser Leu Ser Leu
65                  70                  75                  80
Pro Pro Pro Pro Gln Val Ser Ser Leu Pro Pro Leu Ser Gln Pro Tyr
                85                  90                  95
Val Glu Gly Leu Cys Val Ser Leu Glu Pro Leu Pro Pro Leu Pro Pro
            100                 105                 110
Leu Pro Pro Leu Pro Pro Glu Asp Pro Glu Gln Pro Pro Lys Pro Pro
        115                 120                 125
Phe Ala Asp Glu Glu Glu Glu Glu Glu Met Leu Leu Arg Glu Glu Leu
    130                 135                 140
Leu Lys Ser Leu Ala Asn Lys Arg Ala Phe Lys Pro Glu Leu Pro Lys
145                 150                 155                 160
His Lys Ser Val Val Val Thr Leu Asn Asp Ser Asp Asp Ser Glu Ser
                165                 170                 175
Asp Gly Glu Ala Ser Lys Ser Thr Asn Ser Val Phe Gly Gly Leu Glu
            180                 185                 190
Ser Met Ile Lys Glu Ala Arg Arg Thr Ala Glu Gln Ala Ser Lys Pro
        195                 200                 205
Lys Val Pro Pro Lys Ser Glu Lys Glu Asn Asp Pro Leu Arg Thr Pro
    210                 215                 220
Glu Ala Leu Pro Glu Glu Lys Lys Ile Glu Tyr Arg Leu Leu Lys Gly
225                 230                 235                 240
```

```
Arg Asp Cys Gln Phe Lys Phe Ile Leu Gly Cys Asn Ala Tyr Ile Leu
              245                 250                 255
Phe Asp Asn Phe Ser Arg Glu Lys Gln Arg Leu Ile Lys Ser Asp Gln
          260                 265                 270
Leu Lys Thr Ser Ser Ser Ser Pro Ala Asn Ser Asp Val Glu Ile Asp
          275             280             285
Gly Ile Gly Arg Ile Ala Met Val Thr Lys Gln Val Thr Asp Ala Glu
      290             295             300
Ser Lys Leu Lys Lys His Arg Ile Leu Leu Met Lys Asp Glu Ser Val
305             310             315             320
Leu Lys Asn Leu Val Gln Gln Glu Ala Lys Lys Lys Glu Ser Val Arg
              325             330             335
Asn Ala Glu Ala Lys Ile Thr Lys Leu Thr Glu Gln Leu Gln Ala Thr
          340             345             350
Glu Lys Ile Leu Asn Val Asn Arg Met Phe Leu Lys Lys Leu Gln Glu
          355             360             365
Gln Ile His Arg Val Gln Gln Arg Val Thr Ile Lys Lys Ala Leu Thr
      370             375             380
Leu Lys Tyr Gly Glu Glu Leu Ala Arg Ala Lys Ala Val Ala Ser Lys
385             390             395             400
Glu Ile Gly Lys Arg Lys Leu Glu Gln Asp Arg Phe Gly Val Arg Val
              405             410             415
Leu
```

```
<210> 124
<211> 123
<212> PRT
<213> Homo sapiens
```

```
<400> 124
Met Cys Pro Phe Cys Ala Asp Arg Asp Ser Val Glu Asp Asp Ile Gln
1               5                   10                  15
Phe Phe Asn Gly Val Thr Ala Thr Ser Trp Val Gln Gln Gly Val Gly
              20              25              30
Asp Ser Lys Glu Gln Met Ile Gln Ile Arg Val Arg Trp Val Gln Arg
          35              40              45
Asp Thr Leu Gly Ser Arg Pro Thr Arg Leu Pro Val Ser Leu Ser Cys
      50              55              60
Gly Gly Gly Thr Val Ala Phe Val Cys Leu Pro Leu Ala Gln Thr Pro
65              70              75              80
Glu Leu Arg Val Gly Lys Met Lys Ala Ala Arg Gly Thr Leu Pro Pro
              85              90              95
Pro Thr Leu Ser Ser Arg Thr Ser Ala Asn Glu Arg Ala Thr Leu Ala
          100             105             110
Ser Trp Gly Thr Asp His Phe Leu Ser Ser Leu
          115             120
```

```
<210> 125
<211> 104
<212> PRT
<213> Homo sapiens
```

```
<400> 125
Met Val Trp Val Leu Leu Ala Trp Ser Thr Cys Pro Gly Leu Leu Gly
1               5                   10                  15
Phe Lys Pro Thr Val Glu Ile Glu Gly Thr Val Pro Trp Ser Pro Ala
              20              25              30
```

```
Gly Thr Ser Arg Val Leu Pro Thr Arg Val Ala Glu Ser Leu Gly Leu
        35                  40                  45
Arg Val Thr Ser Gly Gly Thr Arg Ser Ser Ala Pro Glu Ala Pro Thr
    50                  55                  60
Met Lys Gln Ser Asp Ala Ser Pro Gln Glu Arg Tyr Pro Pro Ala Ser
65                  70                  75                  80
Pro Glu Thr Glu Trp Asp Pro Asn Gly Ile Phe Gly Gly Gly Glu Ser
                85                  90                  95
Val Pro Gln Arg Glu Thr Ser Thr
            100
```

```
<210> 126
<211> 147
<212> PRT
<213> Homo sapiens


<400> 126
Met Gln Val Leu Ile Gln Gly Leu Glu Glu Pro Phe Gln Ala Gly Leu
1               5                   10                  15
Val Cys Val Leu Trp Asn Gly Val Gly Gln Ile Thr Ser Thr Ala Val
                20                  25                  30
Phe Glu Gln Cys Val Trp Asn Ile Ala Leu His Gln Gly Cys His Thr
        35                  40                  45
Ser His Val Val Gln Leu Met Gly Leu Gln Asn Arg Arg Leu Pro Arg
    50                  55                  60
Glu Cys Gln Ala Glu Ser Leu Ala Ile Cys Leu Leu Gln Ala Gln Gly
65                  70                  75                  80
Arg His Ala Ala Arg Glu Pro His Met Leu Glu His Gly His Ala Val
                85                  90                  95
Thr Gln Arg Ile Arg Val Met Gln Met Ala Gly Cys Glu Tyr Asp Arg
            100                 105                 110
Thr Thr Phe Ser Val Leu Gln Gln Asn Val Pro Gln Ala Met Thr Gly
        115                 120                 125
Ala Arg Val His Pro Ala Gly Gly Leu Ile Gln Asn Gly Gly Pro Ala
    130                 135                 140
His Gly His
145
```

```
<210> 127
<211> 532
<212> PRT
<213> Homo sapiens


<400> 127
Met Ala Ser His Ala Tyr Asp Lys Asn Gln Asn Ala Asn Val Leu Val
1               5                   10                  15
His Leu Cys Phe Tyr Asn Arg Ile Pro Lys Thr Gly Ala Tyr Tyr Leu
                20                  25                  30
Asp Ser Arg Ser Val Ser Ile Ser Tyr Leu Ile Gly His His Ile Asp
        35                  40                  45
Met Gly Leu Glu Thr Ala Thr Ser Lys Asn Glu Phe Ile Phe Asp Ser
    50                  55                  60
Ala Ser Thr Leu Leu Gly Met Leu Phe Arg Lys Pro Ser Gln His Ser
65                  70                  75                  80
Leu Ser Leu Phe Ser Lys Lys Phe Gln Glu Asn Leu Ile Tyr Leu Glu
                85                  90                  95
Ser Asp Asp Cys Leu Pro Pro Pro Pro Pro Pro Trp Ser Glu Pro
            100                 105                 110
```

```
Pro Ser Phe Leu Thr Trp Thr Ile Val Thr Val Phe Gln Trp Val Ser
        115                 120                 125
Leu Leu Leu Ser Leu Pro Asn Ile Gln Val Ile Leu Tyr Arg Ala Val
        130                 135                 140
Gly Val Val Pro Ser Gln Pro Lys Ser Asp Asn Leu Lys Gly Trp Gly
145                 150                 155                 160
Ser Gly Arg Val Val Lys Glu Lys Leu Arg Ser Glu Ile Pro Asp Trp
                165                 170                 175
Lys Ile Lys Ser Ile His Ile Leu Glu Arg Thr Ala Ser Ser Ser Thr
                180                 185                 190
Glu Pro Ser Val Ser Arg Gln Leu Leu Glu Pro Glu Pro Val Pro Leu
        195                 200                 205
Ser Lys Glu Ala Asp Ser Trp Glu Ile Ile Glu Gly Leu Lys Ile Gly
        210                 215                 220
Gln Thr Asn Val Gln Lys Pro Asp Lys His Glu Gly Phe Met Leu Lys
225                 230                 235                 240
Lys Arg Lys Trp Pro Leu Lys Gly Trp His Lys Ile Gln Lys Gly Lys
                245                 250                 255
Val His Gly Ser Ile Asp Val Gly Leu Ser Val Met Ser Ile Lys Lys
                260                 265                 270
Lys Ala Arg Arg Ile Asp Leu Asp Thr Glu Glu His Ile Tyr His Leu
        275                 280                 285
Lys Val Lys Ser Val Phe Asn Ser Phe Ser Ala Ile Ile Arg Gly Asn
        290                 295                 300
Asp Leu Pro Thr Pro Val Val Lys Ser Gln Asp Trp Phe Asp Ala Trp
305                 310                 315                 320
Val Ser Lys Leu Arg His His Arg Leu Tyr Arg Gln Asn Glu Ile Val
                325                 330                 335
Arg Ser Pro Arg Asp Ala Ser Phe His Ile Phe Pro Ser Thr Ser Thr
                340                 345                 350
Ala Glu Ser Ser Pro Ala Ala Asn Val Ser Val Met Asp Gly Lys Met
        355                 360                 365
Gln Pro Asn Ser Phe Pro Trp Gln Ser Pro Leu Pro Cys Ser Asn Ser
        370                 375                 380
Leu Pro Ala Thr Cys Thr Thr Gly Gln Ser Lys Val Ala Ala Trp Leu
385                 390                 395                 400
Gln Asp Ser Glu Glu Met Asp Arg Cys Ala Glu Asp Leu Ala His Cys
                405                 410                 415
Gln Ser Asn Leu Val Glu Leu Ser Lys Leu Leu Gln Asn Leu Glu Ile
                420                 425                 430
Leu Gln Arg Thr Gln Ser Ala Pro Asn Phe Thr Asp Met Gln Ala Asn
        435                 440                 445
Cys Val Asp Ile Ser Lys Lys Asp Lys Arg Val Thr Arg Arg Trp Arg
        450                 455                 460
Thr Lys Ser Val Ser Lys Asp Thr Lys Ile Gln Leu Gln Val Pro Phe
465                 470                 475                 480
Ser Ala Thr Met Ser Pro Val Arg Leu His Ser Ser Asn Pro Asn Leu
                485                 490                 495
Cys Ala Asp Ile Glu Phe Gln Thr Pro Pro Ser His Leu Thr Asp Pro
                500                 505                 510
Leu Glu Ser Ser Thr Asp Tyr Thr Lys Leu Gln Glu Glu Phe Cys Leu
        515                 520                 525
Ile Ala Gln Lys
        530
```

```
<210> 128
<211> 210
<212> PRT
<213> Homo sapiens


<400> 128
```

```
Met Glu Gly Gly Phe Val Glu Val Ile His Asp Lys Lys Gln Tyr Pro
1               5                   10                  15
Ile Ser Glu Leu Cys Lys Gln Phe Arg Leu Pro Phe Asn Val Lys Val
        20                  25                  30
Ser Val Arg Asp Leu Ser Ile Glu Glu Asp Val Leu Ala Ala Thr Pro
    35                  . 40                 45
Gly Leu Gln Leu Glu Glu Asp Ile Thr Asp Ser Tyr Leu Leu Ile Ser
    50                  55                  60
Asp Phe Ala Asn Pro Thr Glu Cys Trp Glu Ile Pro Val Gly Arg Leu
65                  70                  75                  80
Asn Met Thr Val Gln Leu Val Ser Asn Phe Ser Arg Asp Ala Glu Pro
                85                  90                  95
Phe Leu Val Arg Thr Leu Val Glu Glu Ile Thr Glu Glu Gln Tyr Tyr
            100                 105                 110
Met Met Arg Arg Tyr Glu Ser Ser Ala Ser His Pro Pro Pro Arg Pro
            115                 120                 125
Pro Lys His Pro Ser Val Glu Glu Thr Lys Leu Thr Leu Leu Thr Leu
    130                 135                 140
Ala Glu Glu Arg Thr Val. Asp Leu Pro Lys Ser Pro Lys Arg His His
145                 150                 155                 160
Val Asp Ile Thr Lys Lys Leu His Pro Asn Gln Ala Gly Leu Asp Leu
            165                 170                 175
Val Asp Glu Glu Lys Asp Arg Ser Asn Arg Gly Ala Thr Ala Leu Ala
            180                 185                 190
Glu Thr Phe Asn Asn Asp Lys His His Lys Tyr Gln Asp Val Thr Glu
    195                 200                 205
Ala Thr
210
```

```
        <210> 129
        <211> 515
        <212> PRT
        <213> Homo sapiens


        <400> 129
Met Phe Ala Phe Glu Pro Leu Gly Gly Cys Arg Pro Trp Arg Leu Ser
1               5                   10                  15
Leu Pro Gly Pro Gly Ser Arg Leu Phe Arg Thr Tyr Gly Ala Ala Asp
            20                  25                  30
Gly Arg Arg Gln Arg Arg Pro Gly Arg Glu Ala Ala Gln Trp Phe Pro
        35                  40                  45
Pro Gln Asp Arg Arg Arg Phe Phe Asn Ser Ser Gly Ser Ser Asp Ala
    50                  55                  60
Ser Ile Gly Asp Pro Ser Gln Ser Asp Asp Pro Asp Asp Pro Asp Asp
65                  70                  75                  80
Pro Asp Phe Pro Gly Ser Pro Val Arg Arg Arg Arg Cys Pro Gly
            85                  90                  95
Gly Arg Val Pro Lys Asp Arg Pro Ser Leu Thr Val Thr Pro Lys Arg
            100                 105                 110
Trp Lys Leu Arg Ala Arg Pro Ser Leu Thr Val Thr Pro Arg Arg Leu
    115                 120                 125
Gly Leu Arg Ala Arg Pro Pro Gln Lys Cys Ser Thr Pro Cys Gly Pro
    130                 135                 140
Leu Arg Leu Pro Pro Phe Pro Ser Arg Asp Ser Gly Arg Leu Ser Pro
145                 150                 155                 160
Asp Leu Ser Val Cys Gly Gln Pro Arg Asp Gly Asp Glu Leu Gly Ile
            165                 170                 175
Ser Ala Ser Leu Phe Ser Ser Leu Ala Ser Pro Cys Pro Gly Ser Pro
            180                 185                 190
Thr Pro Arg Asp Ser Val Ile Ser Ile Gly Thr Ser Ala Cys Leu Val
    195                 200                 205
```

```
Ala Ala Ser Ala Val Pro Ser Gly Leu His Leu Pro Glu Val Ser Leu
210                 215                 220
Asp Arg Ala Ser Leu Pro Cys Ser Gln Glu Glu Ala Thr Gly Gly Ala
225                 230                 235                 240
Lys Asp Thr Arg Met Val His Gln Thr Arg Ala Ser Leu Arg Ser Val
            245                 250                 255
Leu Phe Gly Leu Met Asn Ser Gly Thr Pro Glu Asp Ser Glu Phe Arg
            260                 265                 270
Ala Asp Gly Lys Asn Met Arg Glu Ser Cys Cys Lys Arg Lys Leu Val
            275                 280                 285
Val Gly Asn Gly Pro Glu Gly Pro Gly Leu Ser Ser Thr Gly Lys Arg
    290                 295                 300
Arg Ala Thr Gly Gln Asp Ser Cys Gln Glu Arg Gly Leu Gln Glu Ala
305                 310                 315                 320
Val Arg Arg Glu His Gln Glu Ala Ser Val Pro Lys Gly Arg Ile Val
            325                 330                 335
Pro Arg Gly Ile Asp Arg Leu Glu Arg Thr Arg Ser Ser Arg Lys Ser
            340                 345                 350
Lys His Gln Glu Ala Thr Glu Thr Ser Leu Leu His Ser His Arg Phe
        355                 360                 365
Lys Lys Gly Gln Lys Leu Gly Lys Asp Ser Phe Pro Thr Gln Asp Leu
    370                 375                 380
Thr Pro Leu Gln Asn Ala Cys Phe Trp Thr Lys Thr Arg Ala Ser Phe
385                 390                 395                 400
Ser Phe His Lys Lys Lys Ile Val Thr Asp Val Ser Glu Val Cys Ser
            405                 410                 415
Ile Tyr Thr Thr Ala Thr Ser Leu Ser Gly Ser Leu Leu Ser Glu Cys
        420                 425                 430
Ser Asn Arg Pro Val Met Asn Arg Thr Ser Gly Ala Pro Ser Ser Trp
        435                 440                 445
His Ser Ser Ser Met Tyr Leu Leu Ser Pro Leu Asn Thr Leu Ser Ile
    450                 455                 460
Ser Asn Lys Lys Ala Ser Asp Ala Glu Lys Val Tyr Gly Glu Cys Ser
465                 470                 475                 480
Gln Lys Gly Pro Val Pro Phe Ser His Cys Leu Pro Thr Glu Lys Leu
            485                 490                 495
Gln Arg Cys Glu Lys Ile Gly Glu Gly Val Phe Gly Gly Ser Val Ser
            500                 505                 510
Asn Asn Cys
        515
```

```
<210> 130
<211> 155
<212> PRT
<213> Homo sapiens


<400> 130
Met Asn Gly Arg Lys Glu Glu Gly Glu Arg Leu Thr Lys Glu Val Met
1               5                   10                  15
Ser Ser Tyr Ile Gln Ser Glu Phe Ala Ser Val Cys Thr Ser Asn Ser
            20                  25                  30
Ile Leu Asp Leu Phe Arg Thr Pro Ala Ile Arg Lys Val Thr Cys Cys
        35                  40                  45
Leu Met Val Ile Trp Arg Met Ala Pro Pro Ala Gly Arg Glu Leu Arg
    50                  55                  60
Ile Ala Ala Glu Ser Leu Ser Gln Gln Lys Arg Ala Phe Ala Val Ser
65                  70                  75                  80
Arg Arg Ile Gln Glu Arg Thr Phe Ser Ser Gly Ile Leu Asn Ser Gly
            85                  90                  95
Ser Val Ser Pro Ser Arg Lys Glu Glu Gly Gly Arg Arg Ala Ser Pro
            100                 105                 110
```

```
Gly Arg Gln Gly Leu Pro Gln Glu Asp Ala His Ser Trp Thr Arg Val
        115                 120                 125
Arg Arg Ser Pro Leu Ala Pro Gln Ser Arg Asn Cys Ala Ala Cys His
    130                 135                 140
Ala Arg Leu Thr Pro Arg Lys Ser Arg Ala Thr
145                 150                 155
```


        <210> 131
        <211> 145
        <212> PRT
        <213> Homo sapiens

        <400> 131
```
Met Leu Asp Gln Cys Arg Thr Leu Ala Ser Arg Gly Thr Pro Pro Cys
1               5                   10                  15
Lys Pro Ser Cys Val Ser Gln Leu Gly Gln Arg Ala Glu Pro Lys Ala
            20                  25                  30
Thr Glu Arg Gly Ile Leu Arg Ala Thr Cys Val Ala Trp Glu Ser Gln
        35                  40                  45
Leu Lys Pro Glu Glu Leu Pro Ser Met Gln Asp Leu Leu Glu Glu Ala
    50                  55                  60
Ser Ser Arg Asp Met Gln Met Gly Pro Gly Leu Phe Leu Arg Met Gln
65                  70                  75                  80
Leu Val Pro Ser Ile Glu Glu Arg Glu Thr Pro Leu Thr Arg Glu Asp
                85                  90                  95
Arg Pro Ala Leu Gln Glu Pro Pro Trp Ser Leu Gly Cys Thr Gly Leu
        100                 105                 110
Lys Ala Ala Met Gln Ile Gln Arg Val Val Ile Pro Val Pro Thr Leu
    115                 120                 125
Gly His Arg Asn Pro Trp Val Ala Arg Asp Ser Gly Ala Ile Gly Asn
    130                 135                 140
Gly
145
```


        <210> 132
        <211> 288
        <212> PRT
        <213> Homo sapiens

        <400> 132
```
Met Asp Ala Ala Val Thr Asp Asp Phe Gln Gln Ile Leu Pro Ile Glu
1               5                   10                  15
Gln Leu Arg Ser Thr His Ala Ser Asn Asp Tyr Val Glu Arg Pro Pro
            20                  25                  30
Ala Pro Cys Lys Gln Ala Leu Ser Ser Pro Ser Leu Ile Val Gln Thr
        35                  40                  45
His Lys Ser Asp Trp Ser Leu Ala Thr Met Pro Thr Ser Leu Pro Arg
    50                  55                  60
Ser Leu Ser Gln Cys His Gln Leu Gln Pro Leu Pro Gln His Leu Ser
65                  70                  75                  80
Gln Ser Ser Ile Ala Ser Ser Met Ser His Ser Thr Thr Ala Ser Asp
                85                  90                  95
Gln Arg Leu Leu Ala Ser Ile Thr Pro Ser Pro Ser Gly Gln Ser Ile
        100                 105                 110
Ile Arg Thr Gln Pro Gly Ala Gly Val His Pro Lys Ala Asp Gly Ala
    115                 120                 125
Leu Lys Gly Glu Ala Glu Gln Ser Ala Gly His Pro Ser Glu His Leu
    130                 135                 140
```

```
Phe Ile Cys Glu Glu Cys Gly Arg Cys Lys Cys Val Pro Cys Thr Ala
145             150             155             160
Ala Arg Pro Leu Pro Ser Cys Trp Leu Cys Asn Gln Arg Cys Leu Cys
            165             170             175
Ser Ala Glu Ser Leu Leu Asp Tyr Gly Thr Cys Leu Cys Cys Val Lys
        180             185             190
Gly Leu Phe Tyr His Cys Ser Thr Asp Asp Glu Asp Asn Cys Ala Asp
        195             200             205
Glu Pro Cys Ser Cys Gly Pro Ser Ser Cys Phe Val Arg Trp Ala Ala
    210             215             220
Met Ser Leu Ile Ser Leu Phe Leu Pro Cys Leu Cys Cys Tyr Leu Pro
225             230             235             240
Thr Arg Gly Cys Leu His Leu Cys Gln Gln Gly Tyr Asp Ser Leu Arg
            245             250             255
Arg Pro Gly Cys Arg Cys Lys Arg His Thr Asn Thr Val Cys Arg Lys
            260             265             270
Ile Ser Ser Gly Ser Ala Pro Phe Pro Lys Ala Gln Glu Lys Ser Val
    275             280             285
```

```
<210> 133
<211> 255
<212> PRT
<213> Homo sapiens


<400> 133
Met Glu Asn Glu Lys Glu Asn Leu Phe Cys Glu Pro His Lys Arg Gly
1               5               10              15
Leu Met Lys Thr Pro Leu Lys Glu Ser Thr Thr Ala Asn Ile Val Leu
            20              25              30
Ala Glu Ile Gln Pro Asp Phe Gly Pro Leu Thr Thr Pro Thr Lys Pro
        35              40              45
Lys Glu Gly Ser Gln Gly Glu Pro Trp Thr Pro Thr Ala Asn Leu Lys
    50              55              60
Met Leu Ile Ser Ala Val Ser Pro Glu Ile Arg Asn Arg Asp Gln Lys
65              70              75              80
Arg Gly Leu Phe Asp Asn Arg Ser Gly Leu Pro Glu Ala Lys Asp Cys
            85              90              95
Ile His Glu His Leu Ser Gly Asp Glu Phe Glu Lys Ser Gln Pro Ser
            100             105             110
Arg Lys Glu Lys Ser Leu Gly Leu Leu Cys His Lys Phe Leu Ala Arg
    115             120             125
Tyr Pro Asn Tyr Pro Asn Pro Ala Val Asn Asn Asp Ile Cys Leu Asp
    130             135             140
Glu Val Ala Glu Glu Leu Asn Val Glu Arg Arg Arg Ile Tyr Asp Ile
145             150             155             160
Val Asn Val Leu Glu Ser Leu His Met Val Ser Arg Leu Ala Lys Asn
            165             170             175
Arg Tyr Thr Trp His Gly Arg His Asn Leu Asn Lys Thr Leu Gly Thr
        180             185             190
Leu Lys Ser Ile Gly Glu Glu Asn Lys Tyr Ala Glu Gln Ile Met Met
        195             200             205
Ile Lys Lys Lys Glu Tyr Glu Gln Glu Phe Asp Phe Ile Lys Ser Tyr
    210             215             220
Ser Ile Glu Asp His Ile Ile Lys Ser Asn Thr Gly Pro Asn Gly His
225             230             235             240
Pro Asp Met Cys Phe Val Glu Leu Pro Gly Val Glu Phe Arg Ala
            245             250             255
```

```
<210> 134
<211> 68
<212> PRT
<213> Homo sapiens


<400> 134
Met Gly Thr Arg Pro Leu His Gly His Lys Leu Ser Arg Trp Asn Ile
1               5                   10                  15
Met Ser Ser Asn Phe Ser Ser Thr Gly Leu Lys Asp Phe Asn Thr Pro
                20                  25                  30
Lys Ala Leu Phe Ile Arg Lys Gly Leu Gly Arg Gly Glu Lys Thr Leu
            35                  40                  45
Val His Phe Ile Gln Val Phe Ser Tyr Thr Arg Lys Gln Ser Ser His
        50                  55                  60
Ser His Glu Asn
65
```

```
<210> 135
<211> 211
<212> PRT
<213> Homo sapiens


<400> 135
Met Tyr Asp Ile Phe Asn Leu Asn Asp Lys Ala Leu Cys Phe Thr Lys
1               5                   10                  15
Cys Arg Gln Ser Gly Ser Asp Ser Cys Asn Val Glu Asn Leu Gln Arg
                20                  25                  30
Tyr Trp Leu Asn Tyr Glu Ala His Leu Met Lys Glu Gly Leu Thr Gln
            35                  40                  45
Lys Val Asn Thr Pro Phe Leu Lys Ala Leu Val Gln Asn Leu Ser Thr
        50                  55                  60
Asn Thr Ala Glu Asp Phe Tyr Leu Ser Leu Glu Pro Ser Gln Val Pro
65                  70                  75                  80
Arg His Val Met Lys Asp Glu Asp Lys Pro Pro Asp Arg Val Arg Leu
                85                  90                  95
Pro Lys Ser Leu Phe Arg Ser Leu Pro Gly Asn Arg Ser Val Val Arg
            100                 105                 110
Leu Ala Val Thr Ile Leu Asp Ile Gly Pro Gly Thr Leu Phe Lys Gly
        115                 120                 125
Pro Arg Leu Gly Leu Gly Asp Gly Ser Gly Val Leu Asn Asn Arg Leu
    130                 135                 140
Val Gly Leu Ser Val Gly Gln Met His Val Thr Lys Leu Ala Glu Pro
145                 150                 155                 160
Leu Glu Ile Val Phe Ser His Gln Arg Pro Pro Pro Lys Pro Thr Met
                165                 170                 175
His Ser Glu Ile Thr Ser Ser Ile Phe Asn Arg Ile Ser Met Thr Cys
                180                 185                 190
Thr Thr Tyr Tyr Tyr Ser Ser Thr Arg Tyr Lys Tyr Asn Asn Ile Ile
            195                 200                 205
His Lys Asp
210
```

```
<210> 136
<211> 147
<212> PRT
<213> Homo sapiens
```

```
        <400> 136
Met Ser Cys Met Cys Trp Pro Asn Met Leu Asn His Gly Glu Leu Glu
1               5                   10                  15
Gln Ala Leu Leu Leu Leu Lys Leu Leu Ile Met Leu Cys Thr Asn Leu
            20                  25                  30
Glu Ser Ile Gln Ala Gly Arg Arg Gln Val Leu Glu His Arg Val Leu
        35                  40                  45
Ser Leu Trp Thr Arg Tyr Leu Ala Glu Leu Lys Gly Cys Pro Pro Pro
    50                  55                  60
Gln Gly Arg Gly Thr Gln Leu Glu Asn Val Ala Leu His Ala Leu Leu
65                  70                  75                  80
Leu Cys Glu Gly Leu Phe Asp Pro Tyr Gln Thr Trp Arg Arg Gln Arg
                85                  90                  95
Ser Gly Glu Val Ile Ser Ser Lys Glu Lys Ser Lys Tyr Lys Phe Pro
            100                 105                 110
Pro Ala Ala Leu Pro Gln Glu Phe Ser Ala Phe Phe Gln Gly Gln Ala
        115                 120                 125
Pro Pro Leu Pro Pro Leu Gly Ser Thr Pro Lys Pro Arg Pro Leu Pro
        130                 135                 140
Val Val Pro
145


        <210> 137
        <211> 36
        <212> PRT
        <213> Homo sapiens


        <400> 137
Met Ser Gly Arg Val Phe Arg Cys Gln Ala Leu Val Ala Tyr Thr Val
1               5                   10                  15
Leu Ser Glu Leu Phe Thr Glu Ala Lys Glu Gln Arg Leu Ala Thr Asp
            20                  25                  30
Glu Gly Gln Lys
        35


        <210> 138
        <211> 41
        <212> PRT
        <213> Homo sapiens


        <400> 138
Met Ser Gly Arg Val Phe Arg Cys Gln Ala Leu Val Ala Tyr Thr Val
1               5                   10                  15
Leu Ser Glu Leu Phe Thr Glu Ala Lys Glu Gln Arg Leu Ala Thr Asp
            20                  25                  30
Glu Gly Gln Lys Glu Phe Ser Ala Glu
        35                  40


        <210> 139
        <211> 100
        <212> PRT
        <213> Homo sapiens


        <400> 139
```

```
Met Gln Lys Arg Leu Lys Val Val Thr Thr Val Leu Thr Asp Ala Ser
1               5                   10                  15
Lys Gly Ser Leu Asp Gln Gly Ser Glu Ala Thr Ser Ala Asn Ser Leu
            20                  25                  30
Cys Gly Ala Cys Val Cys Ala Ser Ser Glu Leu Arg Ser His Gly Leu
        35                  40                  45
Ser Arg Ser Asp Gly Ser Ser Asp Ser Phe His Val Pro Trp Leu His
    50                  55                  60
Gly Ala His Ala Leu Val Leu Leu Pro Asn Ala Gly Ala Ala Glu Ser
65                  70                  75                  80
Pro Leu Ala Arg Pro His Pro Arg Glu Thr His Val Gly Ala Val Pro
                85                  90                  95
Glu Asp Ser Leu
            100
```

```
        <210> 140
        <211> 53
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 140
Met Ser Leu Lys Gln Ala Leu Gln Ser Pro Gly Leu Phe Leu Pro Ala
1               5                   10                  15
Leu Ala Pro Ala Pro Ser Ser Ser Cys Val Gln Asn Gln Ser Gln Arg
            20                  25                  30
Cys Gly Leu Asn Pro Gly Ser Cys Pro Asp Thr Trp Leu Thr Ser Ser
        35                  40                  45
Phe Ser Leu Pro Ser
    50
```

```
        <210> 141
        <211> 419
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 141
Met Glu Ala Ala Asp Val Ala His Arg Ala His Met Ser Gln Lys Ala
1               5                   10                  15
Gly Gly Phe Arg Asn Ile Ala Ile Gln Thr Ser Pro Ser Leu Arg Lys
            20                  25                  30
His Phe Pro Val Phe Lys Arg Lys Arg Leu Thr Ala Ser Lys Ser Leu
        35                  40                  45
Val Glu Met Pro Thr Ala Ser Gln Ser Ala Ile Gln Val Asn Gly Asn
    50                  55                  60
Leu Ser Glu Gln Asp Ile Val Ser Ser Asp Leu Ala Tyr Leu Arg Leu
65                  70                  75                  80
Ala Gln His Leu Glu Asp Gly Pro Arg Arg Val Lys Val Ser His Ala
                85                  90                  95
Phe Leu Pro Arg Val Pro Lys Val Gln Ser Asn Gly Pro Val Ser Ile
            100                 105                 110
Cys Leu Glu Ala Gly Thr Trp Arg Ser Leu Glu Lys Ala Thr Ala Ala
        115                 120                 125
Ile Gln Val Pro Asp Asp Ile Tyr His Ser Pro Ser Trp Glu Ala Arg
    130                 135                 140
Glu Ser Ala Leu Ser Pro Asp Arg Ser Ala Glu Val Ser Asn Ser Ile
145                 150                 155                 160
His Pro Leu Asp Asp Thr Arg Pro Gly Asp Gly Arg Arg Val Thr Pro
                165                 170                 175
```

82

Leu Asp Ser Glu Lys Ser Thr Ser Cys Leu Asn Ala Thr Ser Val Ala
                180   185   190
Ser His Thr Pro Gly Thr Glu Glu Leu Lys Pro Glu Leu Leu Leu Pro
            195   200   205
Lys Asp Asn Ser Asp Asp Lys Asp Leu Gly Ser Leu Ser Ser Gln Ser
    210   215   220
Lys Glu Thr Cys Val Pro Ser Ser Pro Arg Thr His Ser Ser Pro Ser
225   230   235   240
Gln Gly Ser His Ser Gln Pro Ala His Pro Gly Arg Ala Ser Asp Cys
                245   250   255
Pro Ser Ser Ser Asn Asn His Gln Asn Leu Val Ser Leu Lys Thr Asn
            260   265   270
Ser Ala Ser Lys Ser Ala Pro Gly Cys Gln Glu Gln Thr Ala Asn Asn
            275   280   285
Pro Thr Glu Ser Asp Thr Leu Glu Phe Pro Asn Cys Pro Gly Ser Asn
    290   295   300
His Leu Pro Ser Ser Leu Ser Arg Ser Glu Thr Lys Leu Gln Ser Asn
305   310   315   320
Arg Glu Ile Ser Asp Ile Asn Gln Ile His Leu Ala Arg Gly Glu Leu
                325   330   335
Cys Asp Leu Gln Gly Arg Leu Gln Ser Val Glu Glu Ser Leu His Ser
            340   345   350
Asn Gln Glu Lys Ile Lys Val Leu Leu Asn Val Ile Gln Asp Leu Glu
            355   360   365
Lys Ala Arg Ala Leu Thr Glu Gly Leu Leu Gly Ser Pro Leu Thr Ile
    370   375   380
Glu His Leu Asp Thr Ser Tyr Leu Thr Lys Ser Thr Asp Pro Thr Pro
385   390   395   400
Met Pro Arg Asp Ser Ile His Gly Ser Gln Glu Leu Ala Gly Ile Ser
                405   410   415
Val His Lys

        <210> 142
        <211> 270
        <212> PRT
        <213> Homo sapiens

        <400> 142
Met Asp Ser Gln Glu Val Glu Lys Tyr Pro Asn Thr Ser Val Ala Cys
 1   5   10   15
Glu Glu Ile Pro Phe Ser Gly Ile His Val Ala Gly Gly Lys Ser Gly
                20   25   30
Ala Leu Glu His Gly Lys Asp Asp Leu Asp Glu Pro Ile Glu Asn Pro
        35   40   45
Leu Phe Cys Phe Ser Ser Phe Ser Asn Ala Leu Ala Ile Leu Leu Pro
    50   55   60
Lys Val Phe Leu Lys Asn Ile His Ile Leu Gln Phe Ile Tyr Arg Ser
65   70   75   80
Phe His Leu Leu Thr Met Ala Lys Ala Lys Phe Glu Gly Ala Glu Ser
            85   90   95
Val Glu Pro Val Ser Pro Ser Gln Pro Lys Arg Pro Ser Tyr Val Pro
            100   105   110
Leu Glu Glu Leu Trp Thr Arg Leu Thr Lys Gly Asn Ser Arg Pro Gln
        115   120   125
Gln Arg Asp Arg Glu Lys Gly Gly Trp Met Lys Gly Val Gln Gln Gly
    130   135   140
His Gln Gly Val Gly Lys Gln Glu Glu Gly Ser Glu Asn Ile Lys Glu
145   150   155   160
Lys Ala Gly Asn Trp Gly Asp Gly Arg Arg Trp Gly Arg Asn Gln Gln
                165   170   175

```
Val Leu Ile Asn Lys Ile Thr Phe Lys Gln Thr Ser Leu Asn Tyr Thr
            180                 185                 190
Ser Asn Leu Val Phe Pro Glu Glu Ser Tyr Phe Ser Asn Ala Tyr Ser
            195                 200                 205
Leu Ser Trp Thr His Ile Val Leu His His Cys Glu Ile His Leu Arg
    210                 215                 220
Lys Val Lys Ile Gly Cys Leu Leu Arg Glu Thr Asn Leu Lys Val Arg
225             230                 235                     240
His Ala Leu Ser Val Thr Ser Glu Leu Gly Ala Asp Ile Ser Arg Leu
            245                 250                 255
Ala Gly Phe Asp Glu Ala Tyr Lys Leu Thr Ser Ile Gly Ser
            260                 265                 270
```

```
        <210> 143
        <211> 78
        <212> PRT
        <213> Homo sapiens


        <400> 143
Met Gly Leu Cys Ile Thr Ser Ile Ala Thr Trp Ser Ala Ala Gly Ser
1               5                   10                  15
Pro Thr Gly Cys Leu Ser Ile Lys Tyr Phe Ser Thr Gly Arg Ser Ser
            20                  25                  30
Ser Phe Arg Ala Leu Lys Glu Leu Cys Cys Leu Phe Pro Gly Leu Cys
        35                  40                  45
Leu Pro Thr Ser Leu Thr Val Ile Leu Ala Gly Asn Ile Leu Leu Gln
    50                  55                  60
Lys Thr Leu Trp Leu Phe Val Leu Ile Ser Phe Pro Pro Leu
65                  70                  75
```

```
        <210> 144
        <211> 80
        <212> PRT
        <213> Homo sapiens


        <400> 144
Met Thr Ile Val Arg Asn Gly Val Arg Asp Lys Asp Ile Thr Ala Asp
1               5                   10                  15
Ile Lys Arg Ile Ile Arg Glu Tyr Tyr Glu Gln Phe His Ile His Lys
            20                  25                  30
Phe Thr Lys Ile Gly Asn Ala Tyr Ala Val Leu Ser Asn Pro Glu Lys
        35                  40                  45
Arg Lys Gln Tyr Asp Leu Thr Gly Asn Glu Glu Gln Ala Cys Asn His
    50                  55                  60
Gln Asn Asn Gly Arg Phe Asn Phe His Arg Gly Phe Val Lys Leu Ile
65                  70                  75                  80
```

```
        <210> 145
        <211> 219
        <212> PRT
        <213> Homo sapiens


        <400> 145
```

```
Met Pro Lys Lys Asp Asp Ser Asn Trp Gly Tyr Ala Phe Thr Asp Gly
1               5                   10                  15
Glu Gln Leu Gly Gly Pro Ser Ala Lys Gly Lys Ile Lys Trp Gln Pro
        20                  25                  30
Thr Ile Cys Thr Trp Pro Thr Phe Ala Lys Glu Ser Gly Arg Ser Leu
        35                  40                  45
Ser Leu Pro Gly Arg Ser Val Pro Pro Pro Ile Ser Thr Ser Pro Trp
    50                  55                  60
Val Tyr Gln Pro Thr Tyr Ser Tyr Ser Ser Lys Pro Thr Asp Gly Leu
65                  70                  75                  80
Glu Lys Ala Asn Lys Arg Pro Thr Pro Trp Glu Ala Ala Ala Lys Ser
                85                  90                  95
Pro Leu Gly Leu Val Asp Asp Ala Phe Gln Pro Arg Asn Ile Gln Glu
            100                 105                 110
Ser Ile Val Ala Asn Val Val Ser Ala Ala Arg Arg Lys Val Leu Pro
        115                 120                 125
Gly Pro Pro Glu Asp Trp Asn Glu Arg Leu Ser Tyr Ile Pro Gln Thr
    130                 135                 140
Gln Lys Ala Tyr Met Gly Ser Cys Gly Arg Gln Glu Tyr Asn Val Thr
145                 150                 155                 160
Ala Asn Asn Asn Met Ser Thr Thr Ser Gln Tyr Gly Ser Gln Leu Pro
                165                 170                 175
Tyr Ala Tyr Tyr Arg Gln Ala Ser Arg Asn Asp Ser Ala Ile Met Ser
            180                 185                 190
Met Glu Thr Arg Ser Asp Tyr Cys Leu Pro Val Ala Asp Tyr Asn Tyr
        195                 200                 205
Asn Pro His Pro Arg Gly Trp Arg Arg Gln Thr
210                 215
```

```
        <210> 146
        <211> 214
        <212> PRT
        <213> Homo sapiens


        <400> 146
Met Gly Ala Lys Ala Asp Ser Leu Ala Cys Phe Ser Asp Glu Arg Ser
1               5                   10                  15
Arg Gly Ser Gln Arg Gln Phe Ala Lys Glu Asp Gln Ser Leu Arg Arg
        20                  25                  30
Ser Phe Gly Gly Lys His Ala Val Ser Ala Val Gly Gly Ser Ala Tyr
        35                  40                  45
Gln His His Pro Arg Gly Arg Leu Leu Asp Ala Asp Lys Phe His Pro
    50                  55                  60
Leu Ala Asn Pro Lys Ala Thr His Val Tyr Met Gly Arg Ala Val Arg
65                  70                  75                  80
His Arg Cys Thr Ala Asp Leu Ser Ala Leu Pro Leu Met Phe Leu Leu
                85                  90                  95
Phe Pro Cys Thr Lys Glu Leu Ser Lys Gln Gln Val Arg Arg Gln Gly
            100                 105                 110
His Gly Gly Ser Arg Pro Ala Asp Lys Asp Leu Glu Glu Gly Gly Gly
        115                 120                 125
Leu Glu Ala Glu Ser Pro Lys Gln Ser Pro Asn Leu Cys Val Ile Leu
    130                 135                 140
Arg His Asn Leu Ala Ser Arg Pro Gly Gln Leu Ala Leu Val Thr Val
145                 150                 155                 160
Gly Thr Met Gln Gly Arg Pro Leu Ser His Ser Ser Glu Val Lys Gly
                165                 170                 175
Thr Thr Phe Val Thr His Ser Val Pro Ala Gly Lys Glu Lys Asp Glu
            180                 185                 190
Glu Arg Gly Ile Gly Asp Leu Glu His Ala Arg Asp Leu Arg Asn Ser
        195                 200                 205
```

85

Pro Thr Pro Leu Phe Tyr
    210

        <210> 147
        <211> 125
        <212> PRT
        <213> Homo sapiens

        <400> 147
Met Arg Val Pro Trp Ser Lys Cys Leu Ser Ala Gly Met Pro Leu Pro
  1   5   10   15
Ser Gln Arg Leu Trp Leu Ser Glu Leu Ile Tyr Leu Lys Phe Leu Ala
             20   25   30
Ser Gly Leu Phe Asn Gly Tyr Pro Asn Pro Glu Asn Phe Ser Trp Thr
          35   40   45
Glu Tyr Leu Glu Ala Thr Gln Thr Asn Ala Val Pro Ala Lys Val Phe
       50   55   60
Lys Met Asp Ser Asp Val Gly Glu Asn Arg Lys Ile Leu Arg Asp Glu
 65   70   75   80
Arg Pro Asn Tyr Ser Gln Tyr Thr Pro Phe Ser Arg Cys Asp Asn Ala
                 85   90   95
Ser Tyr Lys Glu Asn Val Phe Leu Gln Lys Leu Glu Arg Asn Thr Pro
            100   105   110
Asp Ile Ala Glu Arg Phe Asp Cys Leu Leu Leu Thr Tyr
          115   120   125

        <210> 148
        <211> 126
        <212> PRT
        <213> Homo sapiens

        <400> 148
Met Cys Lys Ser Trp Gln Cys Ser Val Asn Ala Gln Leu Gln Pro His
  1   5   10   15
Leu Gly Leu Leu Gly Ser Leu Trp Val Met Leu Pro Ser Leu Val Gln
             20   25   30
Leu Ala Ile Ala Arg Arg Lys Val Trp Pro Phe Gly Pro Glu Pro Gly
          35   40   45
His Leu Ile Ser Glu Phe Gly His Phe Glu Gly Thr Val Leu Asp Lys
       50   55   60
Pro Ser Trp Val Thr Cys Arg Ile Leu Gly Gly Gly Arg Leu Gln Gly
 65   70   75   80
Met Gly Trp Leu Thr Ile Asp Phe Ser Pro Gln Ala Ser Lys Arg Ala
                 85   90   95
Leu Thr Ser Ser Ile Met Glu Leu Gly Pro Gly Val Ser Lys Leu Val
            100   105   110
Gln Trp Gln Leu Glu Asn Leu Lys Arg His Cys Gly Pro Leu
          115   120   125

        <210> 149
        <211> 53
        <212> PRT
        <213> Homo sapiens

        <400> 149

```
Met Arg Lys Pro Arg Leu Val Lys Ile Leu Gln Val Ala Gln Gly Pro
1               5                   10                  15
His Arg Leu Arg Asp Lys Ala Arg Leu Gln Ile Gln Ala Ser Val Thr
            20                  25                  30
Leu Glu Cys Val Asp Ser Pro Leu Gln Tyr Thr Thr Ser His His Pro
            35                  40                  45
Cys Lys Lys Lys Lys
    50
```

```
        <210> 150
        <211> 86
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 150
Met Phe Leu Glu Arg Ile Gly Ile Val Leu Cys Glu Arg Glu Phe His
1               5                   10                  15
Phe Glu Phe Leu Pro Gly Val Val Phe Gly Phe Val Lys Cys Phe Thr
            20                  25                  30
Val Met Val Val Leu Arg Lys Cys Ile Gln Ser Leu Leu Tyr Phe Leu
        35                  40                  45
Cys Thr Ala Asn Phe Met Gly Leu Pro Ser Arg Ala Gly Thr Glu Leu
    50                  55                  60
Ala Ala Tyr Thr Asn Arg Asn Ser Ser Thr Pro Pro Asp Thr Ala Glu
65                  70                  75                  80
Ala Ser Pro Cys Tyr Arg
                85
```

```
        <210> 151
        <211> 149
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 151
Met Glu Ser Pro Cys Asn Thr Gly Cys Ser Tyr Gly Asn Cys Tyr Lys
1               5                   10                  15
Thr Arg Ser Gly Phe Thr Arg Val Gly Arg Arg Asn Leu Pro Arg Lys
            20                  25                  30
Pro Gly Ala Gly Val Met Gly Val Asp Val Leu Leu Gly Pro Arg Lys
        35                  40                  45
Val Gly Ser Asp Glu Glu Ala Leu Lys Lys Ser Gln Tyr Asp Asp Asp
    50                  55                  60
Ala Phe Met Val Lys Phe Cys Ala Ser Ser Thr Glu His Phe Leu Asn
65                  70                  75                  80
Asn Pro Gln Thr Asp Ala Val Leu Gly Gln Arg Tyr Gly Arg Glu Ser
            85                  90                  95
Lys Ser Pro Lys Cys Leu Asn His Lys His Arg Asp Leu Thr Pro Val
            100                 105                 110
Thr Val Glu Thr Asn Ala Leu Ala Ser Asp Pro Tyr Arg Ser Ala Phe
        115                 120                 125
Leu Pro Leu Asn Gly Ala Val Arg Gly Glu Leu Gly Cys Arg Thr Gly
        130                 135                 140
Gly Glu Lys Asn Val
145
```

```
        <210> 152
```

87

```
        <211> 48
        <212> PRT
        <213> Homo sapiens


        <400> 152
Met Met Gly Met Tyr Leu Lys Pro Ser Glu Ser His Pro Asp Ser Gly
1               5                   10                  15
Glu Glu Pro Leu Lys Asp Glu Lys Asp Lys Gly Val Thr Arg Gly Gly
            20                  25                  30
Gly Val Val His Cys Asp Ser Ser Ala Val Ala Leu Cys Val His Phe
        35                  40                  45




        <210> 153
        <211> 30
        <212> PRT
        <213> Homo sapiens


        <400> 153
Met His Glu Ser Asn Ala Ile Arg Ile Thr Val Glu Leu Phe Tyr Leu
1               5                   10                  15
Tyr Ala Ser Cys Arg Cys Leu Glu Val Leu His Leu Leu Cys
            20                  25                  30



        <210> 154
        <211> 82
        <212> PRT
        <213> Homo sapiens


        <400> 154
Met Cys Leu Ser Met Gln Pro His Gln Leu Pro Tyr Phe Ser Cys Leu
1               5                   10                  15
His Leu Ser Lys Thr Arg Ala Ala His Pro Ala Pro Pro Asp Phe Arg
            20                  25                  30
Trp Gly Trp Ser Val Lys Thr Gln Ala Arg Arg Lys Thr Pro Ser Pro
        35                  40                  45
Ser Lys Pro Ser Pro Arg Thr Arg Pro Met Cys Arg Pro Lys Ser Lys
    50                  55                  60
Ala Arg Leu Ala Ala Lys Val Gln Ala Val Arg Lys Arg Arg Ser Gly
65                  70                  75                  80
Asn Ser



        <210> 155
        <211> 71
        <212> PRT
        <213> Homo sapiens


        <400> 155
Met Pro Gly Pro Ala Ala Ala Ser His Arg Ala Ser Thr Tyr Val Ser
1               5                   10                  15
Thr Trp Ser Cys Pro Pro His His Ser Trp His Ala Trp Gln Cys Thr
            20                  25                  30
```

```
Val Ala Arg Pro His Leu Gln Thr Ser His Cys Cys Thr Ser Gly Leu
        35                  40                  45
Pro Leu Ala Asp Met Glu Ser Arg Leu Val Ala Ser Pro Ser Glu Trp
        50                  55                  60
Asn Lys Leu Thr Trp Ala Gln
 65                  70
```

```
        <210> 156
        <211> 42
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 156
Met Ile Ser Ser Ala Phe Leu Leu Leu Thr Leu Ile Arg Ser Tyr Leu
 1               5                   10                  15
Leu Leu Arg Tyr Gln Asn Thr Thr Ser Met Thr Glu Leu Asp Pro Arg
                20                  25                  30
Arg Leu His Cys Thr Ile Trp Met Glu Val
        35                  40
```

```
        <210> 157
        <211> 58
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 157
Met Ser Arg Ala Pro Gly Ile Leu Ala Ser Trp Arg Arg Ala Pro Ser
 1               5                   10                  15
Leu Ser Val Gln Lys Gly Ser Gln Thr Ala Arg His Thr Cys His Pro
                20                  25                  30
Glu Val Pro Leu Gly Asn Cys Phe Leu Pro Val Tyr Lys Ala Ser Pro
        35                  40                  45
Leu Thr Val Thr Arg Leu Trp Ala Glu Arg
 50                  55
```

```
        <210> 158
        <211> 85
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 158
Met Gln Arg Ala Leu Arg Arg Asp Thr Gly Gly Ser Gln Ser Asp Tyr
 1               5                   10                  15
Pro Leu Ala Leu Ser Ser Phe Pro Thr Ala Gly Ser Ser Cys Pro Ala
                20                  25                  30
Leu Gly Leu Thr Thr Pro Leu Ala Trp Arg Leu Cys Leu Ile Phe Ile
        35                  40                  45
Thr Gly Arg Glu Thr Arg Ser Ile Pro Lys Glu Arg Glu Pro Arg Met
        50                  55                  60
Pro Glu Arg Lys Ala Ser Pro Arg Arg Trp Asp Asn Phe Pro Tyr Lys
 65                  70                  75                  80
Val Trp Gln Ser Ser
                85
```

```
<210> 159
<211> 82
<212> PRT
<213> Homo sapiens


<400> 159
Met Leu Leu Ala Asp Lys Glu Ala Ser Glu Ala Gly Leu Thr Asn Val
1               5                   10                  15
Pro Asn Asp Ala Asn Tyr Pro Arg Tyr Ser Pro Ala Glu Cys Leu Met
                20                  25                  30
Ala Ile Gly Phe Gly Val Arg Lys Ser Arg Leu Glu His Leu His Leu
            35                  40                  45
Gln Gln Cys Ala Gly Asp Phe Leu Ser Ala Ser Leu Ser Pro Thr Asn
        50                  55                  60
Gln Ile Ser Val Ser Val Trp Ala His Ile His Lys Leu Ala Arg Gly
65                  70                  75                  80
Asn Ser



<210> 160
<211> 27
<212> PRT
<213> Homo sapiens


<400> 160
Met Gly Ala Ala Ala Lys Gly Ser Leu Trp Ala Ser Pro Phe Ser Arg
1               5                   10                  15
Ser Val Leu Pro Leu Cys Leu Gly Ser Ser Leu
                20                  25



<210> 161
<211> 90
<212> PRT
<213> Homo sapiens


<400> 161
Met Trp Asn Met Leu Ser Asp Ser Asn Tyr Gln Gln Phe Pro Ser Asp
1               5                   10                  15
Ser Ala Arg Val Leu Ser Phe Gly Ser Arg Val Leu Tyr Ser Lys Ser
                20                  25                  30
Thr Ser Ser Phe Thr Leu Asn Ser Gln Asp Leu Tyr Ser Trp Thr Gln
        35                  40                  45
Phe Val Thr Thr Thr Ile Phe Gln Ile Cys Ser His Lys His Pro Lys
        50                  55                  60
His Pro Leu Lys Phe Tyr Thr Arg Ile Thr Glu Lys His Pro Ala Asp
65                  70                  75                  80
Phe Leu Leu Ala Ala Ser Lys Glu Gln Leu
                85                  90



<210> 162
<211> 66
<212> PRT
<213> Homo sapiens
```

<400> 162
Met His Cys Ala Val Cys Met Val Ser Phe Gln Pro Pro Pro Lys Trp
1   5   10   15
Phe Ser Pro Lys Ile Leu Lys Arg Asn Phe Met Phe Leu Cys Ile Phe
            20   25   30
Thr Gly Ile Lys Glu Asp Gln Ile His Asn Phe Trp Gln His Cys Ser
        35   40   45
Phe Pro Leu Pro Leu Ala Thr Ser Leu Trp Thr Trp Glu Thr Ser Leu
    50   55   60
Trp Thr
65

<210> 163
<211> 75
<212> PRT
<213> Homo sapiens

<400> 163
Met Thr Ser Arg Glu Asn Thr Asn Gly Ile Asn Ser Ala Val Ser Phe
1   5   10   15
Arg Ser Ser Leu His Arg Cys Phe Ser Lys Leu Met Phe Ser Glu Asn
            20   25   30
Ser Arg His Arg Leu Arg Thr Asn Pro Pro Ser Pro Phe Arg Leu Gly
        35   40   45
Trp Pro Met Gly Trp Ser Val Cys Val Leu Val Gly Pro Ala Val Tyr
    50   55   60
Met Ser Ser Ser Ala Gln Arg Leu His Ser His
65   70   75

<210> 164
<211> 46
<212> PRT
<213> Homo sapiens

<400> 164
Met Ile Leu Thr Thr Leu Met Tyr Gly Tyr Tyr Tyr Leu Asp Asp His
1   5   10   15
Ile Gly Phe Ala Phe Gly Thr Pro Arg Ser Leu Ser Leu Ser Ser Asp
            20   25   30
Phe Leu His Ser Lys Gln Glu Gly Tyr Phe Ser Pro Thr Leu
        35   40   45

<210> 165
<211> 49
<212> PRT
<213> Homo sapiens

<400> 165
Met Ser Ser Val Gly Ser Thr Glu Ala Gly Arg Ser Glu Gln Ala Glu
1   5   10   15
Arg Gly Ile Gly Val Ser Glu Arg Val Gly Val Gln Ala Gln Asp Arg
            20   25   30
Thr Glu Leu Ser Ala Asp Cys Asn Thr Val Thr Pro Lys Val Lys Ala
        35   40   45

Ser

```
        <210> 166
        <211> 56
        <212> PRT
        <213> Homo sapiens


        <400> 166
Met Val His Arg Pro His Ile Ser Leu Gln Leu Asn Phe Gly Pro Lys
 1               5                  10                  15
Arg Ser Arg Leu His Thr Phe Arg Asn Lys Ser Tyr Ser Ser Ala Gln
            20                  25                  30
Asn Gly Ser Thr Arg Leu Asp Leu Pro Thr Arg Pro Ala Trp Pro Leu
        35                  40                  45
Arg Leu Gln Arg Val Ala Leu Asp
    50                  55



        <210> 167
        <211> 8
        <212> PRT
        <213> Homo sapiens


        <400> 167
Met Met Arg Lys Ser Leu Pro His
 1               5



        <210> 168
        <211> 2067
        <212> DNA
        <213> Homo sapiens


        <400> 168
ggaggcagag ctctgggaat ctcaccatgg cctggacccc tctcctgctc cccctcctca      60
ctttctgcac agtctctgag gcctcctatg agttgacaca gccaccctcg gtgtcagtgt     120
ccccaggaca aacggccacg atcacctgct ctggagatgc attgccaaaa aaaacatcct     180
tattggtacc agcagaagtc aggccaggcc cctgtactgg tcatctatga ggacaacaaa     240
cgaccctccg ggatccctgc agagattctc tgcctccagc tcaggacaa tggccacctt     300
gactatcagt ggggcccagg tggaggatga agcggactac tactgctact caacagacag     360
cagtggtaat cataggggggg tgttcggtgg agggaccagg ctgaccgtcc tcagtcagcc     420
caaggctgcc ccctcggtca ctctgttccc accctcctct gaggagcttc aagccaacaa     480
ggccacactg gtgtgtctca taagtgactt ctaccccggga gccgtgacag tggcctggaa     540
ggcagatagc agccccgtca aggcgggagt ggagaccacc acacccggca aacaaagcaa     600
caacaagtac gcggccagca gctacctgag cgctgacgcc tgagcagtgg aagtcccaca     660
aaagctacag ctgccaggtc acgcatgaag gggagcaccg tggaggagac aggtgcccct     720
acagaatatt tattgagggt ttattgagtg caggagaag ggtcttgatg cccttggggt     780
gggaggagaa gacccctctc ccctggggat tcctgcaggt tctagttctt cccgtggggg     840
gggagtgagg ggttgagaaa cctatggaac attcgtgtag ggggcccctg tcttctccca     900
cggtgctccc cttcaatgcc gtgaccctgg caagctgtag ctttctgtgg aactttccac     960
ctggtcaggg cgtcaggctc agatagcctg ctgggccgcg tacttcgttg ttgctttgtt    1020
ttggagggag tggatggtct ccatctcccg ccattgacgg gggctgctat gctgccttcc    1080
caggccactg tacacggctt cccgggtaag aagtcactta tggagacaca ccaagtggtg    1140
gcccttgttg ggcttgaaag ctccctcagc agggagggct gggaacaaga gtgacccgag    1200
gggagcagcc tttgggtgta ccatagggac gggtcagctt tggtcccctc cgccgaacac    1260
agcacacagt gacacagccc cacacacaaa cccctcctga cacaccgac ccgttccccg    1320
```

```
ctgcagcagc ttgggcgccc aggtccagtg gccctgggtc cagagggtca gggtccagtc    1380
tgtgcctgct tcagagatag atgtgggggt agagggcagg gtcttgttgt tgctctgttt    1440
ggagggtgtg gtggtctcca ctcccgcgtt gacggggctg ccatctgcct tccaggccac    1500
ttttacagct cccgggtaga agtcactgat caggcacacc agtgtggcct tgttggcttg    1560
aagctcctca gaggagggcg ggaacagagt gaccgagggg gcagccttgg gctgaccgag    1620
gacggtcacc ttggtgccac tgccgaacac attacactgt gatataacca gggcagcagg    1680
aagcacaaca gagacgtggg taagaatgaa gatgtctggt tccttctgaa gactatttcc    1740
ttgttctgga acattctggc agctgtagct tctgtgggac ttccactgct cgggcgtcag    1800
gctcaggtag ctgctggccg catagttgtt gttgctctgt gtggaggtg tggttgtctc    1860
tatgcccttg gtgactaggg tgccattttc cttcagcatg gccttgttgg cttggagctc    1920
ctcagaggag ggcgggaaca gagtgaccaa gggggtggcc ttgagcggac ctgtgagttt    1980
ccattcccag accttccac aagttcctgg tgatggcacc accatggact tctcacccga    2040
taaactgggc acctggattt tcctcat                                        2067
```

```
        <210> 169
        <211> 1692
        <212> DNA
        <213> Homo sapiens


        <400> 169
atggagaaag gcagcggctt cataaagtac tcaacttaca aacaagggac aattagagtt     60
gcagaagaag cagaaacagc tcacagctct gtcttaattg gtccagaaaa gggcgtggtg    120
cacctggcga cagcggccgt cctaaacgcg gtgtgggact tgtgggccaa gcaggaggga    180
aaggttttgg cagtaggtag ggaactgcag gaggaggaga aagaggagac aggatggcgg    240
aaggcgcagg cagcagtaga gggggggtgtg gggacctggt ggctgacagc cagcattaga    300
gctgccaacg cgtttactgt caggaaaaaa tggggacttt acacatatgt cttacaaatc    360
cttctttttt tacttcaagc ctgtctggaa gttacttgtg gacatgattt gataatgggc    420
tgcattaaaa gtaaagaaaa caaaagtcca gccattaaat acagacctga aaatactcca    480
gagcctgtca gtacaagtgt gagccattat ggagcagaac ccactacagt gtcaccatgt    540
ccgtcatctt cagcaaaggg aacagcagtt aatttcagca gtctttccat gacaccattt    600
ggaggatcct caggggtaac gccttttgga ggtgcatctt cctcattttc agtggtgcca    660
agttcatatc ctgctggttt aacaggtggt gttactatat ttgtggcctt atatgattat    720
gaagctagaa ctacagaaga cctttcattt aagaagggtg aaagatttca ataattaac     780
aatacaccaa tggttctcaa cctgggacag aatcacccag gggatatttg gcagtatctg    840
gagacatttt tggttgtcac agttggggtg ctgccgctgt cttctagtgc ctcaactcct    900
gtatttgatc gagtcaccaa tggagtaact ccaactatca aggatctcac tggctgctgt    960
gttgagaaca gactactgac ttctaatagc agcgacttct ttaccttgat aaaccacagc   1020
aactcctcca aaacacccctt ccagaacaca cgtttggttg tcagcagagg gaattcatct   1080
gaaaaacaat ttgccatacg gtttcaagat gggaagacag atcatgccat ccaactttct   1140
tcagggaaga aaactgccct gggacgtgag gccctggagc atccagaaag cctagactcc   1200
cgcaaagtgg gccagagatc acggtggagc tcccaggctg caagtccat cagtggcccg   1260
attcaggctg agacagcact tctgtgcccc ggtgaccagt ggacacagga attccacaca   1320
tctcctttgc taactgttcc tcatctccct gacatctaca cactggactg ttgccgaaaa   1380
gacttctcca tttacattca ttcctttggt gatatcaccc agtcttatat ctttaaatac   1440
cacctgcaaa ttgatgatta ccagctctgt gcccaggcgc tgaaggatgg ctggaccagg   1500
ccacctcctt tccacactgc tcatctgcac ttctcccttc tgactctcgc ctgtgcagag   1560
acggtcactt ctgcagaaac tccagatgcc cttgccaagt ccaggtttaa agtaaaggtg   1620
ggtgctgatc tccaggatga catgcgaaga tgccaaatca tccgagacat gattggaccg   1680
gaaaagactt tg                                                         1692
```

```
        <210> 170
        <211> 949
        <212> DNA
        <213> Homo sapiens


        <400> 170
ggcacgaggg acgccaccgc cgaggaaaac cgtgtactat tagccatggt caaccccacc     60
gtgttcttcg acattgccgt cgacggcgag cccttgggcc gcgtctcctt tgaggtaagg    120
```

93

```
ggcctggata ccaagaagtg actgctcatc taatccataa agctatgtta acagattgga   180
ggtagtagca tttttcattac aagtgactaa aagaacagct gtttaccccct gatcgtgcag   240
cagtgcttgc tgttccttag aattttgcct tctgtttgca gacaaggtcc caaagacagc   300
agaaaatttt cgtgctctga gcactggaga gaaaggattt gggttataag gggttccctg   360
ctttcacaga attattccag ggtttatgtg tcaggtggt gactgtgaag tcaccataat   420
ggcactggtg gcaagtccat ctacacggag aaatttgaag atgagaaact tcatcctaaa   480
agcatacggg gtcctgggat ctttgtccat ggcaaatgct tggacccaac acaaattggt   540
tcccagtttt tcatctgcac tgccaagact gagtggttgg gatggcaagc cttgtggtgt   600
ttggcaaagt gaaagaaggc atgaatattg tggaggccat ggagcgcttt gggtccagga   660
atggcaagac cagcaagaag atcatcagca ttgctgactg tggacaactc gaataagttt   720
gacttgtgtt tttatcttaa ccaccagatc atttcttttt gtagctcagg agagcacccc   780
tccaccccat ttgctcgcag gatcctaaga attttgtggc tctcgctgca gttcctttgg   840
ggttccatgt tttccttgtt ccctcccatg cctagctgga ttgcagcagt taagcttatg   900
attatgaaat aaaaactaaa taactcacct acaacggatg taattaacg             949
```

```
    <210> 171
    <211> 2331
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> misc_feature
    <222> (1)...(2331)
    <223> n = a,t,c or g


    <400> 171
gccctttttt ttttttttg gtcatttata ttttatttaa gagctgtgcc cagtttttatc   60
atctcacaag aatgaagcaa gggacaaagg taagtgccac gctccctggc cactgggttc .  120
ctggcaagct cccagccact aggtgccaat ctcccttcaa tgtactcctt cttccccaga   180
gtgcagaagc gtatgaagac agttatgaca tggacacatg catgagctat tatgcataat   240
tacaaaagct gaatctgtca tcaaccaaca tctttgtctc atcagtagga gcgaaatggc   300
tggccgggac ggtggcacga tcagcctcgt tcaaagtttt gtcgattacg ggtctatatc   360
ccagggtgac catgaaaaga agagtcttcc cagtggccaa cgtccacata ggacagggtg   420
tgcttcctcc agtggctcct caaaagggct tcttctgttg cccctcggatg ggcttggagt   480
aatcgtactc atcaatccgc accttgtagt cttccctggc atgcgcgccc cgtgactcct   540
tccgcgcctc tggctccgta gatggtcttg aagcgcacac agccatcagg ttctgcagct   600
ccagggtctn cacccaggtc ccgtgttcca gaccattccc cggtcgaacg tcttcaggtg   660
ctttaggtct ccatagagct tgctgatttt cccacaaacc ttctttggaa acaacgcttc   720
cccacacggg aacacggcag catgattttg cattgacttc tgcatgctga gtcgcagttc   780
cgatgttctt atgcttccat cagcaaatct caatttgtca agattcatga cagattcttc   840
cccagcgttt ggtttaattg gagggacttt atctccaggc ctgcatgact cttcgatgct   900
cagggcacat gcccgaccaa agacaaccag gtccaagagc gagtttgccc cgaggcggtt   960
ggcaccatgt accgaggcac aggcggcctc cccacaggcg tacaggccgg gcacaatctg   1020
atcctggcca ttcacgtgcc tcaggacctg ccccttgtag ttggtgggaa tgccgcccat   1080
gttataatgc acggtgggga ggacagggat cggctccttc gtgacgtcca cgccagcgaa   1140
gatcatggct gtctctgaaa tgccaggcag gcgcgtggcc agctgctctg gaggtaggtg   1200
gtgcagctgc aggtagacgt gatctttctc agggccacag cctcttcctt ctcggatctc   1260
cagagtcatc gaccgagaca ccacatctct agacgccagg tccttcgcga caggggcgta   1320
tcgctccata aacctttcgc cttgactgtt aatgagaatg cctccctctc cacgacatcc   1380
ttccgtaatg agacaaccag caccatatat gcctgtgggg tggaactgaa caaactctag   1440
gtcctggcaa ggaaggcctg ccctggtgat catggccgtg ccgtcgccag tgctggtgtg   1500
ggcagacgtg cagctgaagt aggtgcgccc gtagcctcct gtggcaacaa cagtgttctt   1560
tgctcttatg cgatggatgg acccgtcctc tatgcacagt gcgatgacac cacggcactc   1620
cccgttctcc atcaggagat ccaaggcaaa atactccaca aaatagctgg tatcatatcg   1680
cagagaccgt ccatataagg tgtgcaatag cgagtggcca gtccgatcag ccacacagca   1740
gcaccgatgg gcctgcccgc cctttccaaa cttgaggctc tgtccaccaa atgcacgctg   1800
ataaatcttc ccatcttcag ttctgctaaa cggcatgcca taattttcta gctcgaccac   1860
ggcggcgggg gcctgctccg tcatgtagtg gatggcatcc tggtccccca gccagtcgga   1920
gcccttcacg gtgtcgtaga aatgccacct ccagttgtcc tcctccatgt tccccagagc   1980
agcattgatt cctccctgcg ctgcaacagt gtgtgacctg gtaggaaaca gcttggtaac   2040
acatgctgta ttaaaccctg cctcagaaag gccaaatgca gctcgcaagc ctgcccctcc   2100
```

```
agcgcctacc accactgcat caaattcatg atccactact ggatactgag cagaaatgga   2160
atctgaaact ttagcagatg ccctcttgtt cccatcaaca gtgaagtgaa aacctcgggt   2220
tcctgtttgc aacactgttg gccacgcctt ggccagcgcc aggcgccgag cgctcagcag   2280
ccgcgacagg ccccggaccc ccgacatgtc tgctgttgcc gccgcgcagt c           2331
```

```
        <210> 172
        <211> 416
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(416)
        <223> n = a,t,c or g


        <400> 172
gttagagatt acaatttgac tgaagaacag aaggcgatca aggccaagta tccgccagtc    60
aataggaagt acgagtattt ggatcataca gcagatgtcc atggattgta ttacacagag   120
catgaatata cttctttagg ttacacgcat ggggagatac tctggaggaa gcatttgagc   180
aatgtgcaat ggccatgttt ggttacatga cagatactgg gacagtggag cccctccaaa   240
cagtagaagt agaaacccaa ggtggggaga agaattttca ttgtccaagc accctcaggg   300
aacagaagtc aaagcaataa catattcagc aatgcaggtc tataatgaag agaacccgga   360
agttttgtg atcattgaca tttaagacac ccaaaaatan aagactccta cgaaaa        416
```

```
        <210> 173
        <211> 1737
        <212> DNA
        <213> Homo sapiens


        <400> 173
tcaatataag cctgtgtagt ccgtaggcc tctgggaata attagctcaa cagtggactg     60
tgaaacacac actgcttcct tcctggtgag ttctgctctg agctccaatt gcagcccagt    120
tgtcacacac tgaaaagcaa aacgcagttc agctggtttt aaaagaccca ttgacagccc    180
agggcttgta aaacgatgtg tacgggtagc ttcagctggc cccttgcctt ccccagagcc    240
cgcttcggac atggtgtggg ttgcatcctt ctctgcaaac tgcctgtgtg ctctgtggca    300
cggcttccgg caagagattt cctctgcagc attaatgtct cgtggaaggc caagtctctt    360
gctttgtgat cccattccac tcttccacca tgattgtgag gcctccccag ccatgtggaa    420
ctgtaagtcc attaaatctc tttctttgc aaatttccca gtctcaggta tgtctttatc    480
agcatcgtga aaacagactg atacagtaaa ttggtaccag tagagtgggg tgctgctgaa    540
aagataccct gcaaagccac aggggtggag ctgcccaaga ccatgggaac ctacctcttg    600
catcagcatg acctggatgt gagacatgga gtcaaaggag atcattatgg aactcaatgg    660
agacactgca ataggtcact tcttcctgtc caaggaaaaa gcggcgcttt ggaggggata    720
ggccctcctc gagttttct cccccgagta aagagctctt ggcggtcaaa gcgcctcgcg    780
aggggcggag gggcccgggg aacgagtccc ggagcgaacc cagccagcct ctggattccc    840
acggcccagg gctccgccgg acattcctac cgccctcccc tcgacacccc actaaagaca    900
gaagaaccgc ggctcgatcg ggtccgcggc ggaagcgcgg ccaaacgaat gaaattcgag    960
ggtgtaaaga agaggaaggg gaaaaatatc ttgtaccagc ccaggggtga agaagccccc   1020
ggcctgagaa agaaggagga gtgggggagg cgaacagtct cgttgctgcc tctgtgtacg   1080
ctgagggggg agggctcttc ttttcgacta ccctcgctga agattttctc ttccttccct   1140
cgcccaactc tccctcgggg cctctacgga gacccccccc cccatgggt ggcccaaaat    1200
ggagaacgcg gagcagcgca agatggaggc tccgcttctc tgtgtagcag tagatttagg   1260
ttcctttct ccggcaggct cctaagccta ggagagcccg aactggagag agggaacaac    1320
attcatgtga cgggcccctc tgcttctccc ccgccccatc atctccagcg cgtggtgggg   1380
gaactgctgg ggaaggcgat tggcatcgat ctctccatcc cttccgaggc ccgacttcgg    1440
aattgtctta gaagaaagaa ggcaagccac cattttaccc acgtaaatat atgaatatat    1500
ttctgacatt gaggtgttcc agaagatgat aaagaaatga tagcagctcc agaaatacca   1560
actgatttta atctactaca ggagtcagaa acacattttt cttctgacac agattttgaa   1620
cgatatcgca ggaaaaaacc gaactcaggg caaaggcaat acttgtagaa aaggcgaaga   1680
```

95

```
gggcccagca gaaaaggtct gaggtggaaa aggaagagga acacctactt ctgcgcg      1737


        <210> 174
        <211> 6464
        <212> DNA
        <213> Homo sapiens


        <400> 174
ctagttgtgg tgacacgtgt aagatgagca agaacactag attgagctaa tgctgactct    60
tgtctttgta gaatgaccgc cagccttttt tcttttcttt ggaacactat tctgcaggtg   120
catcagctgc ttttttctttt ttctctttgc agttaaaaat tcaagatgtc catttacgct  180
ttgaagatgg tgtcaccaat ctgttgaatg aatgacattc acgaataaag acagtcatcc   240
tattttcttc tttgtctttt ttacctcagg tacagaaact aatgcggaaa aagcaattag   300
acgtagcatt gtaaaagagt gactaccaga aggaaagcca ttcggagcag agcaggtgtt   360
cttgtgacac acaggaggcc atggccagga gcatggagag tcgcagccat cactacgtcc   420
tggagcctgt gtttgcatct gctctttttga agagaaactg ctccaagaag cccctgcata   480
ggtcttaact gagtaaaaga aacaaaccta ttctaaccta gtatctctta acctctaata   540
caaagctgca ataccggcaa atcatggaat tcctcaagct caggagagga gtggggttat   600
gtggattgtc ctggattggt agccttttcg ttgctttttgt tgtaagaagt gattacatcg   660
ttatggacta tttcagctgc cgagaatggt ggtattttgc tttgaatgct aacttgtatg   720
agatcagaga gcagaggaaa cgttgcacct gggactttat gttgcaccgc gctcgtggtg   780
tccagtgtct ctggatctac aacgtttgtg tttttgttta tttgcttttg ttttcaccca   840
aacaggagga aatgtgtcgg attgaagagg aacagagcta acagcagcat atcacagctt   900
gctttttatct ttgagtactc atctctgctc ctttgtgatt gacacagagt ctgcgggagc   960
ctcagtttga ttctccagga gcctgtccgg gagccccaga acccggtgga ggcagtggga  1020
tgctgcagta tctccagtcc tggtttcctg gatggggtgg ctggtacggg cagcagaccc  1080
cagaagaaca tcatcataac tgtgatcagt ctgcttgctg gtgctttttt attcttccac  1140
gttttttctt acagtctttt ctcccttacc atttaggcac tgaggagttt tttgaccccca 1200
ctgcagatgc ctcgtgtatg aacacgtata caaagcgaga tcatgtcttt gccaaactga  1260
atttgcagtt gcagcgaggt acagtgacca caggtctgtt aataaggcta tagttttttgc 1320
cttgttccgt gttcttattc ctgttctttc ctttagctgc agatccagat ggccccgttt  1380
ttgagatgct gtatgagaga aatccggcgc acagccactt tgagaggcgg ctcaatgtca  1440
gcacaaggcc cttgaacatg atgtagcact tttgttcacc cagccgtgtg aaaattctga  1500
ctctgctgtg tatttccaac cttgcaggtt ttggttatca gtctgaactt gagctgagag  1560
tggctgaagc tgcccgaaga caatataaca gcttgagcac catggataaa gctgttgggt  1620
ttcggcagtt atggttaatg actgttttat ttgtacagga ggagagtaaa cgatggaccg  1680
tgcggctgga tatttctgcc cctcaggtga tatttcctga tgatattaca ttaagggaaa  1740
gaggagggaa atagcagaca tatatttgaa tcttctttttt tttatcttca gataactcca  1800
ggaggaaaag tagggatggg tcagcatctg aagagaccca gtttagtgat gatgaatata  1860
agaccccccct ggccacacct cctaacaccc cacctcccga gtcaagcagc agcaacggag  1920
agaaaacacc tccctttttct ggagttgagt tcagtgaaga acagcttcaa gcacatttaa  1980
tgagcacaaa gatgtatgag aggtactcgc tgtcatttat ggacctccag atcatggttg  2040
gacgagtgaa agacaattgg aagcatgtcc aggatattga cgtgggacca acacatgtgg  2100
tagagaagtt caacgttcac ctacagttag agcgtcgatt gatttatact tcagatccca  2160
aatatccagg agccgtgctc tcaggcaact taccagactt aaaaatccac attaatgaag  2220
ataaaatatc tgcactaaag aattgctttg ctctcctcac caccccagaa atgaaaactt  2280
ctgacactca gattaaagaa aagatttttc cccaggagga gcagcgggga agtttgcaag  2340
actccgtaat gaatttaacc cagagcattg tgttgttgga gcagcatacc cgcgaggttc  2400
tggtggagtc gcagctcctc ctggcggaat ttaaagtgaa ctgtatgcag cttggtgttg  2460
agagcaatgg ccggtacatt tctgtgctca aggtgtttgg taccaatgct cactttgtga  2520
agaggcctta tgatgctgaa gtctccctaa ctgttcatgg tttgctcctg gtggatacca  2580
tgcagacata tggtgctgat tttgacctttt tgatggcttc acataagaac ttgagctttg  2640
atattccaac gggaagcctt cgggatagca gggcccagtc tcctgtctct ggaccgaatg  2700
tggcccactt aactgatgga gctacactga acgaccgatc agctactagt gtttcacttg  2760
acaaaattct taccaaagag caagagtccc ttattaagtt ggaatatcag tttgtgagtt  2820
cagagtgccc atcgatgaat ttagacagta ctcttcaggt gatttcccta caggtgaata  2880
atttagatat tatcctcaat ccagagacga ttgtggagct aattggtttt cttcaaaaat  2940
cctttcccaa ggaaaaagat gatttaagtc ctcaaccttt aatgactgat tttgaaagaa  3000
gcttcagaga acaggaact taccagtcta catatgaaca aaacactgag gttgcagtgg  3060
aaatccatag gctgaactta ctgcttcttc ggacagtggg catggcaaat agagagaaat  3120
atggcagaaa aattgcaact gcaagtatag gtggcaccaa agttaatgtc tcaatgggta  3180
```

```
gcacgtttga catgaatggt tctcttggct gtttacagct tatggatttg acacaagata   3240
acgttaaaaa ccagtatgtt gtcagcattg ggaattctgt aggctatgaa aatatcatca   3300
gtgatattgg ctactttgaa tctgtgtttg tcagaatgga agatgcagcc ctcactgaag   3360
ctttgagttt cacgtttgtt gagagatcta aacaggagtg ttttctcaac ctgaagatgg   3420
cttctttaca ttataaccac tctgctaagt ttttgaagga gttgacgtta tccatggatg   3480
aactggaaga aaattttcga ggtatgctga aaagcgcagc caccaaagtc accacagtac   3540
tagctaccaa gactgccgag tatagcgaga tggtatcgct ctttgaaact ccaaggaaga   3600
ctcgggaacc ctttatctta gaggaaaatg aaatatatgg gtttgaccta gcttcgtctc   3660
atttggacac tgtaaagcta atcttgaaca taaacattga atcaccagtt gtttctatcc   3720
ctcggaagcc gggggagtcct gagttgttgg tgggacactt gggacagata ttcatccaga   3780
attttgtggc gggagatgat gaatccagaa gtgaccgtct gcaggtggaa atcaaggaca   3840
ttaaactgta ttctttgaat tgcacccagt tggcaggtag agaagctgtt gggtctgaag   3900
gaagccggat gttttgccca ccttccgggt ctggcagcgt ttaatcagca gtaatgaagt   3960
aaatattaag gttatggtc tatcatttca tctctttat gccagctttt cacatcctga   4020
acaacaccac cattcagttt aaactggaga agatccctat agagagagaa tctgaattga   4080
cttttctca tttatgggca ttacatctac gtgcatttaa taataagagt aactgaattt   4140
ttctcttttc aatacaggtg gtgttagcaa agcatgtata tgagcaggtt ttacaaaccc   4200
tggacaatct cgtgtacagt gaagatctga ataagtatcc agccagtgct acctcctccc   4260
cttgccctga ttctcctctg cctccctca gtacctgtgg agaatcttct gttgaaagga   4320
aggagaatgg attgttcagc cactccagcc tttctaacac ctctcagaag tcattgtcag   4380
tgaaggaagt caaatccttt actcagattc aagccacctt ttgtatatca gagcttcagg   4440
ttcagctaag tggagatctg actttggggg cccaaggtct tgtgagctta aagtttcagg   4500
actttgaggt ggaattcagt aaagaccatc cccagacttt atctattcag attgccctgc   4560
attctctgct gatggaggac ttattggaga agaatccaga ttctaaatat aagaacctga   4620
tggtgtctcg aggagcccct aagccatcta gtttagcaca aaaagaatac ctttctcagt   4680
cttgcccctc agtgtccaat gtggaatatc ctgatatgcc tcggtctctc ccttcccaca   4740
tggaagaagc tcctaatgtc ttccagttgt atcaaaggcc cacctctgcg tcccggaaaa   4800
agcaaaagga agtccaagac aaggactatc ccttgacccc acctccttct ccaacagtgg   4860
atgagcccaa gatacttgtt ggaaagagta aatttgatga ttccttagtc cacatcaaca   4920
tattcttggt agataagaaa catccagaat tctcttccag ttacaatcga gttaaccgga   4980
gcattgatgt tgattttaat tgcttggatg tgctgatcac actgcaaacc tgggttgtga   5040
tattagactt ttttggaatc ggctccactg cagacaacca cgcaatgagg ctgcctcctg   5100
agggcattct gcacaacgtg agccgttttc ctgaaagata cctttttctcc ccagtaatat   5160
tggccttgct ttatcttgtc tgttcctagg ttcattcact ttctctagtg ctccagacat   5220
atttaagttg tgtgacaaaa aaggatacat agtaatgtgt tctaacttta tcatccctag   5280
agggagacct ggccttacag ggcagcattg ggagtctgtc tctaagtgac ctcacatgct   5340
gagttttctt gaaatactaa cttgtgtctt gctgttatct gagtcacact tttatcctaa   5400
ttttagata cggacggcct gaccctctgc tccggagaga acacgacatt cgcgtgagcc   5460
tccggatggc ctctgtgcag tatgtgcata ctcagcgttt ccaggcagag gtggtggcct   5520
ctgaggttat ttggtggtaa aattagggaa ttaattatcc tctgagtcag ttttccttcc   5580
tctttcaggt gagagatcaa gcccagcgct gttcacgggt tctcctggat attgaggctg   5640
gtgctcccgt tctcttgatc ccagaaagtt ccagatcaaa taatctgatt gtagcaaatt   5700
tggagagtcc caccaccagt gctgcccct tcccatttcc tgcattctag ttttattttg   5760
ttccttccca ggaatctgtg ccttcagctt ccccaacggg tattcccaaa cacagtctga   5820
ggaaaacgac aagcacggag gagcccaggg gaacccattc cagggggcag ttcacgatgc   5880
ctcttgctgg aatgagccta ggaagcctga agagtgagtt tgtgcctttg tttagtgcaa   5940
cccctttttg ggtccccttt tcttcattac ctctctttcc ttgggtcctt gtagaagacc   6000
atgtctgcct gctggattgc gttgtcgtgg atctccagga ccatggacca tctttgctgc   6060
ggagagacat ccggagagat tactcgaagg gcaccagagg atagtagtgg agatctgatc   6120
ttcccttcct attttgtgcg gacagacagg aggaagcctc cttaaccgag ccttgtaggc   6180
tgaaattgca ggtggaaagg aatttggaca aagaaataag tcatactgtg ccagacatat   6240
ctatccatgg caatctctcc tcagtccact gctctctgga tctgtataaa tacaagctga   6300
tccgcggctt attagagaac aacctgggag aacccataga ggaatttatg cggccttatg   6360
atttacaaag atccaagaat tcatactgtc ctgagtggag aagtgtacac ctgtatgtgc   6420
ttcctcattg atatggtgaa tgtaagtctg gagcttaaag atcc            6464
```

<210> 175
<211> 1186
<212> DNA
<213> Homo sapiens

```
    <400> 175
tttcgtgcta ccagaagaag tgtcgggtac gtctgcatta cacctggcgg gagctctggt    60
cagccttgat aaatttgctg aagttcctta tgtcaaatga gactgtactt ttggccaaac   120
acaacatttt tacattagcc cttatgattg tgaacctatt taatatgttt atcacatatg   180
gcgacacatt tctgccaacc cccagcagct atgatgaact ttactatgag attatccgca   240
tgcaccagag ctttgacaac ctctactcca tggtcctgag gctttctacc aatgcaggcc   300
agtggaagga agcagctagc aaggtgaccc atgcattggt taatatcaga gccatcatca   360
accactttaa ccccaaaatt gagtcctacg ctgctgtgaa tcacatatcc caactgtcag   420
aggagcaggt gctggaggtg gtgagagcaca actatgacac gctcacgctg aagctgcagg   480
atggcctgga ccagtatgag cgctactcag agcagcacaa ggaagctgcc ttcttcaaag   540
agctggttcg atccattagc accaacgtcc ggagaaacct ggccttccac acactcagcc   600
aagaagtcct gctcaaggag ttctccacta tctcctgagg ccacgcctac ctgagcagcc   660
tctgactgcc cttacccatg aggatcatgg gctggagggg gagcgaaggg agaggggct    720
gcccccgagg ttggagagaa acacagatac caagttctct tggtgaagac cgcacttcaa   780
tggagcttgc gcagcagggg caggagggtc aagccaggga taatcttatt tggggaggaa   840
tgggtgggca cagtggggag aggcctccag gaatgtgggg acttccagag tgggctccct   900
aaacagcccc tcacatttcc aatcttgagg ttacaagctg tagctactga ctaattttcg   960
ggagctggtg aggcaagcct cagggtaatg ccagcaccct gaaagtcagt ggctctgctc  1020
ggcttctgaa aacagatcaa ctctcagata tagctggagc tacatcctgc ttcctttggg  1080
cctggggctg tgcttggctt gaaatctgtg tcccctgcct gcactggcac tttgtccagt  1140
catcgggacc tttggctcag atttagggta agataggaat agggta              1186
```

```
    <210> 176
    <211> 2477
    <212> DNA
    <213> Homo sapiens
```

```
    <400> 176
gcggctttgg tggaccacag tacaagccta tgaccccagg gcagctctcc aacgtgcggg    60
cgccggggtc ggctgagaag ggcagcgggg acacggggga tgcccggccg ccctcggccg   120
cgccgcctgg ggggagcgct ggcgaggcac ggacggggga cgcccggtac ctctgcccgc   180
ggtcctcgct ctcggcgggg gcggcggcga cgcggacctg cggactagcg aacccggagg   240
aggaaggacc ctctgctaaa tgtggcgaga atggtagtgc agagaggact gaccttgggg   300
gaaacaagta caaccaggag aggatacaaa tagagtatgt ggaggtgctg tttgcagatt   360
tctttagaga agtttttgcg atatgtggaa gctgtgatgc tttgggaaac tggaatcctc   420
aaaatgctgt ggctcttctt ccagagaatg acacaggtga aagcatgcta tggaaagcaa   480
ccattgtact cagtagagga gtatcagttc agtatcgcta cttcaaaggg tactttttag   540
aaccaaagga aaacattcat catcgcggtg acttccttgt aacctttcca agttcttcac   600
gttcctcatt tgttcagact ggacagttct ctgggaggga catagacaag gacccaaaac   660
taagtcctgt gggcagggggc tggggtttg aatgggctat agagctatgc atggcagtca   720
aagaggatgt tcgacaggaa gtaggaagcc atataggggtt acttcctgat gttgccatgg   780
catttgtaaa ctgtcgtggc actgatggga gtgtagcagt gaggatgacc agaggtcact   840
ctcattgcca tcttggtttt gcctactgtg ctagtggggtt ctccttggag ccttgtgttg   900
aaaatgactg tgggggcctct tctgcagagg tgcaacaggg cttcgtgttc atcacatctg   960
cctcctcctc ttcctcatat tgcactgagg ccaaaagggt gaagctgaca ctagaaggcc  1020
tggaggaaga tgacgatgat agggtatctc ccactgtact ccacaaaatg tccaatagct  1080
tggagatatc cttaataagc gacaatgagt tcaagtgcag gcattcacag ccggagtgtg  1140
gttatggctt gcagcctgat cgttggacag agtacagcat acagacgatg gaaccagata  1200
acctggaact aatctttgat tttttcgaag aagatctcag tgagcacgta gttcagggtg  1260
atgcccttcc tggacatgtg ggtacagctt gtctcttatc atccaccatt gctgagagtg  1320
gaaagagtgc tggaattctt actcttccca tcatgagcag aaattcccgg aaaacaatag  1380
gcaaagtgag agttgactat ataattatta agccattacc aggatacagt tgtgacatga  1440
aatcttcatt ttccaagtat tggaagccaa gaataccatt ggatgttggc catcgaggtg  1500
caggaaactc tacaacaact gcccagctgg ctaaagttca agaaaatact attgcttctt  1560
taagaaatgc tgctagtcat ggtgcagcct ttgtagaatt tgacgtacac cttcaaagg  1620
actttgtgcc cgtggtatat catgatctta cctgttgttt gactatgaaa aagaaatttg  1680
atgctgatcc agttgaatta tttgaaattc cagtaaaaga attaacattt gaccaactcc  1740
agttgtaaa gctcactcat gtgactgcac tgaaatctaa ggatcggaaa gaatctgtgg  1800
ttcaggagga aaattccttt tcagaaaatc agccatttcc ttctcttaag atggatggaa  1860
tgtgggatgg taacttatca acatattttg acatgaatct gttttttggat ataattttaa  1920
aaactgtttt agaaaattct gggaagagga gaatagtgtt ttcttcattt gatgcagata  1980
```

```
tttgcacaat ggttcggcaa aagcagaaca aatatccgat actatttta actcaaggaa        2040
aatctgagat ttatcctgaa ctcatggacc tcagatctcg gacaaccccc attgcaatga       2100
gctttgcaca gtttgaaaat ctactgggga taaatgtaca tactgaagac ttgctcagaa       2160
acccatccta tattcaagag gcaaaagcta agggactagt catattctgc tggggtgatg       2220
ataccaatga tcctgaaaac agaaggaaat tgaaggaact tggagttaat ggtctaattt       2280
atgataggat atatgattgg atgcctgaac aaccaaatat attccaagtg gagcaattgg       2340
aacgcctgaa gcaggaattg ccagagctta agagctgttt gtgtcccact gttagccgct       2400
ttgttccctc atctttgtgt ggggagtctg atatccatgt ggatgccaac ggcattgata       2460
acgtggagaa tgcttag                                                      2477
```

```
        <210> 177
        <211> 3805
        <212> DNA
        <213> Homo sapiens


        <400> 177
atggagccca ttgagggcaa gagatccagc tgccataaaa caggagaagc tacagcagtt        60
gtccactgtc cacccggctg gaacatcacc atggggggtgg aagcctcatg tgccttcgtc       120
ggccgcgccg gctcccagga tacagtgcgg accggccggg cgctaaaggc gttgacgcaa       180
ctgcgggcgg cgcagggcag gggcagtcag ggagcagcgg cggcagagac agggctgggc       240
gggcgccgcc tgcggagagc accgggaggc gggccctgcg tgggggccgcg cgcagcagcg       300
gcgacgactt tatctgggcc gcggggaca gcgcagggcc atggaggag cggccgcagc        360
tccggtaagg gcgaccagcg cgcgcacgaa ctcgcggcct ggattccccg ggcgacccgg       420
gcccggcaca cgggggctgc gggagccgag ccgtactacc gcgcctgggg ctccgggggaa       480
cagggccgcg gcgtctgccg gggcctactg cgcttgccag ccgggccccc cactccgggc       540
cgagcccgag cgctggcgga acggttgtcc ccgccccggg ccgccccacg ccaagattct       600
tggcccctcc ggggcttcct gccccccgccc cagccgctga accctacatc tgcgtccccc       660
cacccgaggc tcttttctct gcttggcgct cggcctattt ctccgtggac gatggcagcc       720
acgattcagg ccatggagag gaagattgaa tcgcaggctg ctcacctgct ttccctagaa       780
ggtcaaaccg ggatggccga gaagaagctg gctgattgcg agaagacagc cgttggagttc       840
gggaaccagc tggagggcaa gtgggccgtg ctgggaaccc tgctgcagga gtacgggctg       900
ctgcagaggc ggctggagaa cgtggagaac ctgctgcaca acaggaactt ctggatcctg       960
cggctgcccc caggcagcaa ggggggagtcc cctaaggtag ccctggggcg ccctggggtt      1020
ggggaggccg cggccaagcc tgtgagcgtg tggttctctg agcaagtgtg gggcaagctg       1080
gaggactggc agaaggagct ctgcaagcac gtgatgaggg gcaactgcga gatgctggtc       1140
tctttggact acgccatctc caagtccgag gtcctctccc agattgaaca agggaaggag       1200
ccctgcaact ggcgccgccc tggccccaag attccagatg ttcctgtgga ccccagtcca       1260
gccccagtgc ccttgccctt gttttgttca ttgtatccac ctggtgaaat ccatcagtgt       1320
tctgtacctg cagccaaaca gctgcacgtg gtgcagagaa ccagtcctgt gactgctaaa       1380
ctgtcgactc tccagccaaa gccccacttc cacctggtgc tgcatcccac cccatgccag       1440
cttctcaagg gcaacacagt caatcctacc ttgacctcta cccctacagc cacggcctgc       1500
ttctctgctc cgcttcgtgg cagagcccct tggatctata ccatggaagg gaacagatta      1560
aaccagtgtt tccaaactgg gtgctggagg gctcctgggc acatccaggc cggggaagaa      1620
gccccgggga ccgtgtggt gttcacacgc atcacaggtt caggagaatg caggaggggg       1680
cctgagaaga gctgcggatt tggtcactcc cgggaagcgt taggagagga gtggatgatt      1740
cggaaggtga aggtggagga cgaagatcag gaggcagaag aggaggtcga atggccccag       1800
catctatcgt tacttcccca gcccctttcc cgcgcctgac ctggggcatc tggctgccgc      1860
gtacaaactg agccagggg ccccggggggc actgagtggg ctcgcgctgt ctgggtgggg       1920
tccgatgccg gagaagccct acggctgcgg ggagtgtgag cggcgcttcc gggaccagct       1980
gacgttgcga ctgcaccagc ggctgcaccg gggcgagggc ccctgcgcct gcccggactg       2040
cggccgcagc ttcacgcagc gcgcccacat gctactgcat cagcgcagcc accgcggcga       2100
gcggcctttc ccgtgctccg agtgcgacaa gcgcttcagc aagaaggccc atctgacccg       2160
ccacctgcgc acgcacacgg gcgagcggcc ctaccgcgtgc gcggagtgcg gcaagcgctt       2220
cagccagaag atccacctgg gctcgcacca aaagacccac accggcgagc ggcccttccc       2280
ctgcacggaa tgcgagaagc gctttcgcaa gaagacgcac ttgattcggc accagcgcat       2340
ccatacgggc gagaggccct accagtgcgc acagtgcgca cgcagcttca cgcacaagca       2400
gcacttggtg cggcaccaaa gggtgcacca gacggccggc ccggccaggc cctctcccga       2460
ctcgtccgct tctcctcatt ccactgcccc gtccccgacc ccatcctttc ccgggccaaa       2520
gcctttcgcg tgctccgact gcgggcttgag cttcggctgg aaaaagaacc tcgccacgca       2580
ccagtgtctg caccgcagca gagggtcgcc cctttgggtg cgatgagtgc gcactgggcg       2640
ccaccgtgga tgccccgcc gccaagcccc tggccagcgc gcctggcgga ccgggctgcg        2700
```

```
gcccaggatc cgatcccgtg gtgccccagc gcgcccctc gggcgagcgg tccttcttct    2760
gcccggactg cgggcgcggc ttctcccatg ggcagcacct ggcgcggcac ccgcgcgtgc    2820
acacgggcga acggcccttc gcctgcacgc agtgtgaccg ccgcttcggc tcgcggccta    2880
atctggtcgc ccactccagg gcccacagcg gcgccaggcc ttttcgcctg cgctcagtgc    2940
ggccgccgct tcagccgcaa gtcgcacctg ggtccgccac caggcggtgc acactggcag    3000
ccgccccac gcctgcgccg tctgcgcccg cagcagcttc agctccaaaa ccaacctagt    3060
ccgccaccag ggcattccac acaggctccc gcccttctc ctgcccgcag tgcggaaaga    3120
gcttcagccg caagacccac ctggtgcggc accagctcat tcacggcgaa gccgcccacg    3180
cggccgccgg acgccgccct tgcggcccca gcctggtccg ctcccccga ggtggcgccg    3240
cccccgctc ttcttctgag cctagttctc acgaggaccc tttcttgccc cacagtttcg    3300
aaaaggcccg tgcccatgaa gaccgccctg gggtgaagca aggcgaccct ggctgctgcc    3360
cgaagggttt ggccgcgcg ggacacctgt ttccttcccg cagtgtctgc gtccgcacag    3420
catacccagc tcggacctcc taggacagag actcagcgaa cccttgctgg gaaccgctga    3480
gctgaagttc ttggaaggct cccacccagg tgccccgttg gaaagcagat atttcccgga    3540
cccagcgcgg cctcaaccag gggcaggaaa gagtggttat ttatgtactt aaagtttcat    3600
taaagttaaa atcggaaagt tctggggctg ctaaatgaat tggggaggg aacacctgac    3660
tctccttagc cactgtccca cctccatcca cacacagacc acccccctcc acttcccctt    3720
ctgtcctggg tgagttacat ttagccagct gctgttaatt ggttctccac aaataaaaat    3780
gtaatatatt tattcactaa aaaaa                                          3805
```

<210> 178
<211> 4485
<212> DNA
<213> Homo sapiens

<400> 178
```
ccatactgca gtgtcgtgga attcggacag gcagagtgct gatgtgaaaa ataccacgac     60
aaaaccaccc tagttctcca aaatacttat cattcaggtt gaataaacca gttctacaga    120
ctgcttcttc catgcatttc ccaatgatgc taactgccct taaaattctt tcagatttgg    180
aactgtatct gtatggaaac aacagagttt tcttgaagta caactaagga caggtcacca    240
ctaggcacta acatcgctga cttgcatgat tatggagatg gtctatctga tgctgaaaat    300
gtctctagtt ttttgacaac ggctaaataa ccatgggatc aagtggcctt gggaaagcag    360
caacattaga tgaactgctg tgcacttgca ttgagatgtt tgatgacaat ggagagctgg    420
ataatagtta tttgccaaga atagttctac tgatgcaccg atggtattta tcttccactg    480
aattggcaga aaaacttctc tgcatgtatc gaaatgccac tggagaaagc tgcaatgaat    540
ttcgattaaa gatctgctac ttcatgaggt actggattct gaagtttcct gcagagttta    600
atttggatct tggtttgatt cgtatgactg aggaatttcg ggaagtagct agtcaactag    660
gatatgaaaa acacgtcagc ctcatcgaca tatccagcat tccttcctat gactggatga    720
gaagagtcac acagaggaaa aaagtatcca agaagggaaa agcctgtctg ctgtttgacc    780
atctggagcc cattgaattg gctgagcacc tcactttct ggagcataaa tcttttagaa    840
ggatctcatt cactgattac caaagctatg tcatccatgg ctgcctggag aataatccaa    900
ccttggaaag atcgattgct ttatttaatg gaatctctaa gtgggtccag ttgatggttc    960
ttagcaaacc aacccccag caaagggcag aagtcatcac aaagtttatc aatgttgcaa   1020
agaagctcct tcagctcaaa aattttaaca accttattgc aattgtggga gccctcaagt   1080
cataggtcca tttcaggctt caaagggacc cattcctcat ctttcctcag aagtttacaa   1140
agaactggaa tgtgaaatga cagaagtggg tctcctccaa cgggcaatta ctgcaattac   1200
cgcaagccct ttgccgactg cgatggcttc aaaatcccca tccttggagt acacttgaaa   1260
gacttgatag ctgtccatgt catttttccca gactggacag aggagaacaa agtgaacatt   1320
tgtgaaaatg caccagctct ccgttaccct gagtgaacta gtctccctgc agaatgcctc   1380
tcaccactta gaacccaaca tggatttgat caacctgctc acgctttccc tggacctcta   1440
tcacactgaa gatgatattt acaaactgtc actggtgctg gagcctagaa attctaaatc   1500
gcagcctacc tccctacga cgcccaacaa gcctgtggta ccctggagt gggcattagg   1560
ggtgatgcca aagccagacc ccacggtcat caacaagcac ataaggaaat tagtggagtc   1620
tgtatttaga aactatgatc acgaccatga tgggtacatt tcccaagagg actttgaaag   1680
tatagctgcc aattttcct tcttggattc cttctgtgtt ctggacaaag atcaggatgg   1740
cctaattagt aaagatgaaa tgatggctta cttcctgaga gctaaatccc aactacactg   1800
tcaaatcgcg caccaggatt tatccacaat tttcaggaga tgactctatc tcaagccaga   1860
ccttctgcga acactgtgcg ggatttattc tgtggcataa tcaagcaagg atacaaatgc   1920
aaagactgtg agccaattg tcacaaacag tgcaaagacc tcctggttct ggcctgcagg   1980
agaatttgcc cgggcgccct ccttgagcag tggtcatggg tcactgcctg gaagccctc   2040
gctgccccca gcgcagggat taggtgttta agttccctgg agtcactgct gacaacagcg   2100
```

```
attttagaca gcagagccat cacactggtt acaggctctt ctcgcaagaa cttctgtgag   2160
gctacagagg gccaccacca gccaggccac cccagactgg aacctgtctg gtcagaggct   2220
ggctggggg gactcggggt cccacaccct tccctataat agatattcag gttccttgca    2280
caagccacca aaaggcacaa gggctttgca atatgggaaa aatgaaaaag cccagggtgg   2340
catggctggt ggggatgttt aaaacccggg caccggagtt tgaaccttgc cccggatgaa   2400
ggagagaaga ccacacacgg atgggtgagg atgggctgac ttcaaggctg gcggaaaact   2460
tgaaggccaa taatggttgg cttttgggag ggggcaagaa caagaaactc ttgaggaaag   2520
ctcttgcctc tcaggaagtt atcttggaaa gaaccccctg atgttaactt gccttgggga   2580
cactgtggga tctccatgtt tggactatgg gacagagaat tgaccctaac taaactatga   2640
attattatgt gcctcctccc ctaccctag ttaagtgcca caaagactgt gttatgtagt    2700
cagtactttt ttctcatgga tctttctcta gaccatttat atacgggctg aaatgaaagc   2760
cttttgcat gtacttgata ctcagtctgt aaactcagac ttcgcttttt ttgtgagact    2820
atcctttcaa tattttata aacttttgtg tgtgctgtgg caggggaca gttaacaagg     2880
gagtttattt agaggggttt tttcatttt ttgttttct tgttttgttt tgttttgttt     2940
tgttcttctt ggtgtgcttt ttggatggga ccagaactta acattttcct gaggactagg   3000
aagctcatca gacactggaa tgcagtgatt cttctaatga tggtcaactg caaggagaaa   3060
ctgtttacat ccttcccact acacagttgc tatgatatgt aacaaagtca ccacaatttt   3120
tgtatatatc acacaagtct tacccaattc tgcgtcacta gggaagctat agcatggtcg   3180
agaaagctct cctaatactt acttacttaa atagccatgg aagaaaatta tgcttgtccc   3240
ttctgactgg gttaagccat ctttcttaaa gattcctgaa gtagaaatag caattaagaa   3300
attaattcaa gttttgacgg ttaacaaaca tttagcagaa aaacaaacca ttgaataagc   3360
tactaggtga aatgcaaaac aaccatcaat ttttttaaac tcaataattt tgtgaaaaaa   3420
aaaaccacca ccaaactttt ggttgtaaaa gagaaccctt gttcccttcc taagaaactg   3480
ccttccacaa ttaaagaata ctcatagaaa gaaaataatc ataaatcata tttgattaac   3540
atttcattta agctttaaa atatcaattt tttaaatagc tcccatttac ccaaaataac    3600
tagttatggg tctatttctt ccatgattag aggagagaga acttgattca agatactgaa   3660
aaatagagct gggactgagc ctgtgaatga caggaatgat ctattaccag gtgactagtc   3720
ggaaactaca cagaccgtgc actggtctgc atttgggggc taaagtgtat atattccatt   3780
taaaatggaa tttgtttgta tttggggcag tcttcagtaa agcctttctc ctttctttc    3840
tccattgagg accagttctg ctcagccaaa attgttgagt ccctgttctg ggccaggtcc   3900
cacgctatat gcaccaaagt taggaaaaac ttgggtctta agcccttggg gagcttgacc   3960
agcccatggg cattaaggca aagtagttcc cagtgattta aaatacgggt tccaaatacg   4020
ctaaaaccaa acttgtgcca acccagattt acagatgggg aaatactgca gatgatgtga   4080
agttatcagt tgaaggagct gtgatttagg ctggataata agagaacgtg cccatctgta   4140
aagcacctca gaaggcagcc atcccctaga tgttggtttc gatgtatatt acactatcta   4200
ctactatcca taaatgcaat aatatgcatg ttaacaacat taaaaacagc aaacagcaat   4260
ctaagtacag aaaagctttt tgtgtgttta aaaaaattga agaaaattca ggaagaaacg   4320
tgttaataaa cattgtactg ttcttttgct tctcaaagga attattcact tgccactttg   4380
gttatttttg agttttcgta cataggaagt tttatattgc cagccttcct gtgataaaga   4440
tattaaatgt aacttgagta aaaaataaaa aagaataact atgta               4485
```

```
        <210> 179
        <211> 4864
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 179
acgcagctcc gccccgcgtc cgacccgcgg atcccgcggc gtccggcccg ggtggtctgg    60
atcgcggagg gaatgccccg gagggcggag aactgggacg aggccgaggt aggcgcggag   120
gaggcaggcg tcgaagagta cggccctgaa gaagacggcg gggaggagtc gggcgccgag   180
gagtccggcc cggaagagtc cggcccggag gaactgggcg ccgaggagga gatggaggcc   240
gggcggccgc ggcccgtgct gcgctcggtg aactcgcgcg agccctccca ggtcatcttc   300
tgcaatcgca gtccgcgcgt cgtgctgccc gtatggcatc aacttcgacg gcgagccgcag   360
ccctacccaa cgctgccgcc tggcacgggc cgcacgaatc acagctaccg aggtcaccttt  420
tggctcttca gagatgcagg gacacacgat gggcttctgg ttaaccaaac tgaattatttt   480
gtgccatctc tcaatgttga cggacagcct attttttgcca atatcacact gccagtgtat   540
actctgaaag agcgatgcct ccaggttgtc cggagcctag tcaagcctga gaattacagg   600
agactggaca tcgtcaggtc gctctacgaa gatctggaag accacccaaa tgtgcagaaa   660
gacctggagc ggctgacaca ggagcgcatt gcacatcaac ggatgggaga ttgaagattt   720
ctgttgaaac ttacactgtt tcatctcagc ttttgatggt actgatgagt cttgatctag   780
atacaggact ggttccttcc ttagtttcaa agtgtctcat tctcagagta aaataggcac   840
```

```
cattgcttaa aagaaagtta actgacttca ctaggcattg tgatgtttag gggcaaacat  900
cacaaaatgt aatttaatgc ctgcccatta gagaagtatt tatcaggaga aggtggtggc  960
atttttgctt cctagtaagt caggacagct tgtatgtaag gaggtttata taagtaattc 1020
agtgggaatt gcagcatatc gtttaatttt aagaaggcat tggcatctgc ttttaatgga 1080
tgtataatac atccattcta catccgtagc ggttggtgac ttgtctgcct cctgctttgg 1140
gaagactgag gcatccgtga ggcagggaca agtctttctc ctctttgaga ccccagtgcc 1200
tgcacatcat gagcctcag tcagggtttg tcagaggaac aaaccagggg acactttgtt 1260
agaaagtgct tagaggttct gcctctattt ttgttggggg gtgggagagg ggaccttaaa 1320
atgtgtacag tgaacaaatg tcttaaaggg aatcatttgt gtaggaagca ttttttataa 1380
ttttctaagt cgtgcacttt ctcggtccac tcttgttgaa gtgctgtttt attactgttt 1440
ctaaactagg attgacattc tacagttgtg ataatagcat ttttgtaact tgccatccgc 1500
acagaaaata cgagaaaatc tgcatgtttg attatagtat taatggacaa ataagttttt 1560
gctaaatgtg agtatttctg ttcctttttg taaatatgtg acattcctga ttgatttggg 1620
ttttttttgtt gttgttgttt tgttttgttt tgttttttg ggatggagmc tcactcttgt 1680
cacccaggct ggagtgcagt ggcgccatct cggctcactg caacctctgc ctcctgagtt 1740
cacgtaatcc tcctgagtag ctgggattac aggtgcctgc caccacgctg gccaatttt  1800
gtacttttag tagagacagt gtttcgccat gttggccagg ctggtttcaa actcctgacc 1860
tcaggtgatc cgcccacctc agcctcccaa aatggtggga ttacaggtgt gtgggccacc 1920
gtgcctggct gattcagcat ttttatcag gcaggaccag gtggacttcc acctccagcc 1980
tctggtccta ccaatggatt catggagtag cctggactgt ttcatagttt tctaaatgta 2040
caaattctta taggctagac ttagattcat taactcaaat tcaatgcttc tatcagactc 2100
agttttttgt aactaataga ttttttttttc cacttttgtt ctactccttc cctaatagct 2160
ttttaaaaaa atctcccag tagagaaaca tttgaaaag acagaaaact aaaaaggaag 2220
aaaaaagatc cctattagat acacttctta aatacaatca cattaacatt ttgagctatt 2280
tccttccagc cttttttaggg cagattttgg ttggttttta catagttgag attgtactgt 2340
tcatacagtt ttatacccttt tttcatttaa ctttataact taaatattgc tctatgttag 2400
tataagcttt tcacaaacat tagtatagtc tccctttttat aattaatgtt tgtgggtatt 2460
tcttggcatg catctttaat tccttatcct agcctttggg cacaattcct gtgctcaaaa 2520
atgagagtga cggctggcat ggtggctccc gcctgtaatc ccagtacttt gggaagccaa 2580
ggtaagagga ttgcttgagc ccagaacttc aagatgagcc tgggctcata gtgagaaccc 2640
gtctatacaa aaaattttta aaaattagca tggcggcaca catctgtaat cctagctact 2700
tggcaggctg aggtgagaag atcattggag tttaggaatt ggaggcggca gtgagtcatg 2760
agtatgccgc tgcactccag cctgggggac agagcaagac cctgcctcaa aaaaaaaaa 2820
aaaaaaaatt caggccggga atggtggttc acgcctgtaa tcccagcact ttggggggtc 2880
gaggtgggca gatcacctga ggtcaggagt tcgagaccag cctggccaac atggtaaaac 2940
cccatttcta ctaaaaaata caagaattag ctgggtgtga tggcggcatgc ctgtaatcct 3000
agctactcag gaggctgagg caggagaatc acttgacccc aggaggcgaa gattgcagtg 3060
agctgatatc gcaccattgt actccagcct gtgtgacaga gcaatactct tgtcccaaaa 3120
aaaaaaaaaa ttcaaatcag agtgaagtga atgagacact ccagttttcc ttctactccg 3180
aattttagct cctcctttca acattcaaca aatagtcttt tttttttttt tttttttttg 3240
gggatggagt ctccctctgt tgcccaggct ggagtgcaga ggtgcgatct ctgctcacta 3300
caagctctgc ctcccgagtt caagtgattc tcctggctca ccctcctgag ctgggattac 3360
aggcgcctgc caccatgcct ggctaatttt gtgttttag tggagacggg gtttcaccat 3420
gttgtccagg atggtcttga tctcctgacc ttgtgatcca cccacctcag cctcccaaag 3480
tggtgggatt acaggtgtga gccaccgcgt ccagccagct ttattatttt ttttaagctg 3540
tctttgtgtc aaaatgatag ttcatgctcc tcttgttaaa acctgcaggc cgagcacagt 3600
ggctcatgcc tgtaatccca gcattttggg agaccaaggc ggatggatca cctgaggtca 3660
ggagctcaag accagcctgg ctaacatggt gaaacctcat ctccacttaa aatacaaaaa 3720
ttgccggccg cggcggctca tgcctgtaat cccagcactt gggaggcct aggcgggtgg 3780
atcacgacgt caggaaatcg agaccatcct ggctaacacg ggtgaaaccc catccctact 3840
aaaaatacaa aaaaaatta gccgggcgtg gtggtgagcg cctgtagtcc cagctactcg 3900
agagcctgag gcaggagaat ggcatgaacc tggaaggtgg agcttgcagt gagctgagat 3960
ggtgccactg cactctaacc tgggcgacag agtgagactc cgtctcaaaa aaaaaaacaa 4020
aaaccaaaac ttatccaggt gtggcggtgg gcgcctgtga ggcaggcgaa tctcttgaac 4080
ccgggaggcg gaggttgcag tgagccaaga tcacaccatt gcactccagc ctgggaaaca 4140
agagtgaaat tccatctcaa aaccaaattt tcaaaaaaaa aacatgccgc ttgagtactg 4200
tgttttggt gttgtccaag gaaaattaaa acctgtagca tgaataatgt ttgttttcat 4260
ttcgaatctt gtgaatgtat taaatatatc gctcttaaga gacggtgaag ttcctatttc 4320
aagttttttt tgttttgttt tgttttaag ctgttttta atacattaaa tggtgctgag 4380
taaaggaaat aggcagggtg tgttgtgtgg tgttttaact aggcgcttct ctctcagaga 4440
gttttgaaac ctgtttacat aaaggcccaa gatgggaagg agatccaaac ataagccacc 4500
agcctcattc caagtctctt ctctttccaa ccctggattt ttttttttta tttaacattg 4560
tttctttttag ctttattttt cttataaaag aaatgtatca ctataaaaaa ttacacacta 4620
cagaaaaata ttaagaagaa aaacattcac atcggaaaca aagttttttc ccatgaaaac 4680
```

```
agaacccaaa agggtaagtg gttagtattt caccagcaat tatgttgaga ataaggccag    4740
gcgaggtggc tcacgcctgt aatctcagca ctttgggagg ccagggcagg cagatcatct    4800
gaggtcagga gtttgagacc agcctggcca acatggtgaa accctatctc tactaaaaat    4860
taaa                                                                 4864




        <210> 180
        <211> 6397
        <212> DNA
        <213> Homo sapiens


        <400> 180
atgcccgcgc cgcgcgcccg ggagcagccc cgcgtgcccg gggagcgcca gccgctgctg      60
cctcgcggtg cgcggggccc tcgacggtgg cggcgggcgg cgggcgcggc cgtgctgctg     120
gtggagatgc tggagcgcgc cgccttcttc ggcgtcaccg ccaacctcgt gctgtacctc     180
aacagcacca acttcaactg gaccggcgag caggcgacgc gcgccgcgct ggtattcctg     240
ggcgcctcct acctgctggc gcccgtgggc ggctggctgg ccgacgtgta cctgggccgc     300
taccgcgcgg tcgcgctcag cctgctgctc tacctggccg cctcgggcct gctgccgcc     360
accgccttcc ccgacggccg cagctccttc tgcggagaga tgcccgcgtc gccgctggga     420
cctgcctgcc cctcggccgg ctgcccgcgc tcctcgccca gcccctactg cgcgcccgtc     480
ctctacgcgg gctgctgct actcggcctg gccgccagct ccgtccggag caacctcacc     540
tccttcggtg ccgacgcagg tgatggatct cggccgcgac gccacccgcc gcttcttcaa     600
ctggtttac tggagcatca acctgggtgc tgtgctgtcg ctgctggtgg tggcgtttat     660
tcagcagaac atcagcttcc tgctgggcta cagcatccct gtgggctgtg tgggcctggc     720
attttttcatc ttcctctttg ccaccccgt cttcatcacc aagcccccga tgggcagcca     780
agtgtcctct atgcttaagc tcgctctcca aaactgctgc ccccagctgt ggcaacgaca     840
ctcggccagg tcaaagctgt cacaaggcca gcaggggaaac aatggcagtg aaagtaaact     900
ccacctgttg gtggcaaaat ggcagcacac gctgggaagg gtggagttga cagtggctgt     960
ctttggagat gactacacta atattgtccc ttttggaatc tcaaaggaca gtgcaaggct    1020
cttggacaaa aagagagacc gtcaatgtgc ccgcgtgctg gccgacgaga ggtctcccca    1080
gccaggggct tccccgcaag aggacatcgc caacttccag gtgctggtga agatcttgcc    1140
cgtcatggtg accctggtgc cctactggat ggtctacttc cagatgcagt ccacctatgt    1200
cctgcagggt cttcacctcc acatcccaaa cattttccca gccaacccgg ccaacatctc    1260
tgtggccctg agagcccagg gcagcagcta cacgatcccg gaagcctggc tcctcctggc    1320
caatgttgtg gtggtgctga ttctggtccc tctgaaggac cgcttgatcg accctttact    1380
gctgcggtgc aagctgcttc cctctgctct gcagaagatg gcgctgggga tgttctttgg    1440
ttttacctcc gtcattgtgg caggagtcct ggagatggag cgcttacact acatccacca    1500
caacgagacc gtgtcccagc agattgggga ggtcctgtac aacgcggcac cactgtccat    1560
ctggtggcag atccctcagt acctgctcat tgggatcagt gagatctttg ccagcatccc    1620
aggcctggga gtttgcctac tcagaggccc cgcgctccat gcaggcgcc atcatggggc    1680
atcttcttct tgcctgtcgg gggtgggctc actgttgggc tccagcttag tgggcactgc    1740
tgttcctttg cccggggggct ggctgcactg ccccaaggac tttgggaaca tcaacaattg    1800
ccggatggac ctctacttct tcctgctggc tggcattcag gccgtcacgg ctctcctatt    1860
tgtctggact cgctggacgc tatgagaggg cgtcccaggg cccagcctcc cacagccgtt    1920
tcagcaggga caggggctga acaggcccta ttccagcccc cttgcttcac tctaccggac    1980
agacggcagc agtcccagct ctggtttcct ttctcggttt attctgttag aatgaaatgg    2040
ttcccataaa ataaagggca tgagcccttc ctcacgacca tggtccatga caaggggcag    2100
ggcagagggg gccttggatg ggagtccttg tggggacca ggcaggggac ttggatcaac    2160
aagcaccaga cgagtggcgg gggcaggcga gaggctcagt gggacctcca ccctcgttgc    2220
cccagctggt ggctgaccag gtggctgtgg agggtcagga gctgccccg ttcctctcca    2280
tgtagttgcg aagctcctca gggtccttca gccccatgtc ctcacacacc cagcggatgt    2340
cctcctcgcc tgccacaagg atggactgca cagcaggggc ccctacaggc tcctcaggtg    2400
actgggctgg aggggctggc gcaaatgtca caaactctac tcgcttccgc cgccccccag    2460
cctcctttcg gccagggtg cttgaggagc tggtggtgcc cccaggaggg ccaggggcca    2520
gggtaggggc ctcccctcct ccccactct cacagggca gctcccctcc ccttgggcg    2580
ggccagggga ctgccggtcc agctggcggc tcagttcctc ctggtcagtg cccagccaga    2640
cccagttgtg gggctggggg gaggtggggt cagtggcact gtcgggaggt tctttgcgct    2700
gatagcgcag gacgaagacc acaccattga ccaagaagat gaagatggcc acgcagaaga    2760
ctcccagcag ggcgtacatg cccagctcta gctcagtgac atgctgaggg cagggacca    2820
tctcctcctc ctcttcctcc tcctcctccc tggcttcggt ctcctccttc ctggcctcct    2880
cctctgcccg ctcaaacttg cccctcacac ctgtgttgcc cccgacactg cctgccacct    2940
gccgtttacc acccatggtg gcttctgtgg ctggtgggct ccaagcaggg ctggatggga    3000
```

103

```
gagcaggggc tggagtggag gcaggggggca gccccagcca ggcggtgcca gaggccagag    3060
gcacacggtg gcggccccgg cggcagggct cgggcgggtg cagagccaca tgcagcggca    3120
gcccctcggc gcctgcccca ctcaccacca ccccgagctg ggcaccctgc tcctcagctg    3180
gcaggatggc accaggctcc tcggctgaga cggacagtcc caggtcacgg cggtcgtaga    3240
gctcagctgg ggccacagtg tgatcagaga aggacagcca tagggagagg gccacctcct    3300
gctttggggc gggaagggct gactgtgccc agcacgtagc tgtgacctcc ccggggtggg    3360
cagtgccccg gctcaagggt cagcaagatt gcccatcact ggctgcaccc tcagctccag    3420
cactgagacc ttgtcgtccg tcacagccag cgcctgctcc cccaggatgg agtcagacag    3480
tggggaacgc acctcaatgg aggtgacacc gggctcccgg cccaccacga cacggccacc    3540
ctccagagag gctacacgcg agtccagcac gcgggcgtgt ggcgccacga ggtgggacac    3600
gtctagcagc cagtcggggc caagcaggtg cgtgaggcgg cggccgccgt ccagcgggtg    3660
ggccgcgaag ggggcgagga agcgcacacc ggcccgctgg tactgcaggt ggcagccacg    3720
ggcgcgccgc tcggcctcat ccgacgcctc tgcagcgggt tccgcaggcc cttcagcagg    3780
gccaggtacc ctccagccgc ggacctgctc gagggtggtg tcggtgagct cgatacgcag    3840
cggtagcagg ggggcccaca cggtcagccg cagcgaggcg cggagccggc cgccaccaga    3900
agtccacttc gcaccccccg ggcgccccgg ctctccttgc cagccacgaa cacggcatca    3960
caggcctcaa gacacctgca ggacctgtgt gttggcagat tcgcagccga catgctctgt    4020
cacctccacc aaggcccccc cgccgttcca cagtggacaa ggcgcacggg gacatgctgg    4080
ggcactccag tcaagtggtg ctgtattcac cagctcctca gccttggcca gtgggataag    4140
ggctctgatg tcccgctcag acaccaggat ttcccacacc gattttgtcc ttctctgctt    4200
caggggcctg gcctgggtac tccagctgcc acgtgacggg gcgagtgacc gctacgcccc    4260
caccagtgct attctccacc acaaagtcca cccataggaa ctcagacagt tcaaggggac    4320
tgctggaatc tggctctgtg agcccagcac ggtggcaggt gatgagggtg gtgtggtgcc    4380
tggagccctt gaagcggtcc agcttggcag tccagagtgt gggctgggct gggcggggcgg    4440
ctgtcacatg cagcccttc ttcaccttga tccgcagggt caggaggctg gctgtgaagt    4500
tgtgccgaag caggagggta gcactaaaga gctggccggg ccgcactggc atgtcaggca    4560
cccgcagagt cacagcctcg tccagaggta cctcctggta ctgcgggggg tctgctgggc    4620
gcagctccac acccccccact gggagggcct gctccccagg gtcgttctcc tcgccggagc    4680
cacagccccc agggccctca gctgcaggct caagcgtgta ggccagctcg gcccgtgtgg    4740
tggaggcctg tgagaaccag tgcgagggaa gctccagctc caccacgcag gcgcccaggg    4800
atggctggaa gcggcaggct tggtgagcag tgccggcagg gtgtgtggca tggagccggg    4860
cacagggcag gctggtggcc cctggtggcc aatcctgccc tttgaggtgg aagagaaccc    4920
gggcgtaggg ctctgctgga gtcacagccg cttccactga aacggcccgc acgtcccatg    4980
ggactggccg ttggtggggc tcagtgactc gagggggggac cacctgctga gtggcaaaag    5040
gtgggtagga ggcccggaga agtggctggg ccctgggcca gggctgtagg agcagaaagg    5100
tctcagatcg ggagctcaga gaggagttgg caggtgggta gtggcccacc tgctgcacac    5160
ggaagtgttc aggggcgtct aggagctcca gggctgccgg caggtagaca gggtccaggg    5220
gagcctggcc acagtccacc cgaagcacag ggaagttgct gccctttccc gcagtgacag    5280
gaatcctctc aaaggttctg gaaggcaagg atgcggccat ccctctcacg acgtccaggg    5340
cgagggccac caggaggcag agccaggggc cgtagggccc ccgaggggcc gctgttgtgc    5400
gaccggccat ccgcgcgcac atctcctcct ccacactgcg ggccccttg gccgctcgcc    5460
tctggcgcca gcgcagctcc tccacctggc gttccagccc tcgcaccttg gcctcgagtt    5520
gggccccaga ggctcgggag ccagtgagcc ggctcagcag ggcgtagagg atcagcaagg    5580
ccaggagtag cagggcccgg gtggaagggt caggcaccga cctcatcagg gccacgaagc    5640
cggccaggaa gatgacaagc ttcaggcccc acaggatccg ccccagcaag gccaagacca    5700
agccgaggag cagagacagc agccagtaga cgaccagggc ccctgctccc cacagcagga    5760
aggtctggac ctggccaggg ctgagcttca ggccctgggc gaggtaatca ccagctagtc    5820
ccaaggcatt cagcagctgt gcggcgatcc cagacagagc aaagaaggcc acagaaatgg    5880
ctgatgagat ggcccacaac acttgggacg aagactctga caccaggtgc atggtctctg    5940
gcccaatcca ggcatccagt gtccctcgca cagatcgacc tatctgggtc aagacatcaa    6000
ctggggcttc tctcttctgt tggcctggtg gtgcaaagtc tcgacgggac tgggccaatg    6060
ctgagtggag gaggataagg gccactagga ccatcagaat ggctttgaac acatgctttc    6120
cccatggtga actgatgctg gaggctgcca tgactgggtc caggatctca atcttgcctt    6180
tttgcttgtc ccatacccgc atgctgcctt gatagtggac atagtccctg ccctcatgga    6240
gctgaagttc accaacaagc tcaaagtgga aggacatcca gactcctgcc aggaggagca    6300
gggcttttgc aacgggctcc atgaagccat gagcctgagg ctcggggtgc cttcccagca    6360
tgccagcccc accaatccac tgccgaggtt cagacat                              6397
```

<210> 181
<211> 1149
<212> DNA
<213> Homo sapiens

104

```
        <400> 181
tttttttttt  tttttgggg  ccaactgaat  tcaacaagta  tttattgagt  gtctattatg    60
tgctagatac  tgagacacat  cagagaacaa  aaccaaaagc  cctgcccttg  tcgggcttac   120
agtctagcac  ttaccgccag  ttaacctgca  ggctacctgg  agcccgggc   aagtcaccgc   180
acctctgtgc  cctcggtcct  cagctgccca  atgggagaat  aagcagacct  ggctcaaaac   240
atgaatcatg  tgccttggtg  taactgcaag  atgcccaaac  tgcatccccc  acaacccacc   300
acgtaagaca  gcagacaggg  ctggaagttg  atttttaatg  aataaagtac  aatgaaggga   360
gggcagaggg  gctaagccta  gctgtccgg   ggtgctgtgg  tggtggtaaa  atggcctaac   420
acaaactgtt  gctgctgctg  ctgcttcttg  gtgcgtcgcc  ttgctggcga  gggtccttgg   480
ccttctctgt  aagctgccag  tgccgtctcc  tttgccttct  ccttggcttc  cttggctgtc   540
tcaacaagtg  ttttggaagg  ggccgtcgcc  ttgcagctta  gccaagatat  attcaaaacc   600
cttcatagtc  ttggtcacgt  tgcttttgaa  tcgggcaaga  ccaaattcct  gggacagctc   660
tggagacacc  aaattaagct  agaggagacc  caggcttccc  cggcgggatt  tcagtccagc   720
ccactgttgg  tcagagttca  caacagtaaa  acacatcgtt  tcctccacca  ccatcagccg   780
gggcgtgggt  tgatgttcca  gttgaaagta  gtcaaggtct  gattctgtgg  gtccacaata   840
gagtcctcca  ggacgtacac  cgagtgagca  acattggcag  gaaatagtcg  ctcgggccca   900
gcgtgggcat  tcctgttggt  cttggtcaga  gtcgcccggg  acagcagttt  ctggtcaggg   960
gtcacctccc  ggtgtactat  gtcttccgtc  aagacatgtt  tgctataggg  attcgggtac  1020
ccgctgccag  aaggcggcga  acacttggtc  ccaggaactc  cggagcacgc  tctggcccag  1080
gaaatacttc  accatcgtcc  cggccgaagc  gggctcagga  attacgcctc  tctacctagg  1140
gtgtcaaag                                                               1149


        <210> 182
        <211> 2526
        <212> DNA
        <213> Homo sapiens


        <400> 182
tttcgtcgct  gaccagcagc  atggaggacc  ccgccgctcc  tgggaccggg  ggcccgcccg    60
caaatggcaa  tggcaacgtg  tggcggcaaa  gggaagcagg  cggcgcccaa  gggccgcgaa   120
gcgttccgaa  gccagcggcg  ggagtcagag  ggctctgtgg  actgtcccac  tctggagttt   180
gagtatggag  atgcagatgg  gcatgcagcc  gagttgtcag  aattgtatag  ttacactgag   240
aacctggaat  tcaccaataa  caggaggtgc  tttgaagaag  atttcaagac  tcaagtgcag   300
ggcaaggaat  ggctggagtt  ggaagaagat  gcccaaaagg  cctatataat  gggactcttg   360
gaccggctag  aggtggtcag  tagggaacgg  cggctgaagg  cggccgggc   tgttctctac   420
ctggcccaag  gtacttttgg  ggaatgtgat  tcagaggtcg  atgtgctaca  ctggtccagg   480
tacaactgct  tcctgctgta  tcagatgggg  accttctcca  ccttcctgga  gctactccac   540
atggaaattg  acaacagcca  ggcctgtagc  agtgcccttc  ggaaaccagc  tgtctccata   600
gctgatagca  cagagctcag  ggtgctgctg  agtgttatgt  acctaatggt  ggaaaatatt   660
cgcctggagc  gagagacaga  ccctgtgg   tggagaacag  cccgggagac  cttccgcact   720
gaattaagct  tctccatgca  taatgaggag  cctttgccc   ttttactctt  ctccatggtt   780
accaagttct  gcagtggcct  ggctcctcac  ttccccataa  agaaggtcct  gctcctgctc   840
tggaaggtgg  tcatgtttac  cctcggtgga  tttgagcatc  tgcagactct  caaagtacag   900
aagcgggcag  aattgggcct  gcctccactg  gctgaagaca  gtatccaggt  ggtgaagagc   960
atgcgtgctg  cctccccgcc  ctcttacact  cttgacctgg  gagagtctca  gctggcaccc  1020
ccacctcca   agctgcgagg  ccgccgtggc  tctcgaaggc  aactcctcac  taagcaggac  1080
agcctggaca  tctacaatga  aagggatctc  ttcaagactg  aggagcccgc  cacagaggag  1140
gaagaggagt  ctgctggtga  tggagaacga  accttggatg  gagagctaga  cctgctagag  1200
caggaccctc  tggtgccacc  tccaccctca  caggcacccc  tctctgctga  gcgggtggct  1260
tttcccaagg  gcctgccctg  ggccccaaag  gtcagacaga  aggacattga  gcacttcttg  1320
gagatgagca  ggaacaagtt  catcggattc  accctggggc  aggacacaga  tacattggtt  1380
ggattaccca  ggcccatcca  tgagagtgtg  aagaccctaa  agcagcacaa  gtatatctcc  1440
atcgcagatg  tgcagatcaa  gaatgaagag  gagctggaga  agtgccctat  gtctttgggg  1500
gaagaggtgg  taccagagac  gccatgtgaa  atcctctacc  agggaatgct  gtacagcctt  1560
ccgcagtata  tgatcgctct  gcttaagatt  ctgctggctg  cagctcccac  ctctaaggct  1620
aagacagact  ctatcaatat  cctggcagat  gtcctacctg  aggagatgcc  catcactgtt  1680
ctccagagca  tgaagctggg  catcgatgtg  aacaggcaca  aggagattat  tgtaaagagt  1740
atctctaccc  tgcttctgct  actcctcaaa  cacttcaaac  tcaaccatat  ctaccagttt  1800
gaatatgtat  cgcaacattt  ggtatttgcc  aactgcatcc  ccttgatcct  gaagttcttc  1860
```

```
aatcaaaata tcttgtcata catcactgcc aaaaacagca tctcagtcct ggattatcct    1920
tgctgtacca tccaggattt gccggagctt actactgaaa gtctggaagc tggagacaac    1980
agccagttct gctggaggaa cctcttttcc tgcatcaacc tcctgaggct gctcaataaa    2040
ctgaccaaat ggaaacattc ccggaccatg atgctggtag tgtttaaatc ggcaccaatc    2100
ttaaagcggg ccctcaaggt caaacaggcc atgctgcaac tttatgtcct aaagctacta    2160
aagttacaga ccaagtacct ggggcgccaa tggaggaaaa gcaacatgaa aaccatgtca    2220
gccatttacc agaaagtgcg tcaccgcatg aacgatgact gggcttacgg gaatgacatc    2280
gatgccagac catgggactt ccaagcagaa gaatgtacct tgagggccaa cattgaggct    2340
tttaacagcc gtcgctatga cagaccccag gactctgagt tttcacctgt ggataactgc    2400
ttgcagagcg tactggggca gaggttggat ctgcctgaag atttccacta ttcatatgag    2460
ctctggctcg agagagaggt gttttcacag cccatctgtt gggaggagct gctccagaat    2520
cactga                                                                2526
```

```
        <210> 183
        <211> 1692
        <212> DNA
        <213> Homo sapiens


        <400> 183
cccacgcgtc cggaagcact tgaggccaga ggaagacatg cgccttgtca gtgatccctg      60
catccctagg ggggggcagc acgtcattcc tgtgagaggc tggactggag agagagactg     120
ggttggcagc caggctggag aagctgtgac cagcctggaa cgccaggccc aggcaggtgg     180
acttgaaact tactcacaag aagcaaagag ccctgttgga aaggtttgac atctacagga     240
aggtgcccaa ggaccttacg cagccaacgt acaccggggc cattatctcc atctgctgct     300
gcctcttcat cctcttcctc ttcctctcgg agctcaccgg atttataacg acagaagttg     360
tgaacgagct ctatgtcgat gacccagaca aggacagcgg tggcaagatc gacgtcagtc     420
tgaacatcag tttacccaat ctgcactgcg agttggttgg gcttgacatt caggatgaga     480
tgggcaggca cgaagtgggc cacatcgaca actccatgaa gatcccgctg aacaatgggg     540
caggctgccg cttcgagggg cagttcagca tcaacaaggt ccccggcaac ttccacgtgt     600
ccacacacag tgccacagcc cagccacaga acccagacat gacgcatgtc atccacaagc     660
tctcctttgg ggacacgcta caggtccaga acatccacgg agcttttcaat gctctcgggg     720
gagcagacag actcacctcc aaccccctgg cctcccacga ctacatcctg aagattgtgc     780
ccacggttta tgaggacaag agtggcaagc agcggtactc ctaccagtac acggtggcca     840
acaaggaata cgtcgcctac agccacacgg gccgatcat ccctgcaatc tggttccgct     900
acgacctcag ccccatcacg gtcaagtaca cagagagacg gcagccgctg tacagattca     960
tcaccacgat ctgtgccatc attggcggga ccttcaccgt cgccggcatc ctggactcat    1020
gcatcttcac agcctctgag gcctggaaga agatccagct gggcaagatg cattgacgcc    1080
acacccagcc taatggccga ggaccctggg catcgccagc cttgcctcca gtgccctgtc    1140
tcctttggcc ctcaatctgg tcccaaatct ggctgtgtcc caaagggtgt gtgggaagtg    1200
gggggaaagt agaggatggc tcgatgtttt gcagctacct cttttccccg tgtttctttt    1260
tagacaaatt agcactgcct gaagatgcag ttcccctttt tctggagagc cccaagaaca    1320
gagtcaggca gggggtgggg agtccaggga tcttggggac ccctcctagg agagctgcag    1380
tctcttccct caggggaaca tcccagaatg catatcgatc agctctcagc caggcttcga    1440
caatctcgca gcccccacta tgtggacaca ttaatgattt ggtttctccc ctgggcagcc    1500
aacctgcccc agaggcacca aacctgggct ttctagcttt tgggaccagg ctgcccaaag    1560
gtactccttt atacacccgg caccttccac ggagatgggt actttcccaa gcaagcccct    1620
atgatttgtc actatagatg gaaccctgac ttctgcccca tcccttcctg cccaacctag    1680
aacccaggcc tg                                                        1692
```

```
        <210> 184
        <211> 2533
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(2533)
        <223> n = a,t,c or g
```

```
      <400> 184
acagcttttt ttgttttttt tttttcttat acctaaaaca gggatatctg catttaattt          60
cattcagtaa atcaattcca gttaacttac catctcttaa aaatgggaga aagcaaacat          120
aggacgtgaa aagttaaaga tgcgtgacat actggagagt aataagacat actggagagt          180
agtaagtgca cacgtggcaa ttaagggttg taaatttaag atgtaaacac aaggaaaaaa          240
agtaaaaatt actgtaactt tattgcctgt atcctatgcc tttcccccag taatagccta          300
naaataccta caagggaggc ccccacccccc aaaagaagaa aaagtgccca ccttctggtt          360
taaaactgtg gcaccttgat ttcttttttga aatgtcactt tataaggtgt atgtagaaag         420
caaccagcag ccgtttacaa aatgtttgtc tgagttgatt ctgagagctc caaaacaagg          480
gatccgcgta taggctgaag aaaaaaagacg gttcaggtta accagtgcgc cgctgtagga         540
acttttaaca caagtcttcc aggtggaatt tcctgtgtaa accctaagta agaagatgcg          600
actcacggag gaccaaaagg taaaaatctc ttttaccggt ttacaagttt aagtgagggt          660
gggtctgcat tctccgcaaa acgactttac aaaggtacaa ggaaatgttg cgtgtgaggt          720
attaggcata gaatatttca ttttccttac cggaagggag cagcacgggg acaggaaacc          780
tagtggacgc ccgccacca ccttttcccga agatgcacac cccccaggga acgggcagtg          840
caaagcctgg gcagcaagcc acccttacaa ttcttttttgg ttgtttaaaa tacaagggct          900
ttctgacatc ctcaccctag gcgtgtgagc cccactcaac ctgggcaggg ntacaaccca          960
cgtcctcgtt tagttttccc ccttgggaat tttttttacag ggatgcctga cagatacggg         1020
tacaaactag tatgaaatta atgatagttt gcgtttccag aaacggcccc cgtggttaaa         1080
tataccaccc ccatttccaa agaaaggttc aaagttaagg gtgactcaga agcattggca         1140
tcccacagcc gcaagaaaac aggcttctcg ctgaactggg gtggaatcgc ccgactctgt         1200
ccctcaacgg tggtgggggc cttggcaggt gggggcgtc acatccacag tgagtgagga         1260
ggcagcgtct gcctttgcag tagttgtggc agggtcagag ggtgcgttgc tggtgggcgg         1320
gagggaagac agcagctctc ctgagcttgc tgcagaagag ctctctggaa ccaaggggaa         1380
tgacgggagg aactcggatg gccagggga agaggtgcaa tgcccaggta agtttcgggg         1440
aggcatggaa ggaagaggtg gcaaaacccc gggtttaaca aattcctggt aaagcccaac         1500
ccccggccat gaatgtgtgg tgcctgggaa ggttgaaggt tgaaggttgg ggaaggttgg         1560
gcagtccctg cctggtaaaa ggcatcagac ccggtaaatg taagtagctg gattccattg         1620
gtggcacaga agtgagggac tggtttactt gtggtggcaa taactggtac tgttggtaca         1680
cctgtactga gaacactact gacagctggt gggagttgag ctaatagaaa gtccagtcag         1740
actctgttca attcctgtag ttcctggtgg tgacaaagac gggggattaa ctgaggacag         1800
ctggacctct gtaaacccat cttttaagagg tgtaataggt gtaccagcca tttgtcctgg         1860
aagagaaatt ttctttcctt cctcaaatgg gcgtgtaggt attcgatgca aataaccata        1920
tccaatgcca catcctaggc tgccttctcc accccatgca gaatttggtg taataatcac        1980
ttctcgaccg ttactcacgt gtctgtgttg tacacataca gtttcaatgg ttttgcttca        2040
tgtgtttcga taaggctgaa tagatcttca gactcattca tgactgtatc tgctccaatt        2100
atataatcac tgtgtggtct aagacctgcc agtgctgcag gagaatttga ttccacctcc        2160
agcacatgcc aaacattttc atttgcccca tcaaagctgc agaaacgaat gctcactccc        2220
aataagccct ggccgcccca caggttactt ggtgtgactg aggtctctcg cagttccaat        2280
gttttgctgc tatagataag catctttaca ggcttttcaa cgtttgcttt cagcagatcc        2340
ttaagagtgt cattgtcttt atttaatctt gaaccattaa tagaaacaat aaaatcaaag        2400
aaaggctcca aaccagctct gtgtcctggg gaattttctt gtacctcctt caggtagcca        2460
ggtcgtattc atgcttattc cgttgtcgta ttcgttgct gctttgccc cttacgtgta         2520
ctccctctga aac                                                            2533


      <210> 185
      <211> 906
      <212> DNA
      <213> Homo sapiens


      <400> 185
ccggggcccc ccattttaaa ttggtttccc ccacaaggga aaggcccccg ggcaaatgtg          60
acataaaatc tcctttttggg aggggggggg aaaaagaaaa aacccccccg gacccggggg         120
cctttttcccg ggctttccca accgggcctt ttatggcttt tccaaagag gcctggttgc         180
agtcatttgc cctccacccc cattaaggaa atgggtttgc caaaaattca ccatagggtg         240
ggatgggaat cattttcggg tgtcttctta gaagttgact tcaaaatcta caaaaagaaa         300
atgaatgagt ttttctccgt agacgataat aatgaagaag aagaggatgt tgaaatgaaa         360
gaagattcag atgagaacgg tccagaggag aagcaaagtg tggaagaaat ggaagagcag         420
agccaagatg cagatggtgt caacactgtc actgtgcccg gccctgcttc agaagaggca         480
gttgaagact gtaaagatga agattttgca aaggatgaaa atattacaaa aggcggtgaa         540
```

```
gtgacagatc attctgtgcg tgaccaagat catcccgatg gacaagagaa tgattcaacg   600
aagaatgaaa taaaaattga aacagaatcg cagagctcat atatggaaac agaagaactt   660
tcatcaaacc aagaagatgc cgtgattgtg gagcaaccag aagtgattcc attaacagag   720
gaccaagaag aaaaagaagg tgaaaaagct ccaggcgagg acacacctag gatgcctggg   780
aaaagtgaag gctccagtga cctagaaaat actccaggtc ctgatgttga aatgaatagt   840
caggttgaca aggtaaatga cccaacagag agtcaaccct cgtgccaagc atgacgtagt   900
cggggt                                                             906
```

```
<210> 186
<211> 883
<212> DNA
<213> Homo sapiens
```

```
<400> 186
atgggctccc ccaacgtgtg gcctccagtc tcgggcctgt gcattgaggt gctcgtggaa    60
gacagtatct gccggctctc ttcccagcag cctcctccca tctcccttcc ccgaaggcag   120
caacatcccc agcttctaca cagtcgcacc ataggcaagc gtccttggac ctcgccactg   180
tccccagagc aactcttgga gaacaacagt gcagataaag cctctggttc tgtgtccacc   240
acgttgccgg ttgcttataa aaagggagtc aaacatcttt ctgctcttct tgatccagag   300
gtcctgtcca ttttcgtgcc tcctttatc agtaaagagg acagtcaaac ggccggtgcc   360
aactgcggca ctctcggtaa aaccccggatg cgctccttga gaaagaagag agagaagccc   420
agaccagagc agtgggaggg cctcccgggg cccccagag cgccagagcc tgaggatgtc   480
gccgtcccgg cggcgtggga cctcctcacc ctgccgcagc tgtgcttccc aggggggtgtg   540
tgcgtggcca ctgaacctaa ggaggattgc gtccacttcc tggtgctgac cgatgtctgc   600
gggaatagga cctatggcgt ggtggcccag tactaccggc ccctgcatga tgagtactgt   660
ttctacaatg gcaaaaccgc accgggagtg tcctggctgc ttcgtgccct cgcggtgtg    720
cgtggtctcc aggtttccct attacaactc cctcaaggac tgcctttcct ggcactaccg   780
cagacctggg gccactctgc tgtcacccag cagcttggtg actttgcttt tggtgaaagg   840
tcctggagct gctgctgcag acgctgggga gattccagtg tga                    883
```

```
<210> 187
<211> 1464
<212> DNA
<213> Homo sapiens
```

```
<400> 187
tgtagactcc tgcatagcct tccaaagttc ttcatttggt gaatattatg agaaatgaca    60
ccgaggtgac tggcacatgg tcgaggcagc tgcttaggca gcttaagcat gccctgtgaa   120
acatccctgt gggggactcc gaccagccca ggcaacgcgg atcctgagaa cgctcccggg   180
taggcatctg cccctgtggg atgcctcacc agagcagtgt gtggcaggcc cccgtggagg   240
accaacacag tggttgaacc ccgggaaggg acaaggatct tggagtttgg acatctaaaa   300
cttgcacatg taccacccct agaattctg gtaaaccagc accagcctga agatcacgtt    360
ctcatcaaac ggtggaaaga agaaaaactc gagccagcct gggaaggacc ctaccctgtg   420
ctgctaacca ccaagactgc tgttcgtaca gcaaaaaaaa aaaaaaaaaa aaaaaaagat   480
ggactcatca cacccaagtc aagaaagtgc caccccctcc agagtcgtgg gccatagtcc   540
caggggaaaa ccctaccaaa ctaaagctaa gaaaaatgta actcttttca tctattctat   600
tactcttctt tctttcctcg tgctattgct gaccatctag ttattaacat aaccaagtca   660
atttcacctc aaactattgc atttaatgct tgccttgtta tacccgtgtg ggacttgcca   720
agtcaaagac agctctctac ttcagaaaag tacttctgtc cctcctgact ctcctcagac   780
tggacattag taaactagga ccatttaatc cagggagatt tcgataaaga ccccagtgcc   840
aaccaggagt cttgcccccc gatgtagaac tttcatgcca tagttggtcc aacgttctgt   900
ggaccactgc agccaaaacg ccaattttct gctcctactg agaggtgaag ccagctggac   960
ttcctgggtt gagtggggac ttggagaact tttctgtctt acaagaggat tgtaaaatgc  1020
accaatcagc actctgtagc taggactgta aaacacacca atcagtgctc tgtaaaacgc  1080
accaatcagc agaatcctcc ccgtctgtat gcagccacca tgcagcccac ctaggctgtg  1140
ggctctgttg atgccgcctt ggagtgtgcg gcttgctctg ggtgggcctt caggggagg   1200
agggaagttg gaactggcaa tcgagccgta gagagagagc aaatgggaag cagcttgtgt  1260
tccccaggcc tggactagca tgcccttcct ggcatccatt tttcctgctg ggccccaagg  1320
```

```
gacctggccc tgtgcgtcag ttctgtggct gctagacctt gggctctgtg gtcgggtctt     1380
tggacatgac atctgcacgg gctggggggct gaggctgctg gccagggcga gccagggcag     1440
gccaccaggc tgcagaaccc acat                                            1464
```

```
        <210> 188
        <211> 4095
        <212> DNA
        <213> Homo sapiens


        <400> 188
atgaggcgag gtggatggag gaagcgagct gaaaatgatg gctgggaaac atggggtggg      60
tatatggctg ccaaggtcca gaaattggag gaacagtttc gatcagatgc tgctatgcag     120
aaggatggga cttcatctac aatttttagt ggagttgcca tctatgttaa tggatacaca     180
gatccttccg ctgaggaatt gagaaaacta atgatgttgc atggaggtca ataccatgta     240
tattattcca gatctaaaac aacacatatt attgccacaa atcttcccaa tgccaaaatt     300
aaagaattaa aggggggaaaa agtaattcga ccagaatgga ttgtggaaag catcaaagct     360
ggacgactcc tctcctacat tccatatcag ctgtacacca agcagtccag tgtgcagaaa     420
ggtctcagct ttaatcctgt atgcagacct gaggatcctc tgccaggtcc aagcaatata     480
gccaaacagc tcaacaacag.ggtaaatcac atcgttaaga agattgaaac ggaaaatgaa     540
gtcaaagtca atggcatgaa cagttggaat gaagaagatg aaaataatga ttttagtttt     600
gtggatctgg agcagacctc tccgggaagg aaacagaatg gaattccgca tcccagaggg     660
agcactgcca ttttttaatgg acacactcct agctctaatg gtgccttaaa gacacaggat     720
tgcttggtgc ccatggtcaa cagtgttgcc agcaggcttt ctccagcctt ttcccaggag     780
gaggataagg ctgagaagag cagcactgat ttcagagact gcactctgca gcagttgcag     840
caaagcacca gaaacacaga tgctttgcgg aatccacaca gaactaattc tttctcatta     900
tcacctttgc acagtaacac taaaatcaat ggtgctcacc actccactgt tcaggggcct     960
tcaagcacaa aaagcacttc ttcagtatct acgtttagca aggcagcacc ttcagtgcca    1020
tccaaacctt cagactgcaa ttttatttca aacttctatt ctcattcaag actgcatcac    1080
atatcaatgt ggaagtgtga attgactgag tttgtcaata ccctacaaag acaaagtaat    1140
ggtatctttc caggaaggga aaagttaaaa aaaatgaaaa caggcaggtc tgcacttgtt    1200
gtaactgaca caggagatat gtcagtattg aattctccca gacatcagag ctgtataatg    1260
catgttgata tggattgctt ctttgtatca gtgggtatac gaaatagacc agatctcaaa    1320
ggaaaaccag tggctgttac aagtaacaga ggcacaggaa gggcaccttt acgtcctggc    1380
gctaacccc agctggagtg gcagtattac cagaataaaa tcctgaaagg caaagcagca    1440
gatataccag attcatcatt gtgggagaat ccagattctg cgcaagcaaa tggaattgat    1500
tctgttttgt caagggctga aattgcatct tgtagttatg aggccaggca acttggcatt    1560
aagaacggaa tgttttttgg gcatgctaaa caactatgtc ctaatcttca agctgttcca    1620
tacgattttc atgcatataa ggaagtcgca caaacattgt atgaaacatt ggcaagccta    1680
cactcataac attgaagctg tcagttgtga tgaagcgctg gtagacatta ccgaaatcct    1740
tgcagagacc aaacttactc ctgatgaatt tgcaaatgct gttcgtatgg aaatcaaaga    1800
ccagacgaaa tgtgctgcct ctgttggaat tggttctaat attctcctgg ctagaatggc    1860
aactagaaaa gcaaaaccag atgggcagta ccacctaaaa ccagaagaag tagatgattt    1920
tatcagaggc cagctagtga ccaatctacc aggagttgga cattcaatgg aatctaagtt    1980
ggcatctttg ggaattaaaa cttgtggaga cttgcagtat atgaccatgg caaaactcca    2040
aaaagaattt ggtcccaaaa caggtcagat gctttatagg ttctgccgtg gcttggatga    2100
tagaccagtt cgaactgaaa aggaaagaaa atctgtttca gctgagatca actatgggaa    2160
taaggtttac tcagccaaaa gaggcagaag cttttcttct gagtctttca gaagaaattc    2220
aaagaagact agaagccact ggcatgaagg gtaaacgtct aactctcaaa atcatggtac    2280
gaaagcctgg ggctcctgta gaaactgcaa aatttggagg ccatggaatt tgtgataaca    2340
ttgccaggac tgtaactctt gaccaggcaa cagataatgc aaaaataatt ggaaaggcga    2400
tgctaaacat gtttcataca atgaaactaa atatatcaga tatgagaggg gttgggattc    2460
acgtgaatca gttggttcca actaatctga acccttccac atgtcccagt cgcccatcag    2520
ttcagtcaag ccactttcct agtgggtcat actctgtccg tgatgtcttc caagttcaga    2580
aagcttaaga aatccaccga agaggagcac aaagaagtat ttcgggctgc tgtggatctg    2640
gaaatatcat ctgcttctag aacttgcact ttcttgccac cttttcctgc acatctgccg    2700
accagtcctg atactaacaa ggctgagtct tcaggaaat ggaatggtct acatactcct    2760
gtcagtgtgc agttcgagac ttaacctgag tatagaggtc ccgtcaccttt cccagctgga    2820
tcagtctgtt ttagaagcac ttccacctga tctccgggaa caagtagagc aagtctgtgc    2880
tgtccagcaa gcagagtcac atggcgacaa aaaagaaaga accagtaaat ggctgtaata    2940
caggaatttt gccacaacca gttgggacga gtcgttgttg caaataccga gaacctcaag    3000
aatcgaacag tgacgcagga ataaatttaa tagcccttcc agcattttcg acaggtggac    3060
```

```
cctgaggtat ttgctgccct ttcttgctga acttcagagg gagctgaaag cagcgtatga   3120
tcaaagacaa aggcagggcg agaacagcac tcaccagcag tcgagccagc gcatctgtgc   3180
caaagaatcc tttaatatca tctaaaggca gcgagtgaaa gaaaagaaaa gaaacaagaa   3240
gaaaaaaacc attggttcac caaaaaggat tcagagtcct ttgaataaca agctgcttaa   3300
cagtcctgca aaaactctgc caggggcctg tggcagtccc cagaagttaa ttgatgggtt   3360
tctaaaacat gaaggacctc ctgcagagaa acccctggga agaactcttc tggcttctta   3420
ctttcaggtg tgccagggcc tttctagttt gcagtctgac cccagctggg ctgtgtgaga   3480
cctccaccac cccaatctag gctgatgctg ttgaattcaa tgatgtgaag accttgctca   3540
gaggaatggg taactacaat ttcagatcca atggaagaag acattctcca acgttgtgaa   3600
atactgtact gatctaatag aagacaaaga tttggaaaaa ctggatctag ttataaaata   3660
catgaaaagg ctgatgcagc aatcggtgga atcggtttgg aatatggcat ttgactttat   3720
tcttgacaat gtccaggtgg ttttacaaca aacttatgga agccacatta aaagttacat   3780
aaatattacc cagagagcct gatgcctctc tgatagctgt gcccataagt gcttgtgagg   3840
tatttgcaaa gtgccatgat agtaatgcct cggagttttt ataatttaa atttctttta    3900
aagcaagtgt tttgtacatt tcttttcaaa aagtgccaaa tttgtcagta ttgcatgtaa   3960
ataattgtgt taattatttt actgtagcat agattctatt tacaaaatgt ttgtttataa   4020
agttttatgg atttttacag tgaagtgttt acagttgttt aataaagaac tgtatgtata   4080
ttttgtacag gctcc                                                    4095
```

```
<210> 189
<211> 1536
<212> DNA
<213> Homo sapiens
```

```
<400> 189
atggctgaga cggaggagcg gagcctggac aacttctttg ccaagaggga caagaagaag   60
aagaaggagc ggagcaaccg ggcggcgagt gccgcgggcg cagcgggcag cgccggcgga   120
agcagtggag ccgcgggtgc ggcgggcgac ggggcggggc cggggacccg gccgggtgac   180
ggcgggaccg ccagcgcggg ggctgcgggc ggggcgggcc ccaccaaggc tgtgacgaag   240
gacgaagatg aatggaaaga attggagcaa aaagaggttg attacagcgg cctcagggtt   300
caggcaatgc aaataagcag tgaaaaggaa gaagacgata atgaaaagag acaagatcca   360
ggtgataact gggaagaagg tggaggtggt ggtggaggta tggaaaaatc ttcaggtccc   420
tggaataaaa cagctccagt acaagcacct cctgctccag taattgttac agaaacccca   480
gaaccagcga tgactagtgg tgtgtatagg cctcctgggg ccaggttaac cacaacaagg   540
aaaacaccac caaggaccac cagaaatcta ccagtgatac cacagttccc atcccccttgc   600
agtcaacttg ccaaagcatg tagaaagccg gaaggataaa gaaatggaga agagctttga   660
agtagtaaga cacaaaaata gaggtaggga tgaggtttca aaaaaccagg cccttaaact   720
tcagctagac aaccaatatg ctgtgcttgg aaaatcagaa aagcagccac tcacaataca   780
attaaggaat gggctttgct aacccttctg aggtaactag actgcagcta aaccaccacc   840
aacagccatt catcatctga tctctgctgg atctacagac accgatgcag gaccactcgg   900
atttccatga ccggccctat tgcacttatg gaagttaaag tgtcacgacc gccctatgc   960
catattggat ttaggggaat tttccattgt tacataaatg tgtgaaccta gtttccaaca   1020
gtgttccttt catatttact ctgcaaattc caaaaaacca aaacctgcag cccagtgggt   1080
ccatttccaa aatcttttta tggttcagat actgaggcct ttcataaggg ttgactacct   1140
cagatttgct gcactcattg tggacttcat gtggatcaca acttctggat aagaagatta   1200
caactattaa gtgtcgatgt gaaccttgca accagctcta ctggattctt atcagaaatc   1260
ctgcataaaa agtcagccat ctgggttctg atctgctgta aaagatgaag atttaagtga   1320
ccttaattaa cctgtcctgt gccctaccct taaggaatac tcagtatctg aacataaaaa   1380
gattttgaaa tgaccactgc ctgcaggttt tggttttttg tatttgcaga gtaaatatga   1440
aagaccactg ttgaaactag ttcacacatt tatgtaacaa tgaaaattcc cctaaatcca   1500
atatgcatag agcagtcgtg acactttaac ttccat                              1536
```

```
<210> 190
<211> 3498
<212> DNA
<213> Homo sapiens
```

```
<400> 190
```

```
caaggcccaa gaagcacttg ggtcccettg ttattgaacc tagagaccag gaatcacaag    60
acaactacct tttttgagcac caaaggcagt gaggtatttc ctgatgaccc ttcgatattc   120
ttagcacttt catatctcaa gtcttctagc aaaatgtcaa aaacttattc tcccttttt    180
ctccagcctc atgtcttacc caagcagtta atctgcagct cctttgtctg ggcaccatcc   240
aggatggaaa ggaagagggg aaaaagcttc tcacggaagt gtcctgaaag catctcagct   300
gccactggtg aggagtatag cttcccataa aggtaacacc caaatggcag tatgataaaa   360
gcaggtaaaa gggtagtggc agctcctccc acaggtcact caccatgctc cattacaagc   420
tcgtctgcca gagcagggat gaaagggttg acccagctct gacatctgag gattctgaga   480
gactcaagaa cccatagcta ttttctgacc tctttaagag gcgagaacaa ccctggacc    540
gaccaaagcc cgtgtgccgc tgcatcccgc gcacagcacc tacatcccgc tgccgtcgct   600
gctgccacca tgcccaagac aaaggctgaa ggtgatgcta aaggagataa agccaaggtg   660
aaggacgaac cacaagtaac cagagctgca attcagacta atactttcat cttcaagtgc   720
tagatagagc cccaaaagca gatatacata ctatacattc aaaactcatg tcaaatttcc   780
ctcttaatct taccaaaaag cacacttatg aagtggatgc agactctctg atcctgagac   840
accagttgcg gcctggccgc gtttgctgag ggaaatggcc aaacccaggt cttctgaaga   900
aaaggttccg cccgcaccga cacgccgggg tcggcagca gctccagcgc gcaggccagg    960
cacaggcggg gggtcacggg cagcagccag cgcgggtcgt gccggtaatg ggccctctcg  1020
aatagaagcg ccgcctcttc ctctctcctg ggcccgggag tgcccgccgt cgccgcctgc  1080
ctcacagcca tctcctcgct tgccctcagc tgaggcgggt tcccaggtgc ctcctggccc  1140
tggggactct ctgtcttagg aagggtggcc ccagtacagc agtgaccttg cagctgaaga  1200
tccctctgtg aagcagtgtg atctccgatg ctgtcctccc ctgcacgagg atcacccact  1260
atccccactc tatgaatccc tggcagggt tgtgcccctg gctggccaga tgctctccct  1320
ccccacccac cagcaggaag acttcacccc agtgggggac aggattcatc tcaggacagg  1380
gggcagagat gaaaccattc acagccactg cctgttcctg ttcccgggtc ccacatccat  1440
agccagtgaa ggctggaggc catggtaggc tgtgcttcct gcctgtgggc ctctcactcc  1500
cagaacagtc gacttggaga ctgtccctca cagcatcctc tcctctgacc agatccttgt  1560
ttcctcccct tggtgctcga ggctctccaa catcctcatc tgtgcacttt ctctggcttc  1620
ctatatcctg gagttctgca acatcctcaa ctccaccgtc attcttattt ccttgccctt  1680
gtacctggat ctcttcagca atttcaactc ttaactgtcc ctggtcatct cctgcaggag  1740
cctgggtctc tgtaccatca tcagctgtgg tccctctcag ctttttaaca gtctgtttct  1800
tcgctctaag cctccagttt tttcccctaa gcctccagat cattctaccg tcctcgtttc  1860
caacctctct ctggtttctc ttctctgatg cctgatttc tgcaacatcc tttccaatca  1920
gctcccagtt cctcctccct ggtgaatggc tccctccaat ttcactatct aactggtcct  1980
cgttctctct cttaggtctc tgagtcttta caccgtcctc acctccaggt tctctctggt  2040
ttctctccac tggagcctga atttctgttc cattctcact tcccatctgc ttctggctct  2100
tccactctga taaaaggatc tttctaccaa gatcacttct aaactgactc tgggtttctt  2160
tcccaggtgc ccaggtcttt acaccgtcct cacctccaac ttctctcagg tttctcttcc  2220
cttgtatctg aatttctgcc ccattctcac ctccaatctg ctgatctttc ttccattctg  2280
ctgaatgcat ttctccatca atttgacttg ttaatttgcc ccagttccct gactcagata  2340
tctgggtatg tgcaccatct tcgcctctaa tatgttcctg attcttcccc tttggtatgt  2400
gaatctttcc actaaattca tttcctaact gaccctgatt tttcctccca agttcctggg  2460
tgtctttatc atcctcacct ttaacctctc tcctccctag tgactgaatg tctgtaccat  2520
cctcttctct aagtggctca ttgctctgag tctccacatc agttatcacc ttttaattgt  2580
tcctggatct cagcctcggg tgccaggata tttgtgccat cctcacatga ttctcccaac  2640
atagtatctc aaattctcta taaatttcac ttgctacttg tctccggttt ccccaccata  2700
gtgcctggat caccacccaa tccttctctt atctccctga gcttcttctt ggtagctatc  2760
tgggtttcct tagcatcttc atctcttctc aggcccttat ttccccaccc cacttgaatt  2820
tcatgactta attgtttctg gttctctccc ccagatgctt gggtcttctt agctttctta  2880
cttccacctt gatcatgctt ctcccacctt ggtgtctgga tctctgtaac attcccattt  2940
ccaacacatt cctgttttcc ccaatccaag gcctgggtct ctacactatt ctctttttt   3000
acttctccca cgttctccct cccacatgat tgggtttgtg cagcatcctg acctccaacc  3060
tgatccttgt ttctcccctc ttccatctga atttccacat ccgcatcacc tttcatctga  3120
tcttgtttct cccactgtgg tgtctgggtc tcctcaccat tctcatctcc agtctggcct  3180
tgcttcccca atccttgagc ctggatctct tccccatcct cctctccagc ctctttcttg  3240
tccttcttct caaatgtctg ggtctccaca gcatcctcac ttccattctt atcctggttc  3300
tcccactcag gtgtttgggt ctctgcatca attttacatc ttaactgttc ttggttctct  3360
cccatatgtg cctgggtttc agggagattc tcacctccag cctccctctg gtttctattc  3420
cctagttcct gaatgttggt tctactctca actcccatcc ggtcctgggt gtcccaccct  3480
ggtgtcaaga tctcgcca                                                3498
```

```
<210> 191
<211> 5410
```

111

```
<212> DNA
<213> Homo sapiens


<400> 191
attcatcggt agaacaagca tcggttgaag tacctgatgg accaacactc catgacccag      60
acctctatat tgagattgtg aaaaatacga agtctgtccc agaatattca gaggtggctt     120
atcccgatta ttttggtcac attccgcctc cattcaaaga gcctatttta gaaaggcctt     180
atggtgtaca aaggacaaaa attgctcaag atattgaaag gctaatacat cagagcgata     240
tcatagatcg tgtggtatat gacttggata acccaaatta caccattcca gaagagggag     300
atattttgaa atttaactcc aaattcgagt ctgggaatct gcgcagagta attcagatta     360
gaaaaaatga atatgatctt attctgaact cagacataaa cagcaatcat tatcatcagt     420
ggttttactt tggaagtcag tggaatgcga ccaggtgttg cttacaggtt taacatcatt     480
aactagcgaa cagttgcaac aggctgttta attatggtat gcaaccactc atgtattcgg     540
ttcaggaagc attaaatgcc agaccatggt ggattcgtat ggggactgac attcgttact     600
atataaatca tttctcaaga agttcagttg ctgcaggtgg ggcaaaaggg gaaaatccta     660
ctatacaatt acatttactg ttcaattttc cacataaagg atggatgttt gctactttgc     720
tttattcact atccatatac gtatttcaac tttacagatg catcttcaaa aattggaatc     780
agcacacaat cctcagcaaa tctattttcg gaaagatgtg ttatgtgaaa ccctgtctgg     840
aaacagctgc cccttggtga ctataacagc aatgccagag tctaattatt atgaacatat     900
ctgccatttc agaaatcgcc cttacgtttt aatgtatgct cgggtacatc ctgggggaaa     960
cttaatgcaa gttgggggtta tgaaagggaa cgttgggaat atctccatga ggcaattaac    1020
cccactggct tcaggagctt acggaggaat ctttattatt ttttaaaatt gtccctatgt    1080
taaatccaga tggtgtcatc aatggaaatc atcgctgttc tttaagtgga gaggatttga    1140
ataggcagtg gcaaagtcca agtccggatt tacatcctac aatttaccat gctaaggggc    1200
tgttgcaata cttggctgca gtgaagcgtt tacccttggt ttattgtgat tatcatggcc    1260
attcccgaaa gaagaatgta tttatgtatg gttgcagcat caaagagaca gtgtggcata    1320
ccaatgataa tgcaacttca tgtgatgttg tggaggatac gggatacagg acattgccta    1380
agatactgag ccatatcgcc ccagcatttt gcatgagcag ctgtagcttc gtagtggaaa    1440
aatctaaaga atccacagca cgtgttgtag tttgcacggg aaataggagt acaaagaagt    1500
tataccatgg agagtacttt atgtggctgt gatcagggaa aatacaaggg tttacagatt    1560
ggtacccgag aactggaaga gatgggagca aaattttgtg ttggtctttt acagtttgaa    1620
aagactgacc tctccattgg agtataaatc ctgccctccc cagccctgcc ttgacctttg    1680
aaaatgattt aaattgaatc caagcctgca aagtaactag cccctaccca cttatgtcct    1740
tggatgaaga tgaaccctcg attcccttga agaagttgat tacagtgcag aaagtaatga    1800
tgagttagat attgagttgg ctgaaaatgt aggagattat gaaccttctg ctcaagaaga    1860
agtactttct gactctgaat tatcaagaac atacctacct tgagcccgct cgccatctct    1920
ttgttaactg caaagaataa atgaaatatc ttggtgtttt attctcccag gaagcttgag    1980
agaaatgagt ttatacagag ctgactcaaa aagacaaaaa gtaacttggg ccagtttggt    2040
ttcaagataa taaatgtgtt attaattaat gattaaaatt ggcgcctggt tttattttcg    2100
gatattccaa tgcactttat ggtagccatg gaatggatca aaatattggg atttacccytt    2160
taaaaaaaaa aaccctgagt atcattggca tgaaatttta tcctccccta tggttatatc    2220
cctgacatca agtggataat tttgaagtgt gttccagaat ataaaattga aattttagag    2280
ttgttgaaaa tccctgactt gttgaaaact aatatatatg tacatggatt tctatagatg    2340
tgtttgttta gaagtgggta gatattgcag ataagactgt tcttcagaat catgttaact    2400
attgggttgt gactgaagta gtcccagggt ttgccttgaa acccattaca ttctacattt    2460
accaaattaa acaaataaaa actgtattaa atgttgcatt cattttgtca tcttctttaa    2520
ccagctcaga ttatttgatg tatagaactt tgtgagaatg tgataaaaac ccagaattgg    2580
acacagtgat aaaaagttgt ttttaagaaa gtgctgggat tacaggcgtg cgccaccgtg    2640
cctggctaaa tcctttcttg taatgaaacc tacctgggtt ttagccctct tgctgcaaga    2700
atgacttat ttttaaataa aataaagcaa atccattgac tttggataag tgttttaaga    2760
actaagtttc tgatataata aaacaacctc caaaagatac ctcattgcag attttcgcca    2820
ggattcaggt gcttaggttt tggcacatat cttcctcact tttttcctata gtgtttttaa    2880
cctgttataa ttggaatgat agagatgtat ttcagaattt tgcatggtcc aaatcaatga    2940
tttttctttt taatatgtaa agtatttcat taacagtgta gattctttct gatgtttggg    3000
gagccatgtt taaaaatgta gtatggagca attgaaaaag gggtcttttt ccctagccta    3060
attcttacta atctcagaaa acaaagatca aatagactgt gaagttgaac tagtcctctt    3120
agtgtagtaa ccaaatttag gaaagatcag gataatttag gaaggaaagt aatcatttat    3180
ttaattattt ataattataa acaattattt tatgttttgt atattttatg tataaaacaa    3240
ttacatgttt tattatagtt atacttcttc agagagtaga ttatggagcc accatgtcca    3300
tacagttagt tgttccttgg tattcttgga ttgattccag acccccccac agttacccaa    3360
atccacagat gctgaagtct ctgatataaa atggagtagt atttgcattt aacctatgga    3420
catcctcctg tatgctttaa atcatctcta gattacttat aatacctaat acaatataaa    3480
tataaatgct ctgtaaatag ttttattgta tagtgtgtgt gtgtgtgttt taagagacga    3540
```

```
ggactcacaa tgggacactt tgaccaggct ggtctcgaac tcctgggcct acacaatcct   3600
cccacctcgg cgtcgcaagt agctgggact acaggtactc accactatgc ctggcagttt   3660
tttaaatttg cgtttttaaa aattgtttat tatttattga atatttttcta cctgagattg   3720
acttaatctg tggatatgga acctatagat atggagggct ggctgtatat gaatttgttt   3780
ttggctttta caaaattaga aattaaaagt aactacagtt actataatgt gcagaatgac   3840
tcaaatattt ccatttatta tgttagtgta aaaactccta actacgtatt ataatatttt   3900
atattaatga agtactttag catacattat gagcctgaat aaagcttttt attaaatatt   3960
cacaagattg aaggagaaat tctttatagt taggaaatga ttttttcata aacaataaat   4020
agctttgaaa atataaaaaa aaatttaggg ctgggtgcag aggctcatgc ctgtagtccc   4080
agcactctga gaggccgagg cgggtggatc acttgaggtg aggagttcaa gatcagcatg   4140
gccaacatgg tgaaactcca cctccacgaa aaatacaaaa attagccagg catggtggca   4200
tgcgcctgta atcctagcta cttgggtggc tgaggcatga gactcacttg aacctgggag   4260
gcagaggttg cagcagtgag ccgagatcaa gccgctgcac tccagctggg gcgacaaagc   4320
aagactgtct caaaaaataa aaacaaaaaa attaaaataa aatcctaact ttcctagtta   4380
gaaatataat taacttttat tggctattag tagctaaaat tgcccttatt tttgcttctg   4440
tggcctcatt ttttttctcg gttattcagt atttaaatta tggcttagat gtcttcaatg   4500
ctatagtcct gaaaattaat gatctacgtt gtgcagcagt gatgggatct gataaactga   4560
gtctgatgat ggagtttaga tttatttcct ttaccttgca tttggaactt tgaatctctt   4620
aaatgtggtt ttggtctagt ccactggttc tcacgttgta atgtgcatca gaatcttctg   4680
aagacacaga ttgctgatta tgtagacctg gggtggaggt ccaagaatgt gcattccttg   4740
caaattccca ggtggtgatg ctgcagagcc acactttgag aatcactagt ataatccagt   4800
atgctcttcc agcatcacac cttccttcct gagaatcaca ggagttgtga actgcagatt   4860
agcattgggg agaatttaga tcaaactaat ttgtagaatc aaggaggtca agtaaggtca   4920
caggggcact tgggttgagc cagggtttta gcccaggtct tctgacaact gcctcatgtc   4980
cttaccacaa aggagctgct atcctttgcc tttccccaaa gagtgaagac tgcttaaagc   5040
tcaaggatct ttcttgaatt tgtgaaattt gttcaggcaa ggtgaaaagc aaaaacctat   5100
ggttcacatt gactttttgt attgatcatt gtcttttgaa gacaggaagt atgatcagtc   5160
tctgccactt gtgctagttt ttgtgtggtg tttagaaaca tgggcatttg tctggatcct   5220
aattacaaat aagtaaccta gaattctctt cgagatagtg gactaaccac cgatgaatct   5280
attctaaaat ttcaaatatc caaattaaaa tggactgtat taggcattaa ggtactggaa   5340
atgggataat acattaaatg tattaatgga attgtttttg tgcatgatac agaaataaat   5400
gatagtaacg                                                         5410
```

```
        <210> 192
        <211> 3704
        <212> DNA
        <213> Homo sapiens


        <400> 192
atggttgcca ttatcactat catcatcatt atcaaggtag aaaccaaaga catagtggga     60
tggagacaca ctgagctgag actcactttt ctcttcctga atttgaacca ccgtttccat    120
cgtctcgtag tccgacgcct ggggcgatgg atccgtttac ggagtcctgg cgcagcaaga    180
gtgaggcgca ggcctgcgga acgggtcctg ctggaagcag ctggaatgcc ctgcagggcg    240
gggtccgggg ccggtgactc agtgcggctg ccgccgggaa aggcgaaact gctggagcga    300
acccgtgcca ggcgagagaa tcttcagaga aaaatggctg agaggcccac agcagctcca    360
aggtctatga ctcatgctaa gcgagctaga cagccacttt cagaagcaag taaccagcag    420
cccctctctg gtggtgaaga gaaatcttgt acaaaaccat cgccatcaaa aaaacgctgt    480
tctgacaaca ctgaagtaga agtttctaac ttggaaaata aacaaccagt tgagtcgaca    540
tctgcaaaat cttgttctcc aagtcctgtg tctcctcagg tgcagccaca agcagcagat    600
accatcagtg attctgttgc tgtcccggca tcactgctgg gcatgaggag agggctgaac    660
tcaagattgg aagcaactgc agcctcctca gttaaaacac gtatgcaaaa acttgcagag    720
caacgcgcc gttgggataa tgatgatatg acagatgaca ttcctgaaag ctcactcttc    780
tcaccaatgc catcagagga aaaggctgct tcccctccca aacctctgct ttcaaatgcc    840
tcggcaactc cagttggcag aaggggccgt ctggccaatc ttgctgcaac tatttgctcc    900
tgggaagatg atgtaaatca ctcatttgca aaacaaaaca gtgtacaaga acagcctggt    960
accgcttgtt tatccaaatt ttcctctgca agtggagcat ctgctaggat caatagcagc   1020
agtgttaagc aggaagctac attctgttcc caaagggatg gcgatgcctc tttgaataaa   1080
agccctatcc tcaagtgctg aagatgcgtc tttggttaat gcctcaattt ccagctctgt   1140
gaaagctact tctccagtga aatctactac atctatcact gatgctaaaa gttgtgaggg   1200
acaaaatcct gagctacttc caaaaactcc tattagtcct ctgaaaacgg gggtatcgaa   1260
accaattgtg aagtcaactt tatcccagac agttccatcc aagggagaat taagtagaga   1320
```

```
aatttgtctg caatctcaat ctaaagacaa atctacgaca ccaggaggaa caggaattaa    1380
gcctttcctg gaacgctttg gagagcgttg tcaagaacat agcaaagaaa gtccagctcg    1440
tagcacaccc cacagaaccc ccattattac tccaaataca aaggccatcc aagaaagatt    1500
attcaagcaa gacacatctt catctactac ccatttagca caacagctca agcaggaacg    1560
tcaaaaagaa ctagcatgtc ttcgtggccg atttgacaag ggcaatatat ggagtgcaga    1620
aaaaggcgga aactcaaaaa gcaaacaact agaaaccaaa caggaaactc actgtcagag    1680
cactcccctc aaaaaacacc aaggtgtttc aaaaactcag tcacttccag taacagaaaa    1740
ggtgaccgaa aaccagatac cagccaaaaa ttctagtaca gaacctaaag aagtgatacg    1800
tgaaattgag atgagtgtgg atgatgatga tatcaatagt tcgaaagtaa ttaatgacct    1860
cttcagtgat gtcctagagg aaggtgaact agatatggag aagagccaag aggagatgga    1920
tcaagcatta gcagaaagca gcgaagaaca ggaagatgca ctgaatatct cctcaatgtc    1980
tttacttgca ccattggcac aaacagttgg tgtgagttta gtgtccacac ctagactgga    2040
attgaaagac accagcagaa gtgatgaaag tccaaaacca ggaaaattcc aaagaactcg    2100
tgtccctcga gctgaatctg gtgatagcct tggttctgaa gatcgtgatc ttctttacag    2160
atctcaaaga ttcaaagaaa cagaacgtcc atcaataaag caggtgattg ttcggaagga    2220
agatgttact tcaaaactgg atgaaaaaaa taatgccttt ccttgtcaag ttaatatcaa    2280
acagaaaatg caggaactca ataacgaaat aaatatgcaa cagacagtga tctatcaagc    2340
tagccaggct cttaactgct gtgttgatga agaacatgga aaagggtccc tagaagaagc    2400
tgaagcagaa agacttcttc taattgcaac tgggaagaga acacttttga ttgatgaatt    2460
gaataaattg aagaacgaag gacctcagag gaagaattaa ggctagtccc cccaagtgaa    2520
tttattgcca tcccaaagga tcagtttact ttgtcagaaa tccgcttgcc ctaaaaagca    2580
gattttgtct gcagtacggt tcagaaacca gatgcagcaa attactatta cttaattata    2640
cttaaaagca ggagctgaaa atatggtagc cacaccatta gcaagtactt caaactctct    2700
taacggtgat gctctgacat tcactactac atttactctg caagatgtat ccaatgactt    2760
tgaaataaat attgaagttt acagcttggt gcaaaagaaa gatccctcag gccttgataa    2820
gaagaaaaaa acatccaagt ccaagaaaag caacattcat tcttcagtca tggccagtcc    2880
aggaggtctt agtgctgtgc gaaccagcaa cttcgccctt gttggatctt acacattatc    2940
attgtcttca gtaggaaata ctaagtttgt tctggacaag gtccccttttt tatcttcttt    3000
ggaaggtcat atttatttaa aaataaaatg tcaagtgaat tccagtgttg aagaagagg    3060
ttttctaggc tgccctggag gagggcgact ccaaccaaag agacagacca tatttgaaga    3120
tgttagtggt tttggtgcct ggcatcgaag atggtgtgtt ctttctggaa actgtatatc    3180
ttattggact tatccagatg atgagaaacg caagaatccc ataggaagga taaatctggc    3240
taattgtacc agtcgtcaga tagaaccagc caacagagaa ttttgtgcaa gacgcaacac    3300
ttttgaatta attactgtcc gaccacaaag agaagatgac cgagagactc ttgtcagcca    3360
atgcaggggac acactctgtg tttaccaaga actggctgtc tgcagatact aaagaagagc    3420
gggatctctg gatgcaaaaa ctcaatcaag ttctttgtga tattcgcctc tggcaacctg    3480
atgcttgcta caaacctatt ggaaagcctt aaaccggaa atttccatgc tatctagagg    3540
tttttgatgt catcttaaga aacacactta agagcatcag atttactgat tgcattttat    3600
gctttaagta cgaaagggtt tgtgccaata ttcactacgt attatgcagt atttatatct    3660
tttgtatgta aaactttaac tgatttctgt cattcatcaa tgag                     3704
```

```
    <210> 193
    <211> 2319
    <212> DNA
    <213> Homo sapiens


    <400> 193
atgcaaataa atgagacaat ttgggatact gtgggagctg caagcaggca cggtgaaggt      60
gaaaggcaag caaagagcag cacaagggggc tgcacacacc ttgctgaagg gcaggaatt     120
tacctgcagg aggagcagag tccacctgag atgtgcacac gtgttatgga gaaaagggaa     180
ggacttacaa ttgagagaga gagggatcca ctcctaccag tctggaaagc actgggcata     240
caagcgcaca aatgcgtggc acatactaca aatccttcta aagccactgc tgtacacctg     300
cctcacttaa ccatgcagcc tcaaggctgt ctcatgtcat tctttcctac agctgcagag     360
ttttcaacat atggacagga attataccta gaaaataacc aaattgaaga ataactgaa      420
atttgtttca atcataccag aaagatcaat gtcattgtac tacgttataa caaaattgaa     480
gaaatagga ttgctccttt agcctggata aatcaagaaa atctagaatc cattgatctc      540
tcctacaaca agctctatca cgtcccgtcc tatctaccca gtccttgct gcacctagta     600
ctccttggga accagattga acggatccct ggctatgtgt ttggccacat ggaaccaggc     660
ctggaatact tgtacctgtc atttaacaaa cttgctgatg atggcatgga ccgtgtctcc     720
ttctatgggg catatcattc tctgagagaa ttatttctgg atcacaatga cttaaaatct     780
ataccacctg ggatacaaga aatgaaagca ctacattttc tgaggctgaa caacaacaag     840
```

```
atacgaggca ataagcagga aatcaaacag acaagtaagc aggcaagtgc tgtgcagtca    900
gaaaaatggg tgacaatgcg acgagcacac tggggcctga gggccgccag gagactacgg    960
ccaccctcaa cggcctggat taacagcaga tccagaccgg tgcctgtgga gcagacgcac   1020
tgtgggcttg ctgtagcaga agagagaaaa gatctgttca tgttttttccg aagcctgcat   1080
tttttgtgg agtggtttga atatcgtaag cgcacgttta aacatctcaa gtgggatgaa   1140
gactatgacc aagagccaga tgatgattac caaacaggat tcccatttcg tcaaaatgta   1200
gactacggag ttccttttca tcagtatact ttaggctgtg tcagtgaatg cttctgtcca   1260
actaactttc catcatcaat gtactgtgat aatcgcaaac tcaagactat cccaaatatt   1320
ccgatgcaca ttcagcaact ctaccttcag ttcaatgaaa ttgaggctgt gactgcaaat   1380
tcattcatca atgcaactca tcttaaagaa attaacctca gccacaacaa aattaaatct   1440
caaaagattg attatggtgt gtttgctaag cttccaaatc tactacaact tcatctagag   1500
cataataatt tagaagaatt tccatttcct cttcctaaat ctctggaaag actccttctt   1560
ggttacaatg aaatctccaa actgcagaca aatgctatgg atgggctagt aaacttgacc   1620
atgcttgatc tctgttataa ttatcttcat gattctctgc taaaagacaa aatctttgcc   1680
aaaatggaaa aactaatgca gctcaacctc tgcagtaaca gattagaatc aatgcctcct   1740
ggtttgcctt cttcacttat gtatctgtct ttagaaaata attcaatttc ttctataccc   1800
gaaaaatact tcgacaaact tccaaaactt catactctaa gaatgtcaca caacaaacta   1860
caagacatcc catataatat ttttaatctt cccaacattg tagaactcag tgttggacac   1920
aacaaattga agcaagcatt ctatattcca agaaatttgg aacacctata cctacaaaat   1980
aatgaaatag aaaagatgaa tcttacagtg atgtgtcctt ctattgaccc actacattac   2040
caccatttaa catacattcg tgtggaccaa aataaactaa aagaaccaat aagctcatac   2100
atcttcttct gcttccctca tatacacact atttattatg gtgaacaacg aagcactaat   2160
ggtcaaacaa tacaactaaa gacacaagtt ttcaggagat ttccagatga tgatgatgaa   2220
agtgaagatc acgatgatcc tgacaatgct catgagagcc cagaacaaga aggagcagaa   2280
gggcactttg accttcatta ttatgaaaat caagaatag                          2319
```

```
        <210> 194
        <211> 948
        <212> DNA
        <213> Homo sapiens


        <400> 194
atgcctcgcc cccagcgcgc gctcccggcg ccggccccgc ccctcaccc aggcggcgcc     60
gtaaagccgg agaagggcg gggtctcagc tcctacttca ttctacggcc gagaccggag    120
gatgttccct gctcaggagg aggccgacag gaccgtgttt gttgggaatt tagaggcccg    180
agttcgggaa gagattctgt acgagctgtt ccttcaggtg ctctgtccaa gggagatggg    240
aattttatct ataagcccct gactgggggct gctgcctttc tttcagagat gccctgctca    300
gacaggagga atctagagag gcaatcaggc tacagtgact ttgtagccct gagctttgtt    360
tacactgtga ggggaaaacc acctactcaa gcctcagtaa tggcagaagc tcctcctccc    420
accaagctta agcatcccag gtcaacttct gactgctgtg ctggcagtga gaatttcaag    480
ccagtggatc ttagcttgct gggctccgtg gaagagggat ctgctgagca agaccacttg    540
gctccctggc ttcagccccc tttccagggg agggaacagt tctgtctcgt tggtgttcca    600
ggcgccactg gtgtacggaa aaaaaaaaaa caactcctgc agctaactgg gtgtctgccc    660
aaacagctgc ccagatacct cagctgccac gtccagactc ttcccactct cccacctgca    720
agagaaacat cctcaggcca agaatgatg catgccacag ggcagtctgt ccatgagaga    780
acaaacctga ggaatgagaa cccaggtccc aggaacaagc ttccatcatt tgagcagaga    840
attctgggac ctgagtacct agatggtcaa gaagcaggaa atggggagga cactcctagg    900
cagagagcca tgcagggaag gctagagtgg gaactgacta aagcatga                 948
```

```
        <210> 195
        <211> 892
        <212> DNA
        <213> Homo sapiens


        <400> 195
atgagtaggt ggggagcggc ggtggggcag ggcgcactgc gagaagagca cttcgcgcat     60
gcgcatatca ccgagcgaac gcgccgtgtt cgggaaggta ggagaaagag gcggagctcc    120
ttgttaacga catccccaac ctctgctaac gcgcaggcgc acttcctgaa gctgaaggtc    180
```

```
agcatagaca aagggcctca gaatcgcgca ggcgcaattg tgccctggtt cgccaagatg    240
tcgttcccaa agtataagcc gtgcgagcct gcgcactctg ccgtgagacc ctcgacccag    300
ccgaatacaa catatctccg gaaacccggc gggcgcaagc cggagcggtt ggcccatagg    360
agcccagctg caaacgagag tacctgcttc agtacaacga tcccaacacg ccgagggctc    420
atcgaaaatc cgtgccttgc ttcgttgggc ctatgcaaga acaataaatg tttattccta    480
atttcaagcc ccactcctaa aagctcactc atgggagctt ttgtgtggga ttttgggccc    540
ctcatcttca tttttattata ttatcaaaac tgagaggtgg gacccaaatc agagatggct    600
cactgactca agaattttaa aatatgaagc tatcttacta gagagagatg acctgacact    660
aaccactgac aattcactca accctgctgc tttcctaaga ggaaatccaa acccggaaga    720
acctgagcat aaatgcttag atctaatcag ttatcaaact agagtcagac tggatctaag    780
caaaaccccc ttccaaacag ggcgtcacct ctttatagac ggttcctccc tggtcattgg    840
aggaaaaggg cacaacgggt actctgtagt tgatggggaa acccttacaa ag             892
```


```
        <210> 196
        <211> 597
        <212> DNA
        <213> Homo sapiens


        <400> 196
atgcagactt ttacaacatg catcagctac agtgagtatt cttgcatgct tttggccaat    60
gcaagctctc atggcacgct gtactgtaag ctccgggtcg gcatttgttt gttgatggta    120
ccagctgtca aaaaccaagc aagtggcagt gctagaggtg ccacaaaagt gcgaaggaag    180
tgtcaggctg gatgtcaaaa tgaacacctt ggagaactgg atgatggaac agacggtaaa    240
aatcagctaa acatcagaga aaatggagga agaggtcaaa actgtgaaca ggaactagaa    300
gaaagtgtag cagaaaaaga cttgtcacaa acttcgagag atttggagaa aatgatgtca    360
aaacacatct tcctcaagcc catgctgagt atctctgatt tggttaattt cttgatgcaa    420
gtttccaaag ttctggtgaa aacggctgaa ggaatagtgt tacagcaact gcccttggct    480
tttccagctt tacacttcca tgcctatgga aatctcttcc ctgtctgtag ctttaagcat    540
tacatctata tgatcgacca tcccatcttc atctccatcc ctgacttcct aacttga       597
```


```
        <210> 197
        <211> 4442
        <212> DNA
        <213> Homo sapiens


        <400> 197
atgccagttc ccagcaggca tataaatatt ggtcgttctc agagctggga tgctgctggg    60
tggtacgagg gcccctggga gaacgccgag tccctgcggc ctctggggag gagaagctcc    120
ctgacgtatg gcacagcaga ggggacttgg tttgagccaa accaccgacc acaggacgct    180
gccctgcccg tggccgccga gccctacctg taccgggagg ccgtttataa ctcagtggct    240
gcaagaaagg ggtctactcc tgacttcacc ttctacgaca gcagacaggc agtgatgtct    300
ggtcgcagcc ccctgctgcc acgggagtac tacagtgatc cgtctggagc tgctagggta    360
cccaaagagc ctcccctcta tcgggaccca ggagtcagcc ggccggtccc cagctacgga    420
gtgcttggca gcagaacgtc atgggatcca atgcaaggcc ggtcacctgc cctgcaggac    480
gccggtcacc tgtaccggga tcctggaggt aaaatgatcc ctcaggggcg gcagacacag    540
agcagggctg catctcccgg gcggtatgga cgggagcagc ccgacaccag gtatgggggcg   600
gaggtgcctg cctacccccct cagccaggtc ttcagcgaca tcagcgaaag acccattgac    660
cctgcccctg ccagacaggt ggccccgacg tgcctggttg tggaccccag ttcagctgct    720
gcccccgaag gcagcacagg ggtggcccca ggggccctga atcgtggcta cgggcctgcc    780
cgggaaagca tcccatccaa gatggcttac gagacttacg aagctgacct gtccaccttc    840
cagggtcctg gtggcaagag gaccgtgctc cctgagttcc tggcctttct gcgggcggag    900
gggctggcag aggccacgct gggagcccta ctgcagcagg ctttgactc cccggccgtc     960
ctggctaccc tggaggacgc ggatatcaag tctgtcgcac ccaacctggg ccaggcccgt    1020
gttctgagcc gcctggccaa tagctgcagg accgaaatgc agctgcggag gcaggaccgg    1080
ggggggccgc tgccccgggc gcggtccagc agcttcagcc accgaagcga actgctccat    1140
ggtgacttgg cttctctggg cgctgcggct cctctgcaga cagcatcccc ccgagctgga    1200
gacccggctc gccgtccctc cagcgcacca tctcagcacc tcctggagac ggcagccacc    1260
tattctgccc ctggcgtggg cacccatgcc ccacacttcc cctccaactc cgggtacagc    1320
```

```
tctcccaccc cttgcgccct gacagcgcgt ctgagcccca cgtaccccct gcaggcaggg    1380
gtggccttga ctaacccggg cccctcaaac cccttcacc caggccccag aacagcctac    1440
tccacggcat acacggtgcc catggagctg ctaaagaggg agcgcaacgt ggccgcctct    1500
ccgctgccca gccctcacgg cagcccccag gtcttgcgga agccaggtgc acccctgggg    1560
ccatccaccc tgccgccggc cagccagagc ctccacacgc ctcactcacc gtaccagaag    1620
gtggcccggc gcacaggggc acccatcatc gtgtccacca tgcttgcacc agaaccaatc    1680
cagtttgctg gccaagcagt ccagagtgac aacgtgagga aggcgtatgc tgcggggacc    1740
ccagtgcggc ccaccagccc cggtgacaca gacaaatggg ggctccaggc ccgcgctcct    1800
ggacgtgccg tagaccccag gaatatgatt tcagcccagg agcataaagt agttgaatgc    1860
atggcccgaa ggagtgccac ctgctttgtg tttgggcaac tctgccgcct tcacagcact    1920
tcctctgacc ccgtgggtgt ggatttcatt ctgtccatgg aggacgtggg aaggggcaag    1980
agtaggaacc ctgattcctg gtcccccaat gcagttgtgt gggatgccag tggcgttggc    2040
ggggagcgcg tcctgcaata ccagctagat atgaacacgg tgcctccgca gggctggacc    2100
actcgaaaaa cgagagtgtg ctgcaagcat gaggcttctc cctctcccat ctcagccttg    2160
gctgccatag ctaaggagga gggtgttatt ttgcttttgt ggacattcac cctgggaaat    2220
aagaggcttg gaggatcggc cacacgagtg gggtatgcag aggcacaggc agaggctccc    2280
tcctgcaagg ccactactgt gactctgagc agcggttctt ctcatgaatg tgatagctcg    2340
gtcagctcta agactgcaac ctgcagggac ttcatggggc aaccctgggg gcacgcaagc    2400
atcccaccca ctcccaaccc cccacctcca gccgtcgtgc ccggcatctt ttcccagcat    2460
gagaacccgt tggctttttct cttttcccgc cttgccatga aggacctgct gccaggattc    2520
gagcctcaga ccttggacag gtctcgggcc agcctcagcc acgttctgcg tgcccggcca    2580
tcagggaggg tagagggtat ccgcccccag atcatgaacg gccccctgca ccccgcccc    2640
ctggtggcgc tgctggacgg ccgcgactgc actgtggaga tgcccatcct gaaggacctg    2700
gccactgtgg ccttctgtga cgcgcagtcg acgcaggaaa tccacgagaa ggttctaaac    2760
gaagccgtgg gcgccatgat gtaccacacc atcaccctca ccagggagga cctggagaag    2820
ttcaaggccc tgagagtgat cgtgcggata ggcagtggct atgacaacgt ggacatcaag    2880
gctgccggcg agctcggtga gtgcgaggca gcgctggctg cctggagttg tccggagctc    2940
tgtgggccct gctcgggtgg gcttggagaa gcagctggaa ctgggaccac ggagcagccg    3000
cttctggctg tagcaaggtg gctgcctcca ggccgggctg tggagcacct tgcggccctg    3060
ccttcacatg acacaggaat tgccgtgtgc aacatcccgt ctgcagccgt ggaagagaca    3120
gcggactcta ccatctgcca catcctcaac ctgtaccgga ggaacacgtg gctgtaccag    3180
gcactgcggg aaggcacgcg ggttcagagc gtggagcaga tccgcgaggt ggcctcggga    3240
gcggcccgca tccgtgggga dacgctgggc ctcattggct ttggtcgcac ggggcaggcg    3300
gttgcagttc gagccaaggc ctttggattc agcgtcatat tttatgaccc ctacttgcag    3360
gatgggatcg agcggtccct gggcgtgcag agggtctaca ccctgcagga tttgctgtat    3420
cagagcgact gcgtctcctt gcactgcaat cttcaacgag cataaccacc accttcatca    3480
atgactttac cataaagcag atgaggcgag ggagcattcc tttgtggaac gcagcccgtg    3540
gcggcctggt ggacgagaaa gccttagcac aagccctcaa ggagggcagg atacgagggg    3600
cagccctcga cgtgcatgag tcagagccct tcagctttgc tcagggtccg ttgaaagatg    3660
ccccgaatct catctgcact cctcacactg cctggtacag tgagcaggcg tcactggaga    3720
tgagggaggc agctgccacc gagatccgcc gagccatcac aggtcgcatc ccagaaagct    3780
taagaaattg tgtgaacaag gaattctttg tcacatcagc gccttggtca gtaatagacc    3840
agcaagcaat tcatcctgag ctcaatggtg ccacatacag atatccgcca ggcatcgtgg    3900
gtgtggctcc aggaggactt cctgcagcca tggaagggat catccctgga ggcatcccag    3960
tgactcacaa cctcccgaca gttggcacat ccttcccaag cgccctctcc caaccagccc    4020
acaaaacacg gggacaatcg agagcacccc aacgagcaat agcagagaat gccagaaggt    4080
aatcactcag atacacttgg gaccaagaga cagtgaaaaa tagatgaact aagagaaaaa    4140
gaatcggatg gtctttgtaa ctgattctgg acatatgcat cattgatgtt gcagtgttga    4200
aactacaaga gctagaaaac tgaagatgtc gtcttgctta cggaaggcgc tggaaagact    4260
agggtgtgga tttatttaac gaccaacttc tgttattgtg tgttaagttt ttcatctgtg    4320
catcaaatca caaaagaat aaatagagct ttttccttta tcagtcccttt ggggcacagc    4380
cgggtcctga acaccctgct ctacaatgtt gcatcaagag ttcaaacaac aaaataaaaa    4440
at                                                                   4442
```

```
        <210> 198
        <211> 573
        <212> DNA
        <213> Homo sapiens


        <400> 198
ccgaatttcc gtgtcgacga tctcgtagct tcttaagata tcaggaatta ttcttaaaac    60
```

```
gggagagagt cagaatcaac tagctgtgga tcaaatagct ttccaaaaga agctctttca    120
gaccctgagg agacaccctt cctatcccaa aataatagaa gaatttgtta gtggcctgga    180
gtcttacatt gaggatgaag acagtttcag gaactgcctt ttgtcttgtg agcgtctgca    240
ggatgaggaa gccagtatgg gtgcatctta ttctaagagt ctcatcaaac tgcttctggg    300
gattgacata ctgcagcctg ccattatcaa aaccttattt gagaagttgc cagaatattt    360
ttttgaaaac aagaacagtg atgaaatcaa catacctcga ctcattgtca gtcaactaaa    420
atggcttgac agagttgtgg atggcaagga cctcaccacc aagatcatgc agctgatcag    480
tattgctcca gagaacctgc agcatgacat catcaccagc ctacctgaga tcctagggga    540
ttcccagcac gctgatgtgg ggaaagaact cag                                 573
```

```
        <210> 199
        <211> 6286
        <212> DNA
        <213> Homo sapiens


        <400> 199
gacgcgccgg agccggtttt ccagataaca gaaagtaacg tgaaggaatt caggtgactc     60
agacatggag gagagaagac ctcatctgga tgccaggccc aggaattccc ataccaacca    120
cagaggccct gtggatggag agttaccacc aagagctaga aatcaggcca ataacccacc    180
agccaatgct ctccgaggag gagccagcca ccctggaagg catcctaggg ccaacaacca    240
tcctgctgct tactggcaga gggaagagag atttagggcc atgggcagga acccacatca    300
aggaaggagg aaccaggagg ggcatgccag cgacgaagct agagaccaaa gacatgacca    360
ggagaatgac accaggtgga gaaatggcaa ccaggactgt aggaaccgca gaccaccatg    420
gtccaatgac aacttccagc agtggcggac tccccaccag aagcctacag aacagccaca    480
gcaggcgaag aaactgggct acaagttctt agaaagtctt ctgcagaaag accttctga    540
ggtggtcatc acacttgcca caagtttagg gctgaaagag ctcctttctc attcttccat    600
gaaatctaac ttccttgagc tcatctgtca ggttcttcgg aaggcttgta gctccaaaat    660
ggatcgccag agtgttctcc atgtactggg catattgaaa aactccaaat ttctcaaagt    720
ctgcctgcct gcttatgtgg tagggatgat cactgaaccc atccctgaca tccgaaacca    780
gtatccagag cacataagca acatcatctc cctcctccag gaccttgtaa gtgtcttccc    840
tgccagctct gtgcaggaaa cttccatgct ggtttccctc ctgccaacct ctcttaatgc    900
tctgagagcc tctggtgttg acatagaaga ggaaacggag aagaacctgg aaaaggtaca    960
gatctatcat tgaccatctg caggaaaaga ggcgagaggt cactttgaga gtggataccgt   1020
acactctagt gcagcctgag gcagaagacc atgttgagag ctaccgatcc atgcccattt   1080
accctacgta caatgaagtg cacttggatg agaggccctt ccttcgcccc aatatcattt   1140
ctggaaaata cgacagcact gctatctatc tggatacCCa cttccggctc ctgcgagaag   1200
aaatcgtcag acctttacgg gaaggtattt tggaacttct ccaaagcttt gaagaccagg   1260
gcctgaggaa gagaaagttt gatgacatcc gaatctactt tgacaccagg attatcaccc   1320
ccatgtgttc atcatcaggc atagtctaca aggtgcagtt tgacacaaaa ccactgaagt   1380
ttgttcgctg gcagaattcc aaacgattgc tctatgggtc tttggtatgc atgtccaagg   1440
acaacttcga gacatttctt tttgccaccg tatctaacag ggagcaggaa gatctctgcc   1500
gaggaattgt ccagctctgc ttcaatgagc aaagccaaca gctgctagca gaggtccagc   1560
cctctgactc tttcctcatg gtagagacaa ctgcatactt tgaggcctac aggcacgtcc   1620
tggaaggact ccaggaggtc caggaggaag atgttccctt ccagaggaat atcgtggagt   1680
gtaactctca tgtgaaggag ccaaggtact tgctaatggg gggcagatac gactttaccc   1740
ccttaataga gaatccttca gccactgggg aatttctaag aaatgtcgag ggtttgagac   1800
atcccagaat taatgtctta gatcctggcc agtggccctc aaaagaagcc ctgaagctgg   1860
atgactccca gatggaagcc ttgcagtttg ctctcacaag ggaactggct attattcaag   1920
gacctcctgg gaacaggcaa aacctatgtg ggtctaaaaa ttgttcaggc cctcctaacc   1980
aacgagtctg tttggcaaat tagcctccag aagttcccca tcttggttgt gtgttatact   2040
aatcatgctt tgggaccagt ttctgggaag gcatctacaa ttgtcaggaa gaccaggcat   2100
tgtgcgggtg gggtggaagg gagcaacagt ggaaattcct gaaggcagtt tcaccctaag   2160
ggagctgagg aacaagcggg aattccgccg caacctcccc atgcacctcc gaagggccta   2220
catgagtatc atgacacaga tgaaggagtc agagcaagag cttcatgaag gagccaagac   2280
cctggagtgc accatgcgtg tgtgtcctacg ggaacagtac ctgcagaagt acatctcacc   2340
cccagcactg ggaaagtctc atgaatggcc ccagtgcagg atagtgaatg gattttcttc   2400
ccagcactgg aagcattccc atgatgctgg agtggcttag gtcttggtgt cggttctttc   2460
acgcaaagtg tttctccagc aggacctgag aatacagccc caggcagaag gggatgagga   2520
ggaagaaggg gaggaggaga gtttcgcttg attagagatt cgcagaggga agctgaccct   2580
gatttcaagc agaccgggtg attgaggagg aagaggtggt gaggccccag cggcggaaga   2640
aggaagagag tggagcagac caggagttgg ctaaaatgct tctggccatg aggctagacc   2700
```

```
attgtggcac tgggacagca gctggacagg agcaagccac aggagagtgg cagacccagc    2760
gcaaccagaa aaagaaaatg aaaaaaagag tgaaggatga gcttcgcaaa ctgaacacca    2820
tgactgcagc cgaggccaac gagatcgagg atgtttggca gctggacctc agttctcgct    2880
ggcagcttta taggctctgg ctacagttgt accaggctga caccgccgg aagatcctca     2940
gctatgaacg ccagtaccgc acatcagcag aaagaatggc cgagctgaga ctccaggaag    3000
acctgcacat tcttaaagat gcccaggttg taggaatgac aaccacaggt gctgccaaat    3060
accgccagat cctacagaag gtggagccga ggattgtcat agtggaagaa gctgcggaag    3120
tccttgaggc ccataccatt gccacattga gcaaagcttg ccagcacctc attttgattg    3180
gggaccacca gcagctgcgc cccagtgcca acgtgtatga tctggccaag aacttcaacc    3240
ttgaggtgtc cctttttgaa cggctagtga agtaaacat tccctttgtc cgtctgaatt      3300
accagcaccg tatgtgccct gaaattgccc gccttttgac cccccacatt taccaggatc    3360
tggagaatca tccatctgtt cttaagtatg agaagattaa ggggggtgtct tccaacctt     3420
tctttgtaga acacaacttt cctgaacagg aaatccaaga ggcgcaaaag ccatcagaac    3480
cagcatgagg ctcacaatgt ggtagagctg tgcaagtact tcctgtgcca ggaatacctg    3540
ccttcccaga tcaccatcct cactacctat accgggcagc tcttctgcct gcgcaaactg    3600
atgcctgcca agacatttgc tggcgtcagg gtccatgttg tggacaaata ccaaggggaa    3660
gagaatgaca tcatcctcct ctcgctagtg cggagcaacc aagaaggcaa ggtgggtttt    3720
ctgcagatat ccaaccgcat ctgtgtggcc ttgtcccgag ccaagaaggg aatgtactgc    3780
atcggaaaca tgcagatgct ggccaaggtg cccctgtgga gcaagatcat tcatacactt    3840
cgagagaaca atcaaatagg ccccatgctc cggctctgct gccagaacca ccctgaaacc    3900
cacacccttag tatccaaagc ttctgacttc caaaaagtac ccgaaggagg ctgcagcctg    3960
ccctgcgagt tccgcctggg ctgtgggcat gtctgcaccc gtgcctgcca cccttatgac    4020
tcttcacaca aggagttcca atgcatgaag ccatgccaga aggtcatctg tcaggaaggg    4080
caccggtgtc cccttgtttg cttccaggag tgtcagcctt gtcaggtgaa ggtgcccaaa    4140
accattcctc ggtgcggcca tgaacaaatg gtcccttgtt ccgtgcctga gtcagatttc    4200
tgctgccagg agccttgctc caagtctctg agatgtgggc acagatgcag ccacccatgt    4260
ggtgaggact gtgtgcagct gtgttcagaa atggtcacca taaaactcaa gtgtgggcac    4320
agtcaaccgg taaaatgtgg tcatgtggaa ggcctcctgt atggtggtct gctagtcaag    4380
tgtaccacaa agtgtggcac tatcttggac tgcgggcatc cttgcccagg ctcctgccac    4440
agctgcttcg aagggcgttt ccatgaacgc tgtcagcagc cctgcaagcg cctgcttatc    4500
tgctcacaca agtgcccaga aaccatgcat tggtgagtgc ccaccctgcc agcggacctg    4560
tcagaaccgc tgtgtccaca gccagtgcaa gaagaaatgt gaggagctgt gtagtccctg    4620
cgtggaaccc atgtgctcgc gctgccagca ctaccagtgc accaaactct gctctgagcc    4680
ctgcaaccga cccccatgct atgtgccttg tactaagctg ctagtttgtg gccacccctg    4740
cattggtctc tgtggggagc catgccccaa gaaatgccgg atctgccaca tggatgaggt    4800
cacccaaata ttctttggct ttgaggatga gcctgatgcc cgctttgtgc agctggaaga    4860
ctgcagccac aattttgag gtgcaagccc tagaccgcta catgaatgaa cagaaggatg     4920
atgaagtcgc catcagattg aaagtctgcc ctatctgcca ggtgcccatc cgcaaaaacc    4980
tgagttatgg aactagcata aaacagcggc tagaggagat tgaaatcatc gaggaaaagt    5040
atccagggct catcagggga aatggcaacc agccaggaac ggcttaaggc cctgctggag    5100
aggaagagcc tcctccacca gctgcttcct gaagacttcc tgatgttaaa ggagaagctg    5160
gcccagaaaa atctgtcagt gaaggacctg ggtctggttg agaattacat cagcttctat    5220
gaccacctgg ccagcctgtg ggattccctg aaaaagatgc atgtcttaga agagaaaaga    5280
gtgaggactc gactagaaca ggtccatgag tggctggcca agaagcgctt gagcttcact    5340
agccaggaac taagtgacct ccgaagtgaa atccagaggc tcacatacct ggtgaacctt    5400
ctgacccgct acaagatagc agagaagaag gtgaaagata gcatagcagt agaggtctat    5460
agtgtccaga atatccttga gaaacatgt aagttcacc aagaggatga acaacttgtg      5520
caggaaaaga tggaagctct gaaagccacc cttccctgct ctggcctggg catctcagag    5580
gaagagcgag tgcagattgt cagtgccata ggttatcctc gtggtcactg gttcaagtgc    5640
cgcaatggcc atatctatgt gattggcgat tgtgggggag ccatggagag gggcacgtgt    5700
cctgactgta aggaagtgat tggtggcaca aatcatactc tggaaagaag caaccagctt    5760
gcttctgaaa tggatggagc ccagcatgct gcctggtctg acacggccaa caacctgatg    5820
aactttgagg agatccaggg gatgatgtag gaagatggta caccactgcc ttttgccctc    5880
gccactgaat gactgggggc agctccctaa tgaaggaact gaagttgttt tttattatc     5940
atcctttta ggctgggcac agtggcttac gcctgtaatc ccagcacttt gggaggccga     6000
ggcaggcgga tcacctgagg tcaggagttc gagaccaagc ctgaccaaca tggcgaaacc    6060
ccgtctctac taaaaataca aaaataaaat aaaataaat caaaataagc caggcgtggt      6120
ggcgtgcgcc tgtaatccca gctactccgg gaggctgagg caggagagtc acttgaaccg    6180
gggaggcgga ggttacagtg agccgagatc atgccattgc attccagcct gggcgacagg    6240
agcaagactc tgtctcaaaa ataaataaat aaataaataa ataaaa                    6286
```

                        <210> 200

                                 119

```
        <211> 2040
        <212> DNA
        <213> Homo sapiens


        <400> 200
gcgagaactc atcctgtagt caccagatgg agtcccaaac agccaagcag atgtaaggcc      60
tgtgctgtgg ctctgaggcc ctgaatacag aagggtcact ttcttagtgg ccaaagagca     120
gttgttgaca ttgatgtcta attattgaac acgaccagtc attttactga gctgcggtga     180
ggaaacactg accatagaag atcaagccaa atgagggatt gcaaatttcc tgattctttt     240
gaattaggat tccagatggg ggcctcattt ctacagcccc caacattcct atagccgtta     300
tcactgccat caccactgcc accagcatct tcttgcagat tccacccctg ctccccagag     360
acttcctgct ttgaaagtga gcagaaagga agctctcaga aaaatctcta gtggtggctg     420
ccgtcgctcc agacaatcgg aatcctgcct tcaccaccat gggctggctt .tttctaaagg     480
ttttgttggc gggagtgagt ttctcaggat ttctttatcc tcttgtggat ttttgcatca     540
gtgggaaaac aagaggacag aagccaaact ttgtgattat tttggccgat gacatggggt     600
ggggtgacct gggagcaaac tgggcagaaa caaaggacac tgccaacctt gataagatgg     660
cttcggaggg aatgaggttt gtggatttcc atgcagctgc ctccacctgc tcaccctccc     720
gggcttcctt gctcaccggc cggcttggcc ttcgcaatgg agtcacacgc aactttgcag     780
tcacttctgt gggaggcctt ccgctcaacg agaccacctt ggcagaggtg ctgcagcagg     840
cgggttacgt cactgggata ataggcaaat ggcatcttgg acaccacggc tcttatcacc     900
ccaacttccg tggttttgat tactactttg gaatcccata tagccatgat atgggctgta     960
ctgatactcc aggctacaac caccctcctt gtccagcgtg tccacaggggt gatggaccat    1020
caaggaacct tcaaagagac tgttacactg acgtggccct ccctctttat gaaaacctca    1080
acattgtgga gcagccggtg aacttgagca gccttgccca gaagtatgct gagaaagcaa    1140
cccagttcat ccagcgtgca agcaccagcg ggaggccctt cctgctctat gtggctctgg    1200
cccacatgca cgtgcccta cctgtgactc aactaccagc ·agcgccacgg ggcagaaaag    1260
cctgtatggt gcagggctct gggagatgga cagtctggtg ggccagatca aggacaaagt    1320
tgaccacaca gtgaaggaaa acacattcct ctggtttaca ggagacaatg gcccgtgggc    1380
tcagaagtgt gagctagcgg gcagtgtggg tcccttcact ggattttggc aaactcgtca    1440
agggggaagt ccagccaagc agacgacctg ggaaggaggg caccgggtcc cagcactggc    1500
ttactggcct ggcagagttc cagttaatgt caccagcact gccttgttaa gcgtgctggg    1560
acatttttcc aactgtggta gccctggccc aggccagctt tacctcaagg acggcgcttt    1620
gatggtgtgg acgtctccga ggtgctcttt ggccggtcac agcctggggc acagggtgct    1680
gtttccaccc caacagcggg gcagctggga gattttggag ccctgcagac tgtccgcctg    1740
gagcgttaca aggccttcta cattaccggt ggagccaggg cgtgtgatgg gagcacgggg    1800
cctgagctgc agcataagtt tcctctgatt ttcaacctgg aagacgatac cgcagaagct    1860
gtgcccctag aaagaggtgg tgcggagtac caggctgtgc tgcccgaggt cagaaaggtt    1920
cttgcagacg tcctccaaga cattgccaac gacaacatct ccagcccaga ttacactcag    1980
gaccctcag taactccctg ctgtaatccc taccaaattg cctgccgctg tcaagccgca    2040


        <210> 201
        <211> 1505
        <212> DNA
        <213> Homo sapiens


        <400> 201
cccgttgcta cgacgatttc gcagcccctg agtctggagg ctgacatgtg gagcataggc      60
gtcatcacct acatcctctt aagtggagca tccccttttcc tgggagacac gaagcaggaa     120
acactggcaa atatcacagc agtgagttac gactttgatg aggaattctt cagcgcagac     180
gagcgagctg gcccaggact ttattcggaa gcttctgggt taagagaccc ggaaacgggt     240
cacaatccaa gaggctctca gacacccctg atcacgtca aaaggagaag gcagagcccc     300
tgaacagcgg aagacagagc ccacccagct gaagaccaag cacctgagag agtacactct     360
caaatgccac tcaagcatgc ctcccaacaa ctgctatgtc aacttcgagc gttttgcctg     420
tgtggtggaa gacgtggctc gggtcgacct gggatgccgt gccctggtgg aggcccacga     480
taccatccag gacgatgtgg aggccctggt ctccatcttc aatgagaagg aagcttggta     540
ccgagacgag aatgagagcg cccggcatga cctgtcccag ctcaggtatg agttccgcaa     600
ggtggagtca ttgaagaagc tgctgcgaga agacatccag gccacgggat gtagcctcgg     660
aagcatggcc aggaaactgg accatctgca agcccagttt gagattctga ggcaggagct     720
ctccgcagac ctgcagtgga ttcaggagct ggtgggcagc ttccagctgg agagtgggag     780
ctctgagggc ctgggctcca cattctacca ggacaccagt gaatccctgt cagagctgct     840
```

```
cagcagatca tgcactgagg aatttctggc aggctggaag ctctaatcgc cagaatccag     900
tcagtgatgc atcccaagag aaagggtata ctcgccagca gttctgccac gagagtacac     960
cgaacaaaag agacagggtc atttataatc tcacgcgtcc accctactgc tgtgtccagt    1020
ttccactggc tggaacggga cctgacattc tgtatttgtc ccgactggct agcaactcag    1080
aactttttaa aagaggcaaa ggcagaggag aatcaaggaa gcaggaagtt aacttgtgga    1140
atgctgagaa aggtaaaaaa aacttttaaa taaggaagag gaacaggcta tgacctaatg    1200
cttgcttgga ccagtataag catgccaggg caaatattta ggctaaattg tgggagctaa    1260
gaacataaag cacattgatt tctttattac ggctggcaga tatttaaaaa tgttagcacg    1320
ggtctttgaa tcaattttgc ttctaagaga agctactatt tattcttaat tagatgggga    1380
ggaaagtctt tgaaaaggaa cctctacttt actttttagt tactatgagg atcactatat    1440
caatgtttct taattcatat gctaaaggaa ttccaccgca ctggctagga tctcgatgtg    1500
ccgcg                                                                1505
```

```
        <210> 202
        <211> 346
        <212> DNA
        <213> Homo sapiens


        <400> 202
gggaaaagaa ggaggaaatg gtatgtccaa agggtcatgg agggcacaga gctctcaaat      60
gatgagcagg tgatggagtt gtaataggag cctgaagagg cagactatag ctaaaaacca     120
tgtgaggact atgacctcac cttgagagca tgggaaatac ccttgaactg ctgaaagcag     180
gtacctatgg tgccagtttt cagtgtggag aaggatggag aggagctcgg tagcttcagg     240
ccacgctggg ccgattggct gactggatta ctggagtggg tttcagtaga gagcctttct     300
atctattgca tttctcaacc tgtttatatg tgggtggaat aaggct                   346
```

```
        <210> 203
        <211> 207
        <212> DNA
        <213> Homo sapiens


        <400> 203
cggccgcgtc gacgcccaac taaagtgtgc tgcgttctct gggtcctgag gcggcagtct      60
ggccgcagtg accagactaa ctgtgccccg gaggctgctt ggaattccac ttaacgctgg     120
aagcacgcag acgctcttga ggcgggcagc tgcgtagcgt gtggcggagc cgggagagcg     180
cccccccaatg tggcacctga gcgtctg                                       207
```

```
        <210> 204
        <211> 2847
        <212> DNA
        <213> Homo sapiens


        <400> 204
ttaaaacgag gacttggaca aggagggaac cactggagtg acgtgatgca agccctcttc      60
ggtcactctt ggcttccacc aggggtctct gcctccttga tgagaagaga agctggctgg     120
ctccatgatg acctcgatgg cgtacaccct aacatcctca ttcaccagac ccagggtcag     180
ctttaggaag ctcatctggc ggctggctac cagctcctct gtctccttgt cgtgggtagg     240
caggtgcagg tggtggcaga aggtgtagag gaaggccttg gagcagagct gggtgagcat     300
gctctggaca tgcaggtagt aggtgctgcc ccgcttgatc tgtgtgcggt ggtctgccag     360
gcggggcacc agggtgcctc tgtaaagggg gcagcgcagg gttttgttgt caaggtccag     420
gatgctcgtg tagcggctgt agcggctcag ggcatggagg gtaccggcac cggcaggggga     480
ggccactctc tgcaagccaa taagcttcca cttctgaaaa tccataatgt gcaaagggga     540
ggaggcccaa tgtttcacgg cttagcgta gcagccatag ctggggacaa agatagccag      600
tgcagtcacg agtttcctga ctatggcctc atcttccccc aggaccacaa gtgtcctccc     660
actgagcagg gagtagatgg ctgggtgggc aaaggggtac tggcggatga attttaaggc     720
```

```
gttctggcca gccctctttt tatgcctatc ggaagacagg ccagcaggat aagcagaggg    780
gatcctgtct gagctggtgg acgctacact gctcacgtag ctggtggtgt ctgagtagtt    840
gtccaggctg gtcttactga tgtcccggct agccagcagg tggctcgggt ccagctcata    900
agcgggaaac ccttcacaac tgttgtctcg ggaagaaggg ttggcatttt ccactgaaaa    960
gtctacacgg aacccctggt cgttctgcct gtggcgctgt gggggggctgc tcaccacacc   1020
atcctcgtca gagtgtgtgt gggctggagt ggagggcagc accaactgac catcgctctc   1080
cttcccaata cagcagcagg agtctatttg tgatggggtg tattctatgc tgccttcctc   1140
tgtctcaccc agttcttggag gactgatgct tgcctggaag tggatggctc gttcattgcc   1200
atctggatat gattcttctt cattaatggc acttgggtag ctggcccttaa agtcatcagg   1260
gatgagggcc tcagagggcc aggtactgag gacttcaatc ctgtcctcgc tgatggtcct   1320
gtgactgact gctttgctcc ggaccacctg ggggctcaat ggtactgtaa ggcttgcctg   1380
gctgtcagat ttagaaagca cggaggtgga tttctccgtg cccaaacctt caatactttc   1440
accactgctg atactccctt tcatatccat atccaggtag tccaagtttt cctgggggtc   1500
gaaactgctc aactcagtca cttccacttc cttgtactcc tcatctccca gttcctgctc   1560
catcttgatc aacacagact ccacactgga cttgtaagaa ccaacactaa ttaacacttt   1620
aggaattggg cattcttcta gagaactgga aggcggcctg tcttgactgg gcttagaggg   1680
tatgctttct tgtttctcca ccatcctgtc atcgacctcc acaaagtctt caaagagaaa   1740
gtttgttata tgctgttgtt ttagaagtgc tctatcaatc tgactggtca ggaggtaaca   1800
caggtctcct ctgaacatgt gttcaatgtg gctgagctga gccagggtct gggtgaaata   1860
ttcagtgtca cagagctcct ccaaggtctt caacttcttg tcaaaacact tggtggactt   1920
tgctttgata agttttgggg tgtaggctgg tctgcaggtg taaaggtctg tgtcggcaga   1980
ctcatcaggg ttagaggtag tggatgcctg gctggcctga tcctggatgt gctccatctc   2040
accaggacac aaatcatgcc ccttcaactt ccgatgaggg tatgagcgga tctgcttcag   2100
caggtcttga tgttcaatga tggacttctc cacactggcc agtttattgg ctttctcaat   2160
tgcctgagat gagtaaaagc ctttgtcgtt ggctttcttc tggatctccg tttctgtgtg   2220
tagcactgtc ctggtgtaat ccaagtcttt cagctttttt tcaagttccc cagcaaatgc   2280
cttcctgttg ccagtcttca agcactcaga agctctggaa aattcggctc aaagctcctg   2340
gaactgctgc atgattttat gctggtctgc agagatataa gccatgcaaa acggcctcac   2400
gaagccacgg gcctccaggt cgtatagggt aaggtggtgc acgtatgcaa aggcgccctc   2460
cttagaatct cccagcacca ccttggagtc ctccacgaag ttcagcttgg ggtaggcaga   2520
tccaggagga tggcccacga aggaagcctg gtaatccaca gacatgatac gcagggagaa   2580
gtaattgaga tcaaaagtgc caaaaacttt ggtgtcattg gggatggtca gtaagggttg   2640
gggtcccacc tgctcagaga actcggaaat aagaatgaag tccctcgaaa acttggcccc   2700
ggacagtttt gaccaggggt tagcaccctg actggcgaag gggaagagcg gcaccgagta   2760
ctcctcaggc agggccggct cattgtaagg ctcttcttca tactcttcct ctttggtgaa   2820
ggccactacg tcagggcgc tgatcat                                        2847
```

```
        <210> 205
        <211> 7653
        <212> DNA
        <213> Homo sapiens


        <400> 205
agtgtgtata aaggcagacct ggagtggctg cgtggcatcg gctggatgcc agaaggctca     60
gtggaaatga acagagtgaa ggttgctcaa gacctcgtga atgaaagact ctataggaca    120
cgtccagaag ctttgtcatt caccagcatt gtcgacactc cagaagttgt cttggcaaaa    180
gccaattctc tgcaaataag tgagaaactg tatcaggaag cctggaataa agataaaagc    240
aacatcacca ttccttctga tactccggag atgctgcagg cccacatcaa tgccttgcaa    300
atcagcaata aactctacca aaaagactgg aatgacacca gcagaaagg ctatgacata    360
agggcagatg ccattgaaat caagcacgcc aaggcctcca gagaaattgc cagtgagtac    420
aaatacaaag aaggttaccg taagcaactg ggccaccaca tgggtttccg caccctacaa    480
gatgacccca agtcagtatg ggctatacat gctgccaaga tccagagtga cagagaatat    540
aagaaagctt atgagaagtc taaaggaatt cacaacacac cgttggacat gatgtcaatt    600
gttcaagcca agaaatgcca ggtcctggtt agcgacattg attatcgcaa ttatctgcac    660
cagtggacgt gtctgccaga tcagaacgat gtgatccagc gtgatcccaaag ctacgacctg    720
cagagcgatc cattgtatcg caatgcctgg agaaaagaga aggctaatgt gaacgtgcca    780
gctgacactc ccctgatgct gcaatccaaa atcaatgctc tgcagatcag caataaacgc    840
tatcagcaag cttgggaaga tgtcaagatg actggttatg acctgcgagc agatgccatt    900
gggatccagc atgccaaggc ttccagggat attgccagtg attatctgta caaaactgct    960
tatgagaaac agaaaggcca ttacattggc tgtcgcagcg ccaaggaaga ccctaaactg   1020
gtttgggcag caaatgtgtt gaagatgcag aatgacaggc tgtacaaaaa ggcctacaac   1080
```

```
gaccacaaag ccaagatctc catccctgtg gacatggtgt ccatcagcgc tgccaaagaa   1140
ggtcaggcac tggcaagtga tgtggactat cgccattacc tgcaccactg gtcttgcttt   1200
cccgaccaga atgatgtgat ccaagccagg aaagcctacg acctacagag cgacacagag   1260
ccttgctctc tggcccaggc tggagtacag tgggtggccg acatgacggc caggggtcag   1320
agccccctcg cgccgctgtt ggagactttg gaagaccctt ctgcctccca tggagggcag   1380
actgacgctt acctgactct gaccagtcgt atgactggag aagaaggaaa agaagtaatt   1440
acagaaattg agaaaaaact tcctcggctg tacaaagttt taaaggtatc cagtataatt   1500
gattcattag aaatactgtt taacaaagga gagacgcatt ctgctgttgt tgattttgaa   1560
gcattaaatg ttatcgtaag gctaattgaa caagccccaa ttcaaatggg agaagaggca   1620
gtgaggtggg caaaactggt cataccttta gtggttcatt cagcacaaaa ggtacatttg   1680
cggggagcaa ctgctctgga gatgggaatg ccattattgc ttcagaaaca gcaagaaata   1740
gcatctatta cggagcagct tatgactact accttgcatc gaagtgggag tttcatcaat   1800
tctctcttgc aactagaaga acttggattt cgtagtggag cacccatgat taaaaagata   1860
gcttttattg cttggaagag tttaatagat aattttgctt taaatccaga tatactatgt   1920
agtgcaaaaa gactcaagtt gttaatgcag ccttttgagtt ccatccatgt gagaacagaa   1980
actctagcat taacaaaact agaagtctgg tggtatttac tgatgagact tggacctcat   2040
cttcctgcta attttgaaca ggtttgtgtg cctctgattc aaagtacaat aagcattgat   2100
tctaatgcct cacctcaggg caattcgtgt catgtagcta catctccagg tttaaatcct   2160
atgactcctg tacacaaagg tgcttcctcc ccgtacggag ccccgggaac tccccgaatg   2220
aacctgagtt cgaatttagg tggaatggcc acaatcccat ccattcaact tttgggactt   2280
gaaatgttgc ttcatttctt gttgggtcca gaagccttga gttttgctaa gcaaaataaa   2340
cttgtgctga gcttagagcc attggaacat ccgttaatca gcagcccttc ctttttttcc   2400
aaacatgcaa atacacttat cactgctgtt catgatagct ttgttgcagt tggaaaagat   2460
gcccccggta acaaaaaaga gaaaccaggt tctgaagttt tgactctctt attaaagtct   2520
ttggaaagca tagtaaagtc tgaagtattt cctgtatcaa aaacgctggg aactccagct   2580
ttgttcttaa ttcaattaat tttcaacaat ttcttggaat gtggtgtatc agatgaaagg   2640
ttctttctca gtttggaatc acttgtaggc tgtgttcttt ctggtccaac ttcaccacta   2700
gctttcagtg actcagtttt aaatgttatt aatcaaaatg caaagcagtt ggaaaataag   2760
gagcatctct ggaaaatgtg gagtgttata gtcaccccat taactgaatt gattaatcag   2820
accaatgaag taaatcaagg tgatgcctta gaacataatt ttagtgccat ctatggtgca   2880
ttgactttac cagtaaacca cattttttca gaacagagat ttccagtggc caccatgaag   2940
actttgctta gaacttggtc agaattatat agagcatttg ctcgttgtgc tgctttggtg   3000
gcaacagcag aagagaactt gtgctgtgag gaactttctt ccaagataat gtccagtttg   3060
gaagatgaag gctttttctaa tttgttgttc gtggatagaa ttatttatat tattactgta   3120
atggttgatt gcattgactt ctcaccatat aatattaaat atcagcccaa agttaaatca   3180
ccacagagac cttcagattg gtccaaaaag aagaatgagc ccctagggaa attgacttct   3240
ttatttaaac ttattgtgaa agtgatctat tctttccaca cactgagctt caaggaagca   3300
cattctgata ccctcttcac tattggcaac tcaatcaccg gcattatttc cagtgtactt   3360
gggcatattt ctttgccttc tatgatccga aaaatatttg caactttaac aagacctctg   3420
gcattatttt atgaaaactc aaagcttgat gaagttccta agtatatag ttgtctgaac   3480
aacaagttag aaaagctact gggagaaatt attgcttgtc tgcaattcag ctacaccgga   3540
acttatgata gtgaacttct tgaacaactc tccccactat tatgcataat atttctgcac   3600
aagaataaac agattcgaaa acagagtgct cagttctgga atgccacttt tgccaaagtg   3660
atgatgttgg tttatcctga agagttaaaa ccagtactaa cacaagccaa acaaaaattt   3720
ctgctcctgt tgcctggttt ggaaactgtt gaaatgatgg aggaatccag tggaccatat   3780
tctgatggac tgaaacttga atcttcgtct ttaaaagtaa agggtgaaat tcttttggaa   3840
gaggaaaagt ctactgactt tgtgtttata cctccagaag gaaaagatgc aaaggaaaga   3900
atattaactg atcatcaaaa agaagttctc aaaacaaagc ggtttgagga gcaaatggac   3960
agtgacattg tcattcctca agatgtcacg gaagactgtg gtatggctga acatcttgaa   4020
aagtcctccc tttcgaataa tgagtgtggt tctcttgaca aaaccagtcc agaaatgtca   4080
aacagtaata atgatgaaag aaaaaaagct ttaatttcat caaggaaaac atcaactgaa   4140
tgtgcatcta gtacagaaaa ttctttcgtt gtcagcagta gttcagtttc taataccact   4200
gttgctggaa ctcccccata ccctacaagt cggaggcaaa cctttattac tttggagaag   4260
tttgatggtt cagaaaatag accttttagt ccatcccct tgaataatat ttcatcaact   4320
gttacagtga aaaataacca ggaaaccatg attaaaacag attttctacc aaaagcaaag   4380
caaagagaag ggacttttc aaaatctgat tctgaaaaaa tagtgaatgg aactaagaga   4440
tcaagccgga gagctggtaa agctgaacaa acagggaata aaaggtctaa gcccttaatg   4500
agatctgagc cggagaaaaa tactgaggaa tctgttgaag gcattgtagt cttagaaaat   4560
aacccacctg gtttgcttaa tcaaacagaa tgtgtgtcag ataatcaggt tcatctttct   4620
gaatctacaa tggagcatga caatacaaag cttaaagcag caacagtgga aaatgctgta   4680
ttattggaaa ctaatactgt agaggagaaa aatgtagaaa ttaatttgga atccaaagag   4740
aatacacccc cagtagtaat atcagcagat caaatggtaa atgaggatag tcaggttcag   4800
ataactccaa atcagaaaac ccttagacgg tcttcaaggc gacgttcaga agtagtagag   4860
tctaccactg aaagccaaga taaggaaaat agtcatcaaa aaaaggaacg acgtaaggaa   4920
```

                                       123

```
gaagaaaaac ctcttcagaa gagtccattg catataaaag atgatgtgtt acctaaacaa    4980
aaactgattg ctgaacaaac tctacaggag aatttaattg agaaaggaag taatttacat    5040
gagaagactc ttggggaaac tagtgctaat gcagaaactg aacaaaataa aaaaaaggca    5100
gaccctgaga acattaagtc tgaggggggat ggtacccagg acattgtaga taagtcctct    5160
gagaaactag tcagaggccg aacacggtat caaactagaa gagcatctca gggtttgctt    5220
tccagcattg aaaactcaga atctgatagt tcggaggcaa aagaagaagg ttctaggaag    5280
aagagatctg gaaaatggaa aaacaaaagc aatgaaagtg ttgacattca agatcaagaa    5340
gagaaagtgg tgaaacagga atgtataaaa gctgaaaatc agtcacatga ttataaagca    5400
acttctgaag aagatgtaag cataaaatct ccgatttgcg aaaaacaaga tgaaagtaat    5460
actgtaatat gtcaggattc tacagtaact tcagattttgt tgcaagttcc tgatgattta    5520
ccaaatgtgt gtgaggaaaa aaatgaaact agcaaatatg cagaatattc ctttacaagt    5580
ctacctgtgc cagaatcaaa tctaaggact agaaatgcca ttaagagatt acataagcga    5640
gactcttttg ataattgtag tttgggagaa tcctcaaaaa tagggatatc agatatttct    5700
tcgctttcag aaaaaaacttt tcaaacactt gaatgccaac acaagagaag taggagggtg    5760
aggagatcta aaggttgtga ttgctgtggg gaaaaatcac aacctcagga aaagtcactc    5820
attgggttaa agaatacaga aaataatgac gtagagatta gtgaaacaaa aaaggcagat    5880
gtgcaagcac ctgtaagccc atcagaaact tctcaagcta atccatattc tgaaggacaa    5940
ttttttagatg aacatcatag tgtgaatttt catttgggtc tcaaagagga taatgatact    6000
attaatgatt cattaattgt ttctgaaacc aaatcaaaag aaaacactat gcaagaatct    6060
cttccttctg gaatagtaaa ctttagagag gaaatttgtg atatggattc tagtgaagca    6120
atgtctcttg aaagccagga gtcacctaat gaaaatttta aaactgttgg cccgtgttta ·  6180
ggagactcga aaaatgtttc acaggaatct ttggagacaa aagaagaaaa accagaagaa    6240
accccaaaaa tggaactgag tctagagaat gttactgttg aaggaaatgc atgtaaagta    6300
acagaatcca atctagagaa agcaaaaact atggaattga atgtaggaaa tgaagctagc    6360
tttcatggac aagagagaac caaaactggt atttctgaag aagcagcaat agaagaaaat    6420
aaaagaaatg atgactctga agcagacaca gctaaactga atgccaaaga agtagcaact    6480
gaggaattta attcagatat tagtctttct gataatacta cacctgtaaa attgaatgct    6540
caaactgaga tttctgaaca aacagcagct ggggaactag atggaggaaa tgatgtatct    6600
gatctacact catctgaaga aacgaatacc aaaatgaaaa ataatgaaga aatgatgatc    6660
ggcgaggcaa tggctgaaac tggccatgat ggtgaaacag agaatgaggg cataactacc    6720
aaaacctcaa agcctgatga agctgaaaca aacatgttga ctgcagaaat ggacaacttt    6780
gtttgtgaca cagttgaaat gagcactgaa gaaggaatca ttgacgctaa taaaactgaa    6840
acaaatactg agtatagtaa atctgaagaa aaattagata caatcaaat ggtaatggaa    6900
agtgatattt tacaggaaga tcaccatact tcacagaaag tggaggaacc atcacagtgt    6960
ctggcatctg gaacagctat ctctgagcta ataatagaag acaataatgc atctcctcaa    7020
aaactaaggg aacttgatcc ttcacttgtg tcagcaaatg acagtcctag tggcatgcag    7080
acacgctgtg tctggtctcc tttggcttct ccgtctacga gcattttaaa gagaggacta    7140
aaaagatccc aagaagatga aatctcatca cctgttaata aggttcgccg tgtctccttt    7200
gcagatccaa tataccaagc aggattggca gatgacattg atagacggtg ctctattgtt    7260
aggtcccatt cttccaatag ttctcccata ggaaaaagtg ttaaaacttc tcctactaca    7320
caatctaagt cagttgacct ctgtgtaaca gcttctgaaa tttattctaa gatttcagaa    7380
atggccaaag aatccatacc atgcccaaca gaaagtgttt acccaccatt ggtgaactgt    7440
gtggcaccag ttgacatcat tttacctcag attacatcaa acatgtgggc aagaggcctg    7500
ggacaactca ttagagctaa gaatataaaa actattggtg atttgagtac tcttacagca    7560
tctgaaataa aaactcttcc tatccgttct ccaaaagtgt ccaatgtaaa aaaggctctc    7620
agaatatatc atgagcagca ggtaaaaact tag                                 7653
```

```
<210> 206
<211> 2636
<212> DNA
<213> Homo sapiens


<400> 206
gaccatgaac ttggctcccc tcccttgccc ttcctgccca tgattgtgag gcccccccca     60
cccccagaaa cgtggaactg ttaaagtccc aatgaacctc tttccttctg taaattgccc    120
cagtcctcaa gtatgtcttt atcagcagca tgaaactga ctaaaagagt aaaattggtac    180
cagtagaatg gggtgttgtt gaaaagatac ccgaaaatgt gtaagcaact ttggaactgg    240
gtaataggca gagaggttgg aacagtttgg aggactcaga agacaggaaa atgtgggaaa    300
gtttggaact tcctggagac ttgttgaatg gctttgacca aaatgctgat gttatgtgga    360
caataaagtc aaggctgaag tggtctcaga tgaaaatgag gaacttcctg ggaactggaa    420
taaagacatt ggtagcattt ttcccctgcc ctagagatct gtggaacatt gaagttgaga    480
```

```
gaggttattt agggtatctg gtggaagaaa tttctaagca gcaaagtgtt caagaagtga      540
cttgggtact cttaaaagaa ttcagtttta tgcattcaca aagatatggt ttggaatcag      600
aacttatgtt taaaagggaa gcagagctta aaagttcaga aaatttgcag cctgactata      660
caatagaaaa gaaaaacaaa tttctgagg agaaattcaa gctgactgaa gaaatttgca       720
taagtaatga ggagccaaat gttaattgcc aagacaatag ggaaagtgtc ttcagggaat      780
gttggaggtc ttcacagcat ccccttccat catgggtctg gaggcctagg aggaaaaaat      840
ggtttcatga gctgggctca gagacttgct gcattgtgaa gtctcaggac tgcattatgt      900
cccagtcatg gctaaaaggg gccaatgtgc agcctaggcc cttgcttcag agagtgcaag      960
ccccaagcct tgatggcttc cacttggtgt tgtacctgca ggtgcagaga agtcaagaat     1020
tgaggttgga caacctccac ctagatttca gaggatgtat ggaaatgcct agatgtccgg     1080
aaatgcctag atgtccaggc agaagtttga tgcaggaatg gagccctcat gaagaacttc     1140
tgctaggagt cccagctgtg gtactgccta gtggaacagt gggaagaggg ccaggccacc     1200
atcctccaga tcccagaatg gtagatccat tgacagcttg cactgttaat ctggaaaagc     1260
tgcaacggca gcccatgaaa gcagctggga ggattttga taattcggtg tctctttcta     1320
gaggatttca tagcaacaat atcaggtcga tacctgagaa agcatttgta ggcaacccct     1380
ctcttattac aatgattctc ttgatgaaag atgaatctgt tttaaagaat ttagtgcaac     1440
aagaagctaa gaagaaagaa tctgttagaa atgctgaagc aaagattaca aaacttacag     1500
aacagcttca agcaactgaa aaaattctta atgttaacag aatgtttttg aagaagcttc     1560
aggaacaaat tcacagagtt caacagcgtg ttacaattaa gaaagctttg actctaaaat     1620
atggagaaga gcttgctcgg gcaaaggcag tggccagtaa agaaatagga aacgtaaac     1680
tggaacaaga tcgctttggg cagggcatgg tccgcggcgt ctgcgccggg attgccaact     1740
attttgatgt accggtaaaa ctggtgcgta tcctggtggt gctgtcgatt ttcttcggtc     1800
tggcgctgtt taccctggtt gcttacatca ttttgtcatt tgcgcttgat ccaatgccgg     1860
gacaacatgg cctttggtga gcagctacct tccagcagcg aattgctgga tgaagtccga     1920
ccgtgaactg gcggcaagtg aaacgcgttt ccgcgagatg gaacgttatg tcacttccga     1980
tactttcacg ttacgtagcc gtttccgtca actgtgagga aagttatgaa tactcgctgg     2040
caacaggccg ggcaaaaggt aaagcctggt ttcaaattag caggcaagct ggtacttctt     2100
accgcactgc gctatggccc ggcgggtgtg gcgggctggg cgataaaatc agttgctcgc     2160
cgaccgctga aaatgttgct ggctgtggcg ctggaaccgc tgttaagtcg ggctgctaat     2220
aaactggcac agcgttataa aaggtgaggg gagtttcgca aaaattgtta aatctcaggc     2280
gtataatgga tggcaatttt catccataga aggacgctta catgtttaaa aaaggcttac     2340
ttgctctggc actggtgttt tcaatgcccg ttttcgccgc tgaacactgg atcgatgttc     2400
gtgttccaga gcagtatcag caagagcacg ttcaggggc catcaatatt cccctgaagg     2460
aagtgaaaga gcgcattgcc accgccgttc cggataaaaa cgacaccgtg aaagtgtatt     2520
gcaatgccgg acgccagtca gggcaagcaa aagagatcct tagcgagatg ggatataccc     2580
acgttgagaa cgccggtggc ctgaaagaca tcgcaatgcc gaaggtcaaa ggttaa         2636
```

```
<210> 207
<211> 547
<212> DNA
<213> Homo sapiens
```

```
<400> 207
gtcttctcct tcctgccacc ttgtgaagaa gataaaaata aaaatgaagt caccagccct       60
cagggtctg tcaaggcaac acacaaaatc tccagttacc ttctggtgga tgacgtttgg       120
agacacatcg cgtccgtcac aggacacact tccgatggat ttacagcaac tcctgggggt      180
cacgaaggtg tgttccaagg ccacatctcc aacctcacag agaggacagg aagtgatcag      240
taccccaact agcaagagtg gcccgttcat tggccgaggt tcttgaggat agagtgggag      300
gtgggagcgt ccctcgtgct gccttcattt ttcctaccct cagctcaggg tctgtgcta       360
gaggaagaca cacgaaggct actgtgcccc caccacaaga gagggaaaca gggagacgcg      420
tgggtctgga gccaagcgta tctctctgta cccatcgcac acgaatttga atcatctgct      480
ctttggaatc gcctacaccc tgctgcaccc acgatgtggc tgtaactcca ttaaagaatt      540
gaatacc                                                               547
```

```
<210> 208
<211> 3035
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(3035)
<223> n = a,t,c or g


    <400> 208
ttttttcaaa ggggaagagt agcatgtttg tacctaggat ggaccaagag atgtttgccc      60
agaggagggg gttgagcaaa gcgacaggtt aatagtaaaa caattaagat gacaaggaaa     120
attactgggc ttaagatttc taactacatt tacttccttg acgaacgctt cggccgtgcg     180
tagactggtc agcttccggg gtgacttaga gcagggctgt ggtcactttc actggcatct     240
gggtcctgtc cgtaggatca gccggtttgg atggtctggg tcttgctggc atggtccact     300
tgtcctgggc tgctgggttt caagccgact gtggagatcg aaggcacagt tccgtggtcg     360
cccgcgggaa cttcaagggt ccttcctacc cgcgttgctg agagtctggg tttacgcgtc     420
acctcgggcg ggacccgatc ctccgctcct gaggccccca caatgaagca gtcggacgcg     480
tctccccaag aaaggtaccc gccagcctct catttttaaa ggcagagatg tgcgtctcgc     540
catgttgccg cgtctggtct cgagctcccg ggctcaagcg atcttcccgc ctcgacctcc     600
caaggctctg ggagtacaga cgtgagccac agcggccggc ccgtgtttaa ctcagataaa     660
atctgggtaa cacactttca acgcttcaac cccctcgggc gcaccgctct gcgctcattc     720
caactttgaa agcaggaagg aagaaatgcg caggctccag ccgcgtcccc gcaggcccca     780
ctccgtttc ctagcaacgc cgggtcacgt gcgccgccgc ccggattccg tagcgtgagc     840
ctgccggagc cggcgcgtac atgcgagcgt gtgcgcgcgt gcgcaggcgg ggcgaccggc     900
gtccccggcg ctcgccccgc ccccgagatc ccgccgtgcg tgcgcgcgcc cggtccgcgc     960
ctccgccgct ttttatagcg gccgcgggcg gcggcggcag cggttggagg ttgtacgcgg    1020
attccggcga ggaatatgga atcatggcgt ttgcgctgtt cgtgctgctg ggatctcgcg    1080
ctgctgggca cccacggagc catccggggc tgccggcaca gtcttcacta ccgtagaaga    1140
cctttggctc caagatactc ctcacctgca tccttgaatg acagcgccac agaggtcaca    1200
gggcaccgcg tggcatgaag ggggcgtgg tgctgaaaga aagatgcgct gcccggccag    1260
aaaaccggag tttcaaggtg gactccgacg accatgtggg gatgaagtac tcctggcgtc    1320
ttcctccccc gagccccatg ggcacgggcc aaccatccaa gcttccacgg ggcctcccag    1380
agttgaaggc ttgtgaagtt cgttcagaac acattcaacg aggggggaga cgggccttgt    1440
tgggtcttgc aagttcagag ttcgtgccac cttgtcactg actgggggcct tggtacaaga    1500
tcactgactc tgagccacaa ggcccttcat tgaacgctca gagaacaagg ttctttcgta    1560
ggtccctccg caggcccggt caaaagctac caacattgag aacctgaaca cataggggccg    1620
cccccggcca ggaaccggtg caacggcacc agctccaaag ggctccgacc gaggccatta    1680
caattcctcc gcgtcgcgcac agccacctga gcagccctct tggcccttcc tgggcatcgt    1740
gggttgaggt gctggtgctt ggtcaccatt catcttcatc tacgagaagc gccggaagca    1800
ccgaggacgt cctgggatga tgacgacgcc ggctctgcac ccctgaaaga gcagcggggc    1860
agcaccagaa ttgacaaagg caagaaacgt tccgccagag ggaatttttc ctgagggcag    1920
gttggcccga ggacgctcgc ctggttccac tgtctgcgcc gccgccggag ttccactccc    1980
agttgcttgg aagatttcca aggttctcac ctctttaaag aaaacccact cccgtaggaa    2040
tcccattcat tacacttcct tctttttaa aaaaagttgg ggtttcttc catttcaggg    2100
attcttgttt cctttaggtt tttttttcct ttctggaagt gtttacgaga agccccggga    2160
gcttgcttgc ccttgcgggc cccgtctttt ggtttttaag ccctctgggg tctgaagtca    2220
ttggccgggt tggggcgcaa cagccttctt ccactgggcc gggagtcagt gccagggtcc    2280
ttgccccttt gtgggaaagt tcacaggtca acacgaaggg gcccccgtgt ccctgccttg    2340
tctgaaagcc aaatgctgtc tgggttgcgc ccattttgt tgcttttat gttttaattt    2400
ttatgagggc ccacggggtc tgttgttcga ctcagccctc aggggacgaa ttctgaacct    2460
cttgggccac agaggaattc aatttgccca cacccgaggg cgaaccccgt cacagcctca    2520
aagtcactcc caagccccct ccttgttctt gtgcatccgg gggcagctct ggaggggggtt    2580
tgcttgggga actggcgcca tctgccggga ctccagaacc cgcagaagcc tccccagctc    2640
acccctggag gacgggccgg gttctctata gcaccagggg ctcacggtgg gaacccccc     2700
tcccacccac cgccacaata aagatcgccc ccacctccac cctcnnnnnn nnnnnnnnnn    2760
gggggggccc ggggccggaa atcccaaatt ttaaaagggg aaatccggaa aaccccgggg    2820
gggttcttta aagggggggtg ggggccccat caaaattttt ttatttaaaa cccggttggc    2880
ccttttttta ggaaaaaaac cccctaaag ttaaaatttg ggccgggaac ccctgggctt     2940
aaaaaatttt ttaaaggccc aaaaataagg ccccatttt tttttgggccc aaatttttt     3000
aagaaaaaat tttaagaggg ctttattaaa aactt                              3035


    <210> 209
    <211> 939
    <212> DNA
```

<213> Homo sapiens

<400> 209

```
atgaaggtct tattagagtc agttaaagaa agagcggaag aagagaaatt ggcagcagca     60
catcttagga gttttgctgc aaaaaaagca aagaaatatg atagtgtcaa aaaggaaaaa    120
actcttcagg atgtggactt aactcagcat cagcacaaac agacccgagc tctgtctgga    180
ggcctgaaga ggaagctctc ccttggcatt gctttcatgg gcatgtcgag gaccgtggtt    240
ctggatgagc ccaccagtgg ggtggaccct tgctcccggc atagcctgtg ggacattctg    300
ctcaagtacc gagaaggtcg tacgatcatc ttcacaaccc accacctgga tgaagctgaa    360
gcgctgagtg accgcgtggc cgtcctccag catgggaggc tcaggtgctg cggtcctccc    420
ttctgcctga aggaggcata tggccagggg ctccgcctga cactcacgag gcagccttct    480
gttctggagg cccatgatct gaaagacatg gcttgtgtta catccctgat aaagatctat    540
attccacaag catttctcaa agacagcagt ggaagtgagc tgacctacac cattccaaag    600
gacacagaca aggcctgctt gaaagggctc ttccaggccc tggatgagaa cctgcatcag    660
ctgcacctga cgggctatgg gatctcagac accaccttag aagaggcaga agggaggacc    720
gcagcacctg agcctcccat gctggaggac ggccacgcgg tcactcagcg cttcagcttc    780
atccaggtgg tgggttgtga agatgatcgt acgacctggg tccaagcaca gggtgcatca    840
gcaccaggag gacaaaggcc ccaggaggac cttccctcct ttcctcagga tggtagatcc    900
agggcacaat ttaaagatcc tcaccaattt tcaaactga                           939
```


<210> 210
<211> 1746
<212> DNA
<213> Homo sapiens

<400> 210

```
atggcttctc atgcttatga taaaaatcaa aatgccaatg tcttagtcca cttgtgcttc     60
tataacagaa tacccaagac tggagcatat tacctagatt ctaggagtgt gagcatcagt    120
tatttgattg gccatcatat agacatgggt cttgagacag ccacttccaa aaatgaattc    180
attttcgata gtgcaagtac actgctgggg atgctttta ggaaaccctc ccaacactct     240
ctctcccttt ttagcaagaa attccaggag aatctgatat acctggaatc tgatgactgc    300
ttgccacctc ctcccctcc accttggtct gagccaccgt catttctcac ctggactatc     360
gtcacagttt tccagtgggt ctccctgctt ctgtccttgc ccaacataca ggtcattctt    420
tacagagcag ttggagtagt accttcacaa cctaagtcag acaacctgaa aggatgggga    480
tcggggagag tcgttaaaga gaagctcaga tcagagatac ctgactggaa gattaaaagt     540
attcacatac tggagaggac tgcttcctct agcaccgagc cctctgtaag tcggcaattg    600
ctagaaccgg agccagtccc cctctccaag gaagctgaca gctgggaaat tatagaaggg    660
ctgaaaatag gccaaaccaa tgtccagaaa ccagacaaac atgagggctt tatgctgaag    720
aaaagaaat ggcctttaaa aggctggcac aagattcaga aggaaaggt ccatgggagc      780
atagatgtgg gactctcagt catgtcaatt aaaaagaaag ctcgaagaat agaccttgac    840
accgaagagc acatctatca tttgaaggtg aaatcagttt tcaacagttt ctctgccatt    900
atcaggggaa acgatttgcc tacaccagtg gtgaaatccc aggactggtt tgatgcatgg    960
gtctccaaac tgcgacatca tcggttgtat cgtcagaatg aaattgtgag atcaccaaga   1020
gatgctagtt ttcacatatt tccttcaacg tccacagctg aatcctcacc agctgctaat   1080
gtttctgtaa tggatggaaa gatgcaacca aacagctttc cgtggcagtc cccttttacca   1140
tgcagcaata gcctccctgc aacgtgcaca actggccaga gtaaagtggc agcctggtta   1200
caggactcgg aagagatgga caggtgtgca gaagatcttg cacattgcca gtcaaacctt   1260
gtggaactta gcaaactcct gcaaaatttg gaaatacttc agagaactca gtcggcacct   1320
aactttactg acatgcaggc taactgtgta gatatttcaa agaaagacaa gcgggtcaca   1380
agacgatgga gaacaaaaag tgtcagcaaa gatacaaaaa tacaactgca ggttcctttc   1440
agtgctacca tgtcaccagt tcgcttgcat tcctccaacc ccaacctttg tgcagatatt   1500
gaatttcaga ctccccctag ccacctcact gaccctctgg aaagttcaac agattataca   1560
aagctgcaag aagaattttg tctaatcgca cagaaaggaa aggggggcatc aaaaaagcaa   1620
gccaaaagga atgctgctga gaaatttctt gccaaattta gtaatatttc tccagagaac   1680
cacatttctt tagtgagtaa tgttgacagc tatgatgtta atgtcattaa gcatttcttg   1740
cagtag                                                             1746
```


<210> 211

```
        <211>  1251
        <212>  DNA
        <213>  Homo sapiens


        <400>  211
atgctcagaa cgcgtaaagc accccacagc tgggtaaaat catctagcaa cacagtgcac      60
tatagagtat cagttgtttg ccttcatgat catgtaactg actgggagtg gcagctcact     120
gccactgccc gacatccaaa gagagtatca cactacatat tgtgggacca ggagaagacc     180
aaaattaaaa ttcgaaaaga tataatccgc atcctcccca gtctagatgt cgaagtcaaa     240
gacatcactg attcttacga tgctaactgg tttcttcagc tgttatcaac agaagatctt     300
tttgaaatga ctagtaaaga gttccccata gtgactgaag tcatagaagc acctgaagga     360
aaccacctgc cccaaagcat tttacagcct gggaaaacca ttgtgatcca caaaaagtac     420
caggcatcaa gaatcttagc ttcagaaatt agaagcaatt ttcctaaaag acacttcttg     480
atccccacta gctataaagg caagttcaag cggcgaccga gggagttccc aacggcctat     540
gacctagaga tcgctaagag tgaaaaggag cctcttcacg tggtggccac caaagcgttt     600
cattcccctc atgacaagct gtcatccgta tctgttgggg accagtttct ggtgcatcag     660
tcagagacga ctgaagtcct ctgtgaggga ataaaaaaag tggtgaatgt tctggcctgt     720
gaaaaaatcc tcaaaaagtc ctatgaggct gcgctgctcc ctttgtacat ggaaggaggt     780
tttgtagagg tgattcatga taagaaacag tacccgattt ctgagctctg taaacagttc     840
cgtttgccct tcaatgtgaa ggtgtctgtc agggatcttt ccattgaaga ggacgtgttg     900
gctgccacac caggactgca gttggaggag gacattacag actcttacct actcataagt     960
gactttgcca accccacgga gtgctgggaa attcctgtgg gccgcttgaa tatgactgtt    1020
cagttagtta gtaatttctc tagggatgca gaaccatttc tagtcaggac tctggtagaa    1080
gagatcactg aagagcaata ttacatgatg cggagatatg aaagctcagc ctcacatccc    1140
ccacctcgcc ctccgaaaca cccctcagta gaggaaacaa agttaacccct gctaacctta    1200
gcagaagaaa ggacggtaga cctgcccaag tctcccaaga gaagaagata a             1251




        <210>  212
        <211>  909
        <212>  DNA
        <213>  Homo sapiens


        <400>  212
atgtttgcgt ttgaacctct tggcgggtgc cggccatggc ggctctcgct cccgggactt      60
gggagccggc ttttccgcac atatggggct gcggacggca ggagacagcg gcggccgggc     120
cgggaagccg cgcagtggtt cccgccgcag gaccggaggc gtttcttcaa cagcagcggc     180
agcagcgacg ccaggatggg cgacccctcg cagtccgacg atcctgacga tcccgacgac     240
cccgacttcc ccggcagccc ggtgaggcgg cggcggaggt gtcccggcgg ccgagtgccc     300
aaggaccggc ccagcctgac cgtgacccca aagcgctgga agctgcgagc tcgcccaagc     360
ctaaccgtga ccccaagacg cctggggctg cgagctcggc ccccgcagaa gtgcagcaca     420
ccctgtggcc cgctccgact tccgcccttc cccagccgcg actccggccg cctcagcccg     480
gacctcagcg tgtgcggcca gcccagggac ggcgacgagc tgggcatcag tgcctccctg     540
ttcagctctc tggcctcgcc ctgccccggg tccccaacgc caaggacag tgtcatctcg     600
atcggcacct ccgcctgtct ggttgcagcc tcagccgtcc cgagcggcct ccacctccca     660
gaagtctccc tggaccgagc atctctcccc tgctcccagg aggaagcgac aggaggagcc     720
aaggacacca ggatgggcag tgtccgagtc ctgcgtgacc ctgtgggggt caacctctat     780
gagcattcgg tcagcaaatg ccacgtcggc cagccggaca ctgatcccag agagaaggtg     840
aaggctgctc cggaagagct gtgtctgcac gcgctccagc accccgctc tgagcaggct     900
gactgctga                                                             909




        <210>  213
        <211>  1188
        <212>  DNA
        <213>  Homo sapiens


        <400>  213
tcagttcttt tgcttgttaa cgtgtctgct caccgcctcc cgctccccaa agccaggact      60
```

128

```
gtgcagttga tcccaggagc gagcccggcg cggctccctg ccggcagcga agcgaaacat     120
ttggacatgg ccccgatttt ccgggtgcgg ttggcaagtc ccggcgtgcg cgaaccaaac     180
ctgcggttcc cgggggcagct ttgagcgggt cgggtcggct ccataggaga atggccccac    240
tgtttccaga aggatccaag agaggacttt cagctctgga attttgaact caggatctgt     300
ttctccctcg cggaaagagg aaggtggacg aagggcaagc ccaggccggc aggggctacc     360
gcaggaagac gcccattcct ggactcgggt tcgcaggagc ccccttgctc cccagagccg     420
gaactgcgct gcctgccacg ctcggctgac tccaaggaag tccagggcaa cgtgattgtc     480
catggccact tgtgttggtg cattccgaac aaacagtctg ctgcctggct gcacaggtct     540
gaccagtgtg gtcatgggtg ggtgacgatg taacaaggtg cattctggct gctgtttcc     600
agccccagat ccttcttcct cctctcggtc ccaggtggct tccagagtca tcccgctggc     660
tcctcctgca tggcaagtcc cagttagctg tacagaatct gcagaaggtg gctcatcggg     720
gagattggcc tggatctggt catccagctc cacagtccca gcactcttct ctgagaagaa     780
gcgcagcacg aagtcgccct ccttgttggg ctcgaaggtg gagggcacca ccacatactc     840
cccgggtggc aggcggaagc gggtgctgac ctctcgcagg ttgatgaact gctctgagcg     900
cgcccgagac gcattggcca ggaagaagtc acgcttcaag tgtacggccg gctggcccac     960
cagctcgtag accgcgaagc caatagtctc catgtcgcgg ccgaagcggc gctcgcggcg    1020
acggtgcttc tgcataaggg cgagcacgaa gctgcagcct gactcgcggt ccccgtagtc    1080
gtccgggtca tccgtctcat ccagccggat cttgaactga gggttcaccc agaaggtggc    1140
ttctttctta tgatgtaatt tactttgaat aattaaggct ccctccat                 1188
```


```
        <210> 214
        <211> 749
        <212> DNA
        <213> Homo sapiens


        <400> 214
ggggagaatc gatgacatta ggccactgga ggccattagc gagtgagctg agctgcgcgg     60
cgcggcgcgg cgcggcacgg cacggtggga gtgtctccgg ctggcctgca gggagaacac    120
cgactgagac ctctaaccct ggctccagtg gcatgtgata accagtcgtt ctgctcagtg    180
gtgggggtgg tatttgccga gccagaatgt gtgtgctgtt ttaggaatcc gtcacctttg    240
aggatgtggc cgtggagttc atccaggagt gggcattgct ggacagcgca cggaggagcc    300
tgtgcaaata caggatgctt gaccagtgca ggaccctggc ctccagggga actccaccat    360
gcaaacccag ttgtgtctcc cagctggggc aaagagcaga gccaaaggca acagaacgag    420
ggattctccg tgccacatgt gttgcctggg aatctcaact taaacccgaa gagttgcctt    480
ctatgcagga tcttttggaa gaagcatcct ccagggacat gcaaatgggg ccggggctgt    540
tcctgaggat gcagctggtg ccctccatag aagagaggga gacaccattg actcgagagg    600
accgaccagc tctccaggac ccgccttggt ctctgggatg cacgggactg aaggccgcta    660
tgcagattca gagggtggtg ataccagtgc ctactctggg ccaccgcaac ccatgggtgg    720
ccagggattc tggtgccatt ggaaatggg                                       749
```


```
        <210> 215
        <211> 723
        <212> DNA
        <213> Homo sapiens


        <400> 215
cccctgcctc ttgatcaaag gctcctggcc agcattacac cctcaccttc aggccaatcc     60
atcatccgaa cccaacctgg agcaggggtc cacccaaagg ctgatggtgc tctgaaggga    120
gaagctgagc aatctgcagg gcaccctagt gagcacctct tcatctgtga ggaatgtggg    180
cgctgcaagt gcgtcccctg cacagcagct cgccctctcc cctcctgctg ctgtgcaac    240
cagcgctgcc tttgctctgc tgagagcctc ctcgattatg gcacttgtct ctgctgtgtc    300
aagggcctct tctaccactg ctccactgat gatgaagaca actgtgctga tgagccctgc    360
tcttgtgggc ctagttcttg ctttgtccgc tgggcagcca tgagcctcat ctccctcttc    420
ctaccctgcc tgtgctgcta cctgcctacc cgtggatgcc tccatctgtg ccaacagggc    480
tatgatagcc tccggcgacc aggctgccgc tgcaagaggc acaccaacac tgtgtgcaga    540
aagatctctt ctggtagtgc acccttcccc aaggcccagg aaaagtctgt atgaccttcc    600
aacaaggtgg atccagagct tttctccttc tagtccccaa cagcaaagca taggcctcat    660
ctttggagag ggggaggagt gataaactag ccaaagttag ggcctctctt ttgttcctgc    720
```

agg   723

```
<210> 216
<211> 1572
<212> DNA
<213> Homo sapiens


<400> 216
atgaagacgt gccttgcttt tcccttggcc ttccaccatg attcaaacgg atcggcggtc     60
ctaagacttc aagcaaccca cggaatttct agtgacagcc ctctcccatc tgtagaaaag    120
gcgagccatt ctccggaccc cagcgaatac tttaggaagc acccacctgt tcgcagatca    180
gggctccgga ctaagcgcac gagcccaggc ccgggagccc gcgtacctgg cagtcagtct    240
ttccgcagcg ccgaggcttg cggtgtggcc gccctggaat gttggcgccg tcgtgtccct    300
gtcccccttt cgtcgccagc tgaggtgcag gtcttgctca agaaggcgct tcgacctgaa    360
agcaggcctt tcagaaatca gatcttacac aattgtgaga gaaactgggg gaataaaggt    420
tggaaagggc tcgttggaag atcggagtcg caaaccggac aatctgagaa gctgagcatg    480
tccagccacc acagagggac tgtgcgggag gagctggtgg tagaggaata tatagggggt    540
tggtgcctct gtgggtctgc atggaagctt ctggtgacag ggctggagca gctgctcttc    600
agcaggaccc gccctcagga ggaggctgtg gacaaaacct ggaggacagc caggcagctg    660
gagtcaggga cactttgtg tcgtcattgc atcacattgc cctggccttc tgagaggaat    720
ggtggttgtt tcctttctcc ctccaacatg cttgtctgtg agttaagggt tctttctgtc    780
atcgttgcat ccccagagcc tagtacagaa catacacagg aacacttatc tggagatgaa    840
tttgagaaat cccaaccaag tcgaaaagag aaaagtttag gattattgtg tcataagttc    900
ttagcacgat atcctaatta tcccaacccc gctgtgaata atgacatctg ccttgacgaa    960
gtggcagagg aacttaatgt tgaacgtcga cgcatttacg atatcgtgaa cgtcctagag   1020
agtttacata tggtgagccg cctcgccaaa aacaggtaca cttggcacgg gcgacacaat   1080
ctcaacaaaa cccttggcac cttgaagagc atcggggagg agaataagta cgccgagcag   1140
attatgatga tcaaaaagaa agaatatgag caagagtttg actttattaa gagttacact   1200
tctgtaaaca gccgcaaaga caagtcttta agggtaatga gccagaaatt tgtgatgctg   1260
ttttttggtgt caacgcctca gatagtaagc ctagaagttg ctgccaagat tttaattggg   1320
gaggaccatg tggaagattt ggataaaagc aagtttaaaa ctggctccct ggttcggctc   1380
tttgccccctt gcctctctgg tgctggcagc aagcttccag gcctggtaga ggcactggcc   1440
tttgaggtat cattggctgc cttctcagtg gtggcatctg tggagtcttt tgagccagta   1500
gctttagaag agtgggtggt gcacaccgtt gggctcaggc cttggggtgg cgtcacactt   1560
tggtgggctt ga                                                       1572


<210> 217
<211> 719
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(719)
<223> n = a,t,c or g


<400> 217
agcccgggtt tgcattaaat tttttaaaag gccatagtct cctcaactct attgaattgg     60
ggttaataag actccacaaa attgtcaagc agaccaatta actagggaca aatttcaaaa    120
cctaaaaatt tagtttgcgt gtaacgtggg actgcacaca agtttggaaa tcatggcaaa    180
acatcaatta cctaggacta caaaacatta atttcttctt ttaagcagag agaatatgga    240
tttaattgtt taccataaga aaagtgacat atccaaccaa ccatccatcc ccacctgtgc    300
cctattcttt ccttgtgttt ctttagagcc ttttcagcta tttcctgtga agcaaactgc    360
acgaaggcct cccccgtact cctccctgg gaagtccacc ggcaatgtta tcccatttgg    420
gcacggattt ccaacccttc aacccaaggg ncaaataacc ccagtagggg ggcaatatta    480
acatcacaag cccagaaatg attcttctta taggctttaa ataaaccagg actttttaac    540
tttagggtga atgggtatgc tttcaacaag tactctttaa atatgcattg caataatatg    600
aagttccatt attataaagt ataactattc ttaacacacc catggtacag tatatattaa    660
```

```
aaaaaacttg ctgaacacag gatgcattaa gaattcaaca acttaagaac acatatctt        719
```


```
        <210> 218
        <211> 1755
        <212> DNA
        <213> Homo sapiens


        <400> 218
atgaggcaaa ccaagacaga atacatccaa gagtttaacc aggaggccac agttgcaagg        60
gctttggaag gtcaggaaaa gcccaccgaa gggccaagaa acacctgcct ggggagcaac       120
aacatgtacg acatcttcaa cttgaatgac aaggctttgt gcttcaccaa gtgcaggcag       180
tcgggcagcg actcctgcaa tgtggaaaac ttgcagagat actggctaaa ctacgaggcc       240
catctgatga aggaaggttt gacgcagaag gtgaacacgc ctttcctgaa ggctttggtc       300
cagaacctca gcaccaacac tgcagaagac ttctatttct ctctggagcc ctctcaggtt       360
ccgaggcagg tgatgaagga cgaggacaag ccccctgaca gagtgcgact tcccaagagc       420
cttttccgat ccctgccagg caacaggtct gtggtccgct ggccgtcac cattctggac        480
attggtccag ggactctctt caagggcccc cggctcggcc tgggagatgg cagcggcgtg        540
ttgaacaatc gcctggtggg tttgagtgtg ggacaaatgc atgtcaccaa gctggctgag        600
cctctggaga tcgtcttctc tcaccagcga ccgccccta acatgaccct cacctgtgta         660
ttctgggatg tgactaaagc gcttgtgggt ggttatgaca tccttgccat ctatgaggtg        720
gagcatttcc aacaagagca gtgtgtggcc gtgatctccg tgtgctcccg cggggggaaag      780
ggcagtgctg agtgtgggca ctggggcaag ggcctgacca ccgagcactc ctcacctgtg        840
cctgcagtca cccacctttc cttggcaagg atagcggaaa aaggcaaagc cggatgccct        900
gcacgggcct gccgggtgca ctcctgggtc cttgtgctat cggggaagcg cgaggtgcct        960
gagaacttct tcatcgaccc attcacagga catagctaca gcacccagga tgagcacttc       1020
ctgggcatcg aaagcctgtg gaaccacaag aactactgga tcaacatgca ggattgctgg       1080
aactgctgca aggtgcctag ggaggggggag ctgggtgacc ctgaggaacg gctcgctcat      1140
ttgtttggtg gcttggactg tctgtccatc tgcatggcgg acgtagccag tctgctgctc       1200
ctgaactccc gtctcaccat cctgtcccag ctgccctcat ggtgtatgag cctcttcctg       1260
caacaacagg acttgatctt tgacctgggt gaccctgtga gatgggagta catgctcctg       1320
gggactgata agtctcagct gtccttgact gaagaagacg acagtgggat aaacgatgag       1380
gatgatgtgg aaaatctggg caaggaggat gaggataaga gcttcgacat gccccactcg       1440
tgggtggagc agattgagat ctccccggaa ggtaccaata ttttggagat aaaggagtgg       1500
taccagaacc gggaagacat gctggagctg aaacacataa acaagaccac agacctgaag       1560
acagactact tcaagcctgg ccaccccag gctctgcgcg tgcactcgta caagtccatg        1620
caacctgaga tggaccgtgt cattgagttt tatgaaacgg cccgtgtgga tggcctgatg       1680
aagcgggagg agacacccag gacaatgaca gagtactatc aaggacgccc agacttcctc       1740
tcctaccgcc atgcc                                                        1755
```


```
        <210> 219
        <211> 1437
        <212> DNA
        <213> Homo sapiens


        <400> 219
atggagatca gaaggtccac cctttcagca ccccctctcc agggacaccg gccttccaca        60
ttcccacaac cttctcccct gctgcaggac ctgggcatca cttacctatg gaccctggag        120
agggcttggc agaaggacct gggttacctg cagcagtggc tgaaggcctt tgtaggtgcc        180
ttcaagaaga gcatctcact gtcctctctg gagccacgaa ggccagagga ggcaggtgca        240
gaggtcccgc tgctaccact ggatgagctg catgtgctgg ccgaacagct gcaccaggct        300
gacctggagc aagcccctcc gctgctcaag ctcttcatca ttctctgcag gaacctggag        360
aacatagagg caggccgggg ccaagtgcta gtgccccgag tgctggcact gttgaccaag        420
ttggtggcgg agctgaaagg atgcccacca ccccaggggcc gaggcacgca gttggagaat       480
gtggccctac atgctctgct tctctgcgag ggcctctttg acccttacca aacctggcgg        540
cgccagcgca gtggggaagt catcagctcc aaggagaaga gcaaatacaa gttccctcct        600
gctgctttgc cccaggaatt cagcgccttc ttccaagacc ccagacacag gaaccaggat        660
tctaaaccca gaccccagat ccaggactca agccccagga ctctaaaccc agacttccag        720
gactgcaaac ccaaacccca gacccaggac ccaggacaag ggctgacgga tttccagatc        780
```

```
agcgtggccc tgtgtggaca aggccagtgg gaaggggcac cggggggtca cactcttggc      840
aacagcgggg gtagctgctt ggcagacctc cctggtagcg ttcagaaggg catgaagaat      900
gtccatcatc ctgtcagagc caatttgggg agctcagact atggttgcca cgtggagggt      960
gggcagaagg agtctccgca ggcagccatg gcccgccctg cctgccggt cccgccctc       1020
ctggcccaca gcctctgggc tgggacgcag gcccacactt cccggaggag tcgagaacac     1080
ggcctgggcc agacccagag ccttagaagg accacgggac ggtgctctaa ctcacccaaa     1140
gaaagcacag agatgggcac aaagaaccca ggaccaaaat acaacttcct gtccccggag     1200
ctgagggcca gacttgcccc ccagagccct gggctggggc ccacaggagg aacgcaaact     1260
ggcaggccca aggctcgagg agagaaaggc cttcaggttt tcagactccc aggagccact     1320
gggtacccag tgctggcaga tcaggctttc ttgggcctca gttttcctgc ctgtgacaca     1380
ggcaagaacc acctccagcc cccctctgat ttctctgggt gccttaaact tgagtga       1437
```


```
        <210> 220
        <211> 357
        <212> DNA
        <213> Homo sapiens


        <400> 220
gtgcgattca tctttctgtc tctaggtctt agcatgtgca cggcacagag caggcgctca       60
gagtgccttc agtgaaggaa taaatgacca taccaccagg cacagagtga ggcctttaga      120
aaccctgagc atcatcgggt gcgcccacca cttctgtatg tgactcaaag taagtgtaag      180
gaaatccagt tctgttttgt ttctgaaata ctagatgtca ggaagggtgt ttaggtgtca      240
ggctttggtg gcctacactg tgctttcgga attattcact gaggcgaaag aacagagatt      300
agctactgat gaaggacaaa aagaattttc tgctgaatcc tgaatttgcc aggatga        357
```


```
        <210> 221
        <211> 339
        <212> DNA
        <213> Homo sapiens


        <400> 221
gtgcgattca tctttctgtc tctagttctt agcatgtgca cggcacagag caggcgctca       60
gagtgccttc agtgaaggaa taaatgacca taccaccagg cacagagtga ggcctttaga      120
aaccctgagc atcatcgggt gcgcccacca cttctgtatg tgactcaaag taagtgtaag      180
gaaatccagt tctgttttgt ttctgaaata ctagatgtca ggaagggtgt ttaggtgtca      240
ggctttggtg gcctacactg tgctttcgga attattcact gaggcgaaag aacagagatt      300
agctactgat gaaggacaaa aagaattttc tgctgaatc                             339
```


```
        <210> 222
        <211> 2485
        <212> DNA
        <213> Homo sapiens


        <400> 222
ggggaagtac tacaagctgt cctcaggtac tgcccctacg tgtgtttccc tgggatgggg       60
ccttgctaga ggtgattctg ctgccccagc attgggaagc aggaccagtg catgtgcccc      120
atgcagccac ggtacatgga agctgtcact tgagccatca gaccggctca gcccatgtga      180
ccggagctct gaagaggcac acacgcatgc cccgcacagg ctgttagcac ttgtcgcctc      240
gctgccctgg tccagactac ccttgcttgc cccacagagc cactcagagg ctgaagccac      300
ttcacagccc actggtgttg agaatcatca tcagaaaacc agatatgtca aggcaggtgg      360
tccagtcatc tgccggagtc tgcctgagtc caggggggttt ttatgggctt cagagggggag     420
gaagtgcatg ctgattggtt cgtgggcagc catgggcagg ctcagaaaaa gcaccataag      480
ttctcgtttt gggccccaga ctctagctgg aactggcaga cctcaggcca tccctgtctt      540
gaagaaacac agtgatgcag tcctgcttgg ggtgtgcttc ctgaagctac tgcaccagca      600
tcaccaggaa cttggtgaaa atgcagattc tcagaccccta ccccagaccc actgggagtt     660
```

```
tatattgtca gaagattata acaagatgac tcctgtgaaa aactatcaag tgttggaagt    720
tctggccagg gcaatgaggc aggagaagca aataaagagt attcaattag gaaaagagga    780
agtcaaattg tctgtgtttg cggatgacat gattgtgtat ctagaaaacc ccattgtctc    840
agcccaaaat ctccttaagc tgataagcaa cttcagcaaa gtctcaggat acaaaataaa    900
tgtgcaaaaa tcacaagcat tcctatacac caataacaga caaacagaga gccaaatcat    960
aagtgaactc ccattcacaa ttccttcaaa gagaataaaa tacctaggaa tccaacttac   1020
aagggatgtg aaggacctct tcaaggagaa ctacaaacca ctgctcaacg aaataaaaga   1080
ggacacaaac aaatggaaaa acattccatg ctcatgggta ggaagaatca atatcatgaa   1140
aatggccata ctgcccaggg taatttatat attcaatgcc atctccatca agctaccaat   1200
gactttcttc acagaattgg aaaaaactac tttaaagttc atatggaacc aaaaaagagc   1260
ccgcattgcc aagacaatcc taagccaaaa gaacaaagct ggaggcatca cgctacctga   1320
cttcaaacta tactacaagg ctacagtaac caaaacagca tggtactggt accaaaacag   1380
aggtgtagat caatggaata gaatagagcc ctcggaaata ataccacaca tccacaacca   1440
tctgatcttt gacaaacctg acaaaaacaa gaaatgggga aaggattccc tatttaccaa   1500
atggtgctgg gaaaactggc tagccatatg tagaaaactg aaactggatc cgttccttac   1560
accttataca aaaattaatt caacatggat taaagactta aacgttagac ctaaaaccat   1620
aaaaacccta gaagaaaacc taggcattac cattcaggac ataggcatgg gcaaggactt   1680
catgtctaaa acaccaaaag caatggcaac aaaagccaaa attgacaaat gggatctaat   1740
taaactaaag agcttctgca cagcaaaaga aactaccatc agagtgaaca ggcaacctac   1800
agaatgggag aagattttta caatctaccc atctgacaaa gggctaatac ccagaatcta   1860
caaagaactt aaacaaaatt tacaagaaaa aatcaaacaa ccccatcaaa agtgggcaa   1920
aggatataaa cagacatttc tcaaaagaag acatttatgc agccaacaga cacatgaaaa   1980
aatgttcatc atcactggtc atcagagaaa tgcaaaacaa aatcacaata agatacatct   2040
cacaccagtt agaatggcga tcattaaaaa gtcaggaaac aacagggaca tggatgaagc   2100
tggaaaccat cattctgagc aaactattgc aaggacagaa aaccaagcac cgtatcttct   2160
cactcatagg tgggaattga acaatgagaa cacttggaca caggttgagg aacatcacac   2220
gctggggcct atcgtgggtg tgatctgtag aaaagtattc cctggaaatt cagggccttc   2280
aaaacccagt gggcttcact tctcccagcc cctaccccaa gttacttcag ttgtggcaaa   2340
aataacaatt gtcccctggg aaatgaagct cattgctatg ggtgttcaag atgaactcaa   2400
cattgccttc cacaaaaatc acttactgat gaatgacacc accattcata tgacaccccta  2460
catccagcca gcccccaagt cctga                                        2485
```

```
<210> 223
<211> 2086
<212> DNA
<213> Homo sapiens


<400> 223
atgagggtgt gcgcgcgcgc tcggcgagcc cgggttcttt gtgtgtccga gcccatgcgc     60
gcgatgggtg atgctgagag ctgcctgctc agacaacaga cacgcgaggt caggaagaag    120
ccgcttataa attaccgctt ccttcgcgcc gccgccaacg ccgagccccg aggaccgcaa    180
gcccagagga caagctgcgc caagagggag tgcggagcgt tcacccagcg ggggtcagcc    240
ctccacaagg cagtccgggc tctggggact ctgttttcta acctgaactt gtccgcctgt    300
cagtttgtca aaggatttgg gaggtgtact tctctgaaag tctttccaaa agtcctgaat    360
gataagaaac ttatccagaa ccagaaccac agcccttctg aggagctccc aaacccctgc    420
cggcttcgtg acctggagga gtcacagaac taccctgagc ctcaggtgag aaaactgggg    480
ctcaggaagg cagtgagaaa ctggaagtca gccacgtgtc aggacaggag cctggattta    540
gcccacatct ttggctttgg ttttgcacac agctgctgct gggagctggg ccagggcag     600
gcagaaataa tcctgggctc tgcagagcct gtttcaggct catggtctac cctaccccgc    660
ccccattttcc ggcaaaacca ggctgagggc tgggctgcta gcgaagctga cagcaagagt    720
gacagccctg tcctgtcgct gcaacaggaa aacaacccca aaaccccagc cttaagagca    780
agtccaacag tgcgcgactc cccaggtcag gagaagcccc gatgtgtgca gaatctgcag    840
atggggctgc tctcggccct gcctctggct gtggaaacag gcctccaagt acccaagagc    900
cgagcttctg ggtttgaatc cagctgtatg accctgggca gtggcttta cttctctggg    960
cctctttcca tcatccgggc tggtgaggaa attcactttc actacgacca gaatattttt   1020
gctcattgtt tcggctttgt tccgggcaaa acaatgcctg gcttcctgga tgacctcacc   1080
gggacaagcc atcagggctg taggccagcc tggtcagcat ctccgcacga gcccattctt   1140
ccctttgcca cggccacctt agtcaagccc ctgcttgtca ccggcctgcc tgggaccctt   1200
ggagcagccc tcctgtccca cgactttacc ccaaagagcc tctagtctg caccccctgtc   1260
tctgattcat cacccaacat ccatcaggtt ggcagctgta caaacagtc ccaggtctca   1320
gggctcaaca caaggaagag gcagccgctg ctgctggttg tcgtgtgtct ggtccagaga   1380
```

```
cactctaaac atcgtttaca caaatgggag cgtgtgatgc tgcccgcacc ccagattccc   1440
ttacatggag gccccgctgg ctatttcgca acacccactg gcattcactt agggcgctct   1500
gatctctcgc tgaagcaaac catgctggtg aactcccttg cctgtgtgtc atttcacatg   1560
tcggaaaaat cacctgaaag gaatggaaaa cttatgccta cacaaaaagt gcatgtggat   1620
gtctacagta gctttttcca taattgccaa aacctggaag caaccaagat gtccttcagc   1680
agcgccaagc tggaaacaac ccacacatct aacaacagga gactgggcaa atggcctggg   1740
gtagttttct acaagggaat atgtgacagc atgagagcga acgaaccaga gcaaaccaga   1800
cacaaccacc tgggtgaatc tcacagatgt gcagttgagc aacagcagcc aagcaccaag   1860
gggtgtttcc actactctgc agttcccagt gttggggaca gtggacaagt ctggtgttac   1920
catgaccttt tgggtttaaa atggcagcat agcccagtgg tcaagggcat agcttggtgc   1980
cagctgtgtc ctctcagtga gtcctcaact tcctcgttgc ttcagctgga agatgcagag   2040
gccaaagttc agcaagccga gggacctgcc ttgggtctcc cagctg              2086
```

```
<210> 224
<211> 942
<212> DNA
<213> Homo sapiens


<400> 224
atgggcaata agacttatgg aggacaaaat cagatgttga ttttttgcttt cactttgcat    60
tccctctttc ttaattctgg agatggcaga ttgtcctttg agagctcgtc ccagaagcca   120
gggggctttc gcaacattgc aatccaaact tcccccagtc tcaggaagca tttcccagtt   180
ttcaaaagga agagactcac agccagtaag tccgtggagg aaatgccaac agcctcccaa   240
agtgccatcc atgtcaacgg taacctctct gaacaggaca ttgtgtcttc tgaccttgcc   300
tacttaaggt tggctcagca tcttgaggat gggcctcgaa gggtcaaggt gtcccatgca   360
ttcctcccaa gggtccccaa ggtgcaaagc aatggtcctg ttagcatatg cttggaagca   420
ggaacttgga ggtccttaga gaaagccaca gctgccattc aggttccaga tgatatttat   480
cacagtcctt cctgggaagc tagagagtct gctctcagcc cagacaggtc agctgaacat   540
aacagcctca gcaggccatc tgaccctggg ctgtctctcc agcctcagct tctgcccact   600
ctttgtctcc cgttccatgt actctacacc aggagtcccc agtccctggg ccacgggccc   660
atagcagtcc atggcctgtt gggaaccatg ctgcgcagca ggaggacatg gagctttctg   720
tatcccgggt tcttgccttg gtgttctgga agaatcggat cacgtgtggg cttggagaat   780
gagtgcaagg tttcattgag tggaagtagc tctcagccaa tgggagagcc agaagggaga   840
tggtcttccc ctgaagttg accactcgcc agccccggct ctccctgat agcctgggcc   900
aaactccgct ttgtcccgcc tgtcgatgac ctgccagtgt ga                      942
```

```
<210> 225
<211> 1528
<212> DNA
<213> Homo sapiens


<400> 225
atggacagtc aagaagtaga gaaatacccc aacacttctg tagcttgtga ggaaatcccc    60
ttttcaggaa tccatgttgc tggtgggaaa tcaggagcat tagaacatgg aaaggatgac   120
cttgatgaac ccattgaaaa tcccctcttt tgtttctcaa gctttagcaa tgcacttgca   180
atattgcttc caaaagtgtt ccttaagaat attcatatac tgcaattcat ctacaggagt   240
tttcaccttt tgacaatggc aaaagcaaag tttgaaggtg ctgagtctgt ggagccagtg   300
tcaccttcac agcccaaaag gccatcctat gtccccctag aagagctatg gacgaggtta   360
acaaaaggga acagcaggcc tcagcagagg gacagggaga agggaggatg gatgaaggga   420
gtgcagcaag gccatcaagg agtaggaaag caggaggaag gttcagagaa catcaaagaa   480
aaagctggga ttgttgtctg tgaggtgcct aacaacaagt tagataaatt catgggaatc   540
ctttcttgga aagacagcaa gcattccctc aacaatgaga agataatcct gagaggctgc   600
atcctgagaa ataccagctg gtgtttggga atggttattt ttgcaggtcc tgacactaaa   660
ctaatgcaga atagtggtaa gacaaagttt aaaaggacaa gcattgatag attgatgaat   720
actctagtac tatggattat gctaatttct caaccagtgg tagaatttat catgagagga   780
cacagttatt ttataaactg ggaccggaag atgtattatt ctcgaaaagc aatacctgca   840
gtggctcgaa cgaccacgct caatgaggaa ctgggccaga ttgagtacat tttctccgac   900
aaaacgggta ccctcactca aaacatcatg acctttaaaa gatgttccat taatgggaga   960
```

```
atctatggtg aagtacatga tgacctggat cagaagacag aaataactca gttaatacat      1020
agatggctag ctagactaaa aaagaagaag agagagaaga atcaaacaga cacaataaaa      1080
aatgataaag ggaatatcac cactgacctc gcagaaacac aaactaccat cagagaatac      1140
tataaacacc tctacactaa taaactagaa aacctagaag aaatggataa attcctggat      1200
gcatacacct tatcaagact aaaaccagga gaagttgaat ccttgagtag accaataaca      1260
agctctgaaa ttgaggcagt aattaatagc ctaccaacca aaaaaagccc aggaccagac      1320
agattcacag ctgaattgta ccagaaatac aaggaggagc tggaaaaaga gcctgtggat      1380
ttctcagtca aatctcaagc ggatagagaa tttcagttct ttgaccacaa tctgatggaa      1440
tccattaaaa tgggtgatcc caaagttcat gaattcctta ggttacttgc tctctgccac      1500
actgtaatgt cagaagagaa tagcgcag                                         1528
```



```
         <210> 226
         <211> 515
         <212> DNA
         <213> Homo sapiens


         <400> 226
attcccgggt cgacgatttc gtctccttcc cccttccgga agctatagac acttccgaga       60
gagcgcgaac ttgcggagca ctttgcatgc gcgccgcggg taggactgga cggtcggatt      120
tgtaggcaat tctgacaccg agctcccggg ctcggttggc agaagatcgc tttgggaatc      180
ctcctactct acgaggacca gaaaccaagg acgccaagcc atacaaattc agcacagctg      240
actcagagag gtggaaagga aatcaggaca aaaagccaca atgtcttctg gaggaggata      300
ttgccagcca gaataactgt gagagatgca agcatagtcc tggaaacaaa cagcacaatt      360
cctttaaagc cctaaaggat gaagatcttc ctgtagagaa gtatttaatg gaaaggcagc      420
ctgtaggtga gccagctgcc gaccaggtag ctatggatgt gatgcacagc cccatcctcc      480
aactggaaag gaaacacaaa gtctcaagtg acagc                                  515
```



```
         <210> 227
         <211> 1023
         <212> DNA
         <213> Homo sapiens

         <220>
         <221> misc_feature
         <222> (1)...(1023)
         <223> n = a,t,c or g


         <400> 227
gtagtgtaca ttcttttta aatggaagag ctggttatag ccaacaacat cagcatcgac       60
atagtggaca tgaaagagaa gaggaaagag gagattggaa ctgggcaaac tattaaaatg      120
caaacagaaa acttgggtgt tgtttattat gtcaacaagg acttcaaaaa tgaatataaa      180
ggaatgttat tacaaaaggt agaaaagagt gtggaggaag attatgtgac taatattcga      240
aataactgct ggaaagaaag acaacaaang gcaattaggc aggagaagga aataaagggt      300
attcaattag gaaaagagga agtcaaattg tccctgtttg cagatgacat gattttatat      360
ctagaaaacc ccattgtctc agcccaaaat ctccttaagc tgataagcaa cttcagcaaa      420
gtctcaggat acaaaatcaa tgtacaaaaa tcacaagcat cttatacac taacaataga      480
caaacagaga gccaaatcat gagtgaactc ccattcacaa ttgcttcaaa gagaataaaa      540
tacctaggaa tccaacttac aagggatgtg aaggacctct tcaggagaa ctacaaacta      600
ctgctcaagg aaataaaaga ggatagaaac aaatggaaga acattccatg ctcatgggta      660
ggaagaatca atatggtgaa aatggccata ctgcccaagg taatttacgg attcaatgcc      720
atccccatca agctaccaat gatttttcttc acagaattgg aaaaaactac ttcaaagttc      780
atatggaacc aaaaaagagc ccacatcgcc aagtcaatcc taagccaaaa gaacaaagct      840
ggaggcatca caccacctga cttcaaactg tactacaagg ctacagtaac caaaacagca      900
tggactagaa aaatttattc agctaagaaa cgtaaagtca aaatttcagt ggaacctgtt      960
tacagcggtg tgacactaac tacagcaata cagcttgttc ctcttctgtg cacagctctg     1020
taa                                                                   1023
```

<210> 228
<211> 936
<212> DNA
<213> Homo sapiens

<400> 228
atggactacg agaaagcaga caagagacca actccttggg aagcagcagc aaagtctcct   60
ctcggtctag tggatgatgc tttccaaccc aaaaacatcc aggaatccat tgtggcaaat   120
gtggtttcag cagctcggag gaaggtgctt ccagggcctc cagaggattg gaatgaaaga   180
ctgtcctata ttcctcaaac ccagaaggcc tatatgggct catgtggaag gcaagagtat   240
aatgtcacag ccaataataa tatgtccacc acctcccaat atggttcaca gttgccatat   300
gcatattata ggcaggcttc aagaaatgat tctgcaatca tgtccatgga aaccaggcac   360
ttgtacactc gccagcttta ctgttacagc tttggagact ctggaaactt ctgtgaaaat   420
acaaatggca gacctgcagc agatgctgtc aggggcctga ctatcctctc actctccacc   480
acttccatac catccagtgg aataagtgag gctttgatat ctgaaaatga aaacaaaaac   540
ctcgagcatc tcacacatgg gggttatgtg gaaagtacca ccctgcagat tcgaccggcc   600
acaaagaccc agtgcacaga attcttcctc gccctgtca agactgaagt tcccctagct   660
gagaaccaaa gaagtggtcc cgactgtgca ggcagcttga agaagaaac aggcccgagc   720
taccaaaggg ctccccaaat gcctgactcc caaagaggac gcgtggcaga agagctgatc   780
ttaagggaga aagtagaagc gagtactcag aacaattact atgtaggtga gctgacaggt   840
gtaaccttac aaaaatggtta tggagaaaaa cccatccttg ctactcaagg tgaggctcac   900
agaccatcag caatggaatc acctggaggc ttgtga   936

<210> 229
<211> 1448
<212> DNA
<213> Homo sapiens

<400> 229
ttaactttgc aataatatgc agccagctaa ttgaaaattc tagtgccata aatgtttta   60
attgcttact atgtgtcagg cgttgtacta ggcactgggg aaaactgtaa ataaaagaga   120
cccagttcct tccttttttt caggttgcag tctatcagga aaggcagaca tttaaaaagg   180
gtcttgtgag gactgttatg aaacaggaag tacgagtgcc atttctatac cttagtacaa   240
tcactcgttt taattcacat cttccatggt ggcaagtttg cctcagtgtc agccggtcaa   300
ttgccactca aggggatcag aacatttatg tatctggaat gcttgaatat ttaagagaaa   360
acctttttgg ccgctttgat aatgataatt tttgtctatt gaatggtgat gctgtgattt   420
tcaggatgta tgtatcatgg aaactggtag agaaagaaag aactgagatc atgctgaagt   480
atactggggc ccaccaagag gtagagctga gtgcaccaat tgtcaccaaa atggcaaccc   540
aatatttaag agaaaacctt tttggccgct ttgataatga taattttgt ctattgaatg   600
gtgatgctgt gattttcagg atgtatgtat catggaaact ggtagagaaa gaagaactg   660
agatcatgct gaagtacact ggggcccacc aagagacttg gttaaaagac cttgaggaat   720
ccccccttta cgaagcctta tccatgagag gacaagataa ggagacccct ggtttgtgga   780
ttcagcttcc atggtgccct ggggtaaag ctgtccagat gcacatgaac ccctcctctt   840
ttcagctgga caccaagcca ggaaaaggag agcttgctgg ccgccttatc attccacacc   900
aggaagccag catccttgag ttgtccttac ttcttatgac ctgctgtgta gaaagagagg   960
ggaaaaccag tgtccgagtg gctgctgtgg gtgagtgcac agccagcgag acacccaatc   1020
agggagcagg aaggctgtcc ctgtggcagc agttaaccag taagaaagag accataatgg   1080
agaaagaaca cactgactgt gtttcacaga ctgttgccct catctccact tgtgttaaag   1140
aaggagggtc ccgacctgcg gataaagacc tagaggaagg gggaggcctt gaggcggagt   1200
cccccaagca gagccccaac ttgtgtgtga tcctgcgcca caacttggcc agccggcctg   1260
gacagctggc tctggttact gtgggaacaa tgcaaggaag gccgttgtca cattcctctg   1320
aggtcaaagg cacaaccttc gtcacacact cagtccctgc tggcaaagag aaagacgagg   1380
agcgtggaat cggagacctg gagcatgcga gggacttgag aaattcacca actcccttgt   1440
tttactga   1448

<210> 230
<211> 906

136

```
     <212> DNA
     <213> Homo sapiens


     <400> 230
atgagtgaac tcccattcac aattgcttcc aagagaataa aatacctagg aatccaactt       60
acaagggatg tgaaggactt cttcaaggag aactacaaac cactgctcaa tgaaataaaa      120
gaggaaacaa acaaatggaa gaacattcca tgctcatggg taggaagaat caatatcgtg      180
aaaatggcca tactgcccca gaggttgcct catggttttc tgccaaatat gaaacttgaa      240
gttgtggata aacggaaccc caggttaatt cgtgttgcta cgattgtaga tgttgatgac      300
caaagagtaa agcactcaat gacagccagc tcagggtctg gggtttcggc agatctcaac      360
acagccagcc agcccctatg gcttctgaaa actgcactgg ctgtgtcttc ctctgtcaaa      420
gtccatcccc ctgtgtcagg tttgatcttc agctcctcca gaaccctgct ttcctttatg      480
ggaattatga gagaagactt agggtttttcc aggaggcaga tcctccattt ccccatggct      540
ttgtccaaga gtgcaggaag aagatctaag attggtcaat tggatgctct ttcccaggac      600
tttggcttga gggacagaga ctctagcaag aagggaacag gttatcccaa tccagaaaat      660
ttttcctgga cagaatacct ggaagctact caaaccaatg cagttcctgc caaagttttt      720
aaaatggaca gtgatgttgg ggagaacaga aagattctcc gggatgaaag acctaattac      780
agtcagtata ctccatttag tagatgtgat aatgcatctt acaaagaaaa tgtgtttcta      840
caaaagctgg agagaaacac accagatatt gcagaaagat ttgactgttt attactgaca      900
tattag                                                                906



     <210> 231
     <211> 1117
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> misc_feature
     <222> (1)...(1117)
     <223> n = a,t,c or g


     <400> 231
ccatggaata gatgatgagt tggtcctctg cagagaaggg acccgaaggg cacaggcgaa       60
gggagtggcc aatgccagtg ggaagatgag ccatgaaacc agaatgggga gtccagaaaa      120
aaagagagaa aagagaaaag aagaaaagag acatgagagg agaggagagg tgagaaaaga      180
gagaagagag aaaagaaaag gagaagggag ggaaggatgt ccatatcttt tgcgaggagg      240
tacagcatac tctagagcac gggtcccccag tccccaggcc acgaaccggt acagctctga      300
agcaataact gccctccaac tgtttaatga gactcaagct cttatgcaag ctatagaatt      360
gtccaaaggc ctccggagag aagaaaccag atgcatgcag tctggtacca acacagcatc      420
caatgcaaca ctgttatact gtgcatcaga tcttgtgact cttgtggcag acattaccac      480
ttgccatgga tatccaagtt cccaatcctt gcaggaactc tgggaaaaag catcaccctc      540
aaatgtggac aagataatga gggccacaga gaacacagat gtgctgggtg ctccaaaagt      600
atgtgtgttt gtgattcaga atatacacaa tgggccagga gcagtggctt acgctggtaa      660
tcagagcttt gggaagcgaa gtttatcccc acataattta aggagtaatg ctctcctggc      720
agtggactca gaacctaaat tcccccttct taagccactt gagttttgcc ctggagtaag      780
catgacatca gggtgcttgc tgcttcctcc agtggcccga gctctgtgtg cctttgttga      840
acaaggtttt cgtggagctg aggtgactct catgaacaga gaatacctgt ccttcataca      900
gagaagcacc caaatgcaaa catctacttt ttctggtgtt caaccnagaa ttcttggagg      960
aggtagacta caggggatgg gctggttgac gattgacttt ctcctcaag catctaaacg     1020
tgccctaacg tcttccatta tggagctggg gccaggtgtc agcaaactgg ttcagtggca     1080
gctggagaac ctaaaaaggc attgtgggcc tctgtag                             1117



     <210> 232
     <211> 4707
     <212> DNA
     <213> Homo sapiens
```

```
    <400> 232
tcacaggcac ctgctgctgc tgctgctgcc tctgctcttg ccctcagtcc ccgtctttcc     60
acctgggtcc ccttgcactt tcatgcctga ggctgcactg gtggccaagt ctaaactgag    120
ggtcctcccg cagaccgaga gccgccgcag cgcctcggag gcggcctcca cgggcatgct    180
ggagcgctgt tccagcagca tctccagcag tgagctcatc tccgagacaa aggtgctggc    240
cagcctcgtg cctgttgggc tcagctctgg tgcctctgcc ttgccgaacg tctggaaggt    300
ccttggctcc tccgtggctg cagcatccgg ggagatcaca ttgtcacggt agttggtggt    360
gaggggcaaa gagagtctcg ccatccaggc cgggtcaggg gcgctcagcc ggtccagggc    420
cagacctgtg ctggggtcca gcagacttga cagctcttct tctagcagtt gcttcacaga    480
gaggtcctct tcaggatcca aaggcccttc ctcctgttct gggtctgtct ggcctccagc    540
ccttgcactt gggccatctg tgtctgggat tgcactcctg aggggtttta aggcgtagga    600
gtccttctgt ttgtttggtt ttgttcccct gtagccattt ctgctgctgc tgcctcctgg    660
cttggccaag tacttatttc ctcggtggtt tggtttgggc tggaattggc cctgatgcag    720
caaggacagc agctgggaga tttgctgaac aggaggagaa tccacagtga gctcctccac    780
gggggttccgc tcggcgaagg cagccacaga cagccggacc aggctccgca ggatctgacg    840
gggccctgat tctttctcag gggacacttt gccattgaga tgtcgctgcc gtctcagggt    900
tgcagaggag gctggtggcc tctgtggggc ttcctcactg ccctggtctc cagccagcct    960
ccctgtgggg ctgcctgcaa ccttcagagg cctgaacgt ggctggcctg tggcaggctg   1020
gggctcggga aggttcaggt tctcccggga ggcattcctc tgcctgggat ggttgaaaag   1080
gaggttgacc gtgtcttgca gcacctctcg gctctccgcc ggtgctccct ggttgccttg   1140
attacgcagc gtcctgtaca gggtcggggt gaggtggaag ggggcctgca ggcaggggtc   1200
ccagcctgct tccatcatcg cctccttgtc cacatctttg tgggactgcc cgacttcaca   1260
aggctcacct gcctgacccc tgagcacagg cacgaggtgg atgtctgcct tctgaatgtg   1320
tttctggggc ctcttgggct gctggcggta ggtggactcg gcctcccgac agttgtaggc   1380
cctgttgtcc ttctttctg tccggcagat ggacatgaac aaagccagga tcaacccgaa   1440
gatgcccaac agtacagcca ggcagatcac cgtcagcatc gacatgctca aggccccagg   1500
cttgcgggct gagtccctca ggtggtccac actggtgaca aacatgaccc tcaacagggc   1560
tcgggtctgt aaggggggggc ttccctggtc ctctactact atctccagct cccactcact   1620
cccaatgagg ctgctggcat tggtgacatt gacgaacagc tgccccgtat gagggttgag   1680
gatgaagagg tgggcttcat ttccactgcg gatgctgtag aggggctctc catttgcccc   1740
cgagtctgca tctcttgcca caatggttgt caaaaggaat ggccgggagc tgtgagtggc   1800
cagtggaggt gtgtcagtgc ccgctgggcc caagccattg ggagtctcga tgggcaccag   1860
caggtggcct gtggaggcat tcacaagcac ggagaggctg gcttttccat cgctgagcac   1920
aggctggacc acctctgggt cattatcatt ggcatccaag aggctgaccc acacagagac   1980
actggatgca agcatggctt gcccgctgtc ctctgcgatc acctggaact caaagccggc   2040
catctcttca tagttcagtg acctctgagc agtgacctct cctgtgttgg agtcaatagc   2100
tactaagtga gcaactgggg agtcctggat gcggtatgag actttccat taatgcccaa   2160
gtctgcatca tgagccttga tggtaatgag gtgaagagag ggtaagttgt tttcccgcgt   2220
ggagacttca tacctgcttt tctcaaacac aggtgcattg tcgttgatgt cactgatctg   2280
aatgctgagc tgtttcttgg ctgataaggg ctggagtcct tggtcttggg ctaacagagt   2340
gagggtatat ttgggccact gctctctgtc cagtgtggca ttggttagca acatgtatgt   2400
gttgccatta gttcttttca gcctgaagtg gcccagctct tggctcagcc agcagtggac   2460
caaaccattg tgtcctgaat ccaagtcatc tgccatgaca agagcaataa aactgtcctt   2520
gggaagagct tctgacacca gtgatggctg ggaggcccat gtgacgtgga tgcttgggat   2580
gttgtcattg acatccagaa ccttgatgag aactttgcaa tgggctggga taggattggg   2640
acccaggtcc cttgcctgaa catccacctc gtaggcaggg ttctttttcat agtctagagg   2700
tcgacgcaga atgacctggc ctgtcttggc atcaatactg aaggtgtcca gcacctctgg   2760
aggcatgtgc ttactgagga agaactccac ctccccattg gggccttggt cagggtctgt   2820
ggcggtcagt tttatgagaa gcgtaccagg tgcagcatct tcttggattt ccagtgccag   2880
tgaactctca gcaaacgcag ggctattgtc attggagtcc aagacgttga ccttgaccaa   2940
gctggtacct gacttggggg ggttcccatt gtcataggca gttaacacca gatcaaaaaa   3000
tgaatggatt tccctgtcca gctccttcac cactatgagt tctgcatgtt tggtctcatc   3060
agggcccaca atgacatcca aggcaaagtg ctcactgctg ctgctgctgc tgcctctgct   3120
cttgccctca gtccccgtct ttccacctgg gtccccttgc actttcatgc ctgaggctgc   3180
actggtggcc aagtctaaac tgagggtcct cccgcagacc gagagccgcc gcagcgcctc   3240
ggaggcggcc tccacgggca tgctggagcg ctgttccagc agcatctcca gcagtgagct   3300
catctccgag acaaaggtgc tggccagcct cgtgcctgtt gggctcagct ctggtgcctc   3360
tgccttgccg aacgtctgga aggtcctcgg ctcctccgtg gctgcagcat ccggggagat   3420
cacattgtca cggtagttgg tggtgagggg caaagagagt ctcgccatcc aggccgggtc   3480
aggggcgctc agccggtcca gggccagacc tgcctgaccc ctgagcacag gcacgaggtg   3540
gatgtctgcc ttctgaatgt gtttctgggg cctcttgggc tgctggcggt aggtggactc   3600
ggcctcccga cagttgtagg ccctgttgtc cttcttttct gtccggcaga tggacatgaa   3660
caaagccagg atcaacccga agatgcccaa cagtacagcc aggcagatca ccgtcagcat   3720
cgacatgctc aaggccccag gcttgcgggc tgagtccctc aggtggtcca cactggtgac   3780
```

```
aaacatgacc ctcaacaggg ctcgggtctg taagggggg cttccctggt cctctactac   3840
tatctccagc tcccactcac tcccaatgag gctgctggca ttggtgacat tgacgaacag   3900
ctgccccgta tgagggttga ggatgaagag gtgggcttca tttccattgc ggatgctgta   3960
gaggggctct ccatttgccc ccgagtctgc atctcttgcc acaatggttg tcaaaaggaa   4020
tggccgggag ctgtgagtgg ccagtggagg tgtgtcagtg cccgctgggc ccaagccatt   4080
gggagtctcg atgggcacca gcaggtggcc tgtggaggca ttcacaagca cggagaggct   4140
ggcttttcca tcgctgagca caggctggac cacctctggg gcattatcat tggcatccaa   4200
gaggctgacc cacacagaga cactggatgc aagcatgggt tgcccgctgt cctctgcgat   4260
cacctggaac tcaaagccgg ccatctcttc atagttcagt gacctctgag cagtgacctc   4320
tcctgtgttg gagtcaatag ctactaagtg agcaactggg gagtcctgga tgcggtatga   4380
gacttttcca ttaatgccca agtctgcatc atgagcttga tggtaatgag gtgaagagag   4440
ggtaagttgt tttcccgcgt ggaacttcat acctgcttgt cttttttttt gtctttctcg   4500
tgcgttggtg tgacccccc ccacttcctt cccgtacggg gtgtctgccg tcggagacg   4560
ctcctcactt cccagatggg ttgttgctag agcaggtgat tcaatcttcc ttaggtaatg   4620
ccgtggtcca aaggcgatcc cacgcagcac cacattaaga cgcgtttctg ccacaggcac   4680
aggttcgggt tgttttacct gttccat                                        4707
```

```
          <210> 233
          <211> 1287
          <212> DNA
          ·<213> Homo sapiens


          <400> 233
gcgtcgaccc acgcgtccgc aggaggaagg tgggtctgaa tctagcacca tgacggaact     60
agagacagcc atgggtttga tcatagacgt cttttcccga tattcgggca gcgagggcag    120
cacgcagacc ctgaccaagg gggagctcaa ggtgctgatg gagaaggagc taccaggctt    180
cctgcagctc tctggcccag ggctgggtca tcagcacacc ctgctgctgc tgttcagatc    240
tgcatcctgg tcccgcttgg tcccacagtg agaacgcttt gctatcacat gggcaggctc    300
tgagagccct gccggcctgg ccttctcaaa gaagacctga gagcttggga cccaagcaga    360
gaggaagaac agggctcagg gtgcttgctc catgctcgct ccacacctgg ggctcaaccc    420
tggctttccc cggctccctg tgtgacttca gggcaggtcc cttgggccct ctgggcctta    480
tcatcttcat ctgtaacagg gcgatgcctc tgccgtgtct ggtggtgttg aggagttcct    540
gtttgtgtaa gcagctagtt cagtgccagc acgagatggg aggcccatga agttagcagt    600
gcacaaaaaa tagagcaaag actggatgca tttcctgaga acaaccatca ctgtaaagca    660
ctttacaaat ccaaagacaa cccccggcaa aaactcaaaa tgaaactccc tctcgcagag    720
cacaattcca attcgctcta aaaacattac aagttagttc atgtcatgcc agatagctga    780
aggcagcttc acaagttctt aaggccagga atgccatgtg tctgctatgc acagctgggc    840
cctggccctt gaggcctgga atggacaggc aaaggttgac ggcagatgtt gggtgccctg    900
cttccttgcc ccagcagcag tgcttggtgg aggctgaggc cctgcacagg caccctcact    960
gctgaccttg agcctctctc tcctctaaag tgggaaaaac aagggaatcc gtggataaaa   1020
atggctcaag gacctgggac gccaatggag atgcccaggt gggacttcag tgagttcatc   1080
gtgtttcgtg ggctgcaatc acgtttgcc tgttcacaag tatttgaga aggcaggact    1140
caaatgatgc cctggagatg tcacagattc ctgggcagag ccatggtccc aggcttccca   1200
aaagtgtttg ttggcaatta ttccctagg ctgagcctgc tcatgtacct ctgattaata   1260
aatgcttatg aaatgaaaaa aaaaaaa                                        1287
```

```
          <210> 234
          <211> 2640
          <212> DNA
          <213> Homo sapiens


          <400> 234
atggtggaag gcaaggagga gcaagtcaca tcttacgtgg atgtccagag agcttgtgca     60
ggtattcgag gtgcctttga aaagccccag ggtgctgtgg ccagggttca cattggccaa    120
gtcatcatgt ccatctgcac caagctgcag aacaaggagc atgtgattga ggccctatgc    180
aaggccaact ttaagttccc tggccgccag aatatccact ctctcagagaa gtgggacttt    240
accaagttca gtgtggatga atttgaagac atgatggctg agaagcagct tatcccaata    300
actgtggggt caagtatacc cccaatcgtg accctccgga caagcgggat ggagtcgccc    360
```

```
tgcaacacgg gctgctccta tggcaactgc tacaaaacaa gatcaggctt caccagggtc    420
gggagaagaa acctcccaag aaagccaggc gctagagtca tgggtgtgga tgtcctttta    480
gggcctagga aagtagggtc tgatgaggag gcattgaaga aaagccagta tgacgacgat    540
gctttcatgt actcccccat ctgccaccaa ccacctatcc gtggtttcgc caccacccac    600
ctatccgtgg tttctccacc accctgcttc ctgggatgca gcaaccccca aacagatgca    660
gttttgggcc agcgttatgg aagagaaagc aaatccccca aatgtctgaa tcacaaacac    720
agagacctca cccccgtgac agtggaaaca aatgccctgg cctctgaccc ctacagatcc    780
gcgttcctgc ccctaaacgg tgcagtgagg ggagagctgg gctgcagaac aggtggagag    840
aagaacgtga agagcaaaag agagaagagg ggtgttaccc agagggtaga agctgcagca    900
gtccccgggc tggagctgct gaatgtctgg agacgtcccc actgctgggg agcggaagcc    960
aatcctgtgt ctccgctgga gcctcagatg cttctcgggc ccctgttgt atacagtcac   1020
tggtaccgct gccgctggag ccagaatttc gacatgacag ctcgccagtt tcacaatgca   1080
taccttcctt atcagagacc gttgatgatg gagatgctct ggccagtcta tagagaatgc   1140
acagaggatt ttcggtcctc tgcttcacct tctgatgtca gaaggctgaa aactccacac   1200
tcagattatg ctaatgctgc catttgtgta catgtgaccc atgaagagca actctcctct   1260
ggcgtgacag ccggcatgga ggatccacag agtaaagagc ctgccggcga ggccgtggct   1320
ctcgcgctgc tggagtcgcc gcggccggag ggcggggagg agccgccgcg tcccagtccc   1380
gaggtgagga gtcgacccgc gcctggctgt tggcgccagc tgccccgtcc ccaaagcgcc   1440
ctcggcaccc ctttcttctc aggtgtcccg cagaaggtgc agctgtgcgc ccttggaccc   1500
cagcctcttc ctcggtgccc agctccctgg ctttatcctc gggaaactca acagtgtaaa   1560
tttgatggcc aggagacaaa aggatccaag ttcattacct ccagtgcgag tgacttcagt   1620
gacccggttt acaaagagat tgccattacg aatggctgta ttaatagaat gagtaaggaa   1680
gaactcagag ctaagctttc agaattcaag cttgaaacta gaggagtaaa ggatgttcta   1740
aagaagagac tgaaaaacta ttataagaag cagaagctga tgctgaaaga gagcaatttt   1800
gctgacagtt attatgacta catttgtatt attgactttg aagccacttg tgaagaagga   1860
aacccacctg agtttgtaca tgaaataatt gaatttccgg ttgtttttact gaatacgcat   1920
actttagaaa tagaagacac gtttcagcag tatgtaagac cagagattaa cacacagctg   1980
tctgatttct gcatcagtct aactggaatt actcaggatc aggtagacag agctgatacc   2040
ttccctcagg tactaaaaaa agtaattgac tggatgaaat tgaaggaatt aggaacaaag   2100
tataaatact cacttttaac agatggttct tgggatatga gtaagttctt gaacattcag   2160
tgtcaactca gcaggctcaa ataccctcct tttgcgaaaa agtggatcaa tattcggaag   2220
tcatatggaa atttttacaa ggggggaacat ccgcatccaa gagacgcctg cagtccaggg   2280
ggctccagag ggagggagtc ctgtggatgt ggaagatacg cttttgtctg agagtcatga   2340
gattggactg tgggtccctg ttgttgttaa ccctgtgtg atcttgggca attcactgtt   2400
cctgtctta cctctacttg ctccctcagta agtcagagtg aactgagatc tcttcctgaa   2460
attacttagc ctaattctat ggttggtttc tggtggccag gaaccagaaa taaatctctc   2520
agcaaaattt tgcttatgga ccatgaatct tagagtatcc atggtatcac tgatatcttt   2580
aattcccaga tattttccag taatgaaatt catataataa agccaggatc aatggttctt   2640
```

```
        <210> 235
        <211> 426
        <212> DNA
        <213> Homo sapiens


        <400> 235
atgtctcgcc gcaagcaagg caaaccccag cacttaagca aacgggaatt ctcgcctcgg     60
gaccgcgagg aggtcaccac gtgctttccc tgcccacccc ccacccgcc cggtctggtc    120
accagtcccc ctgcgccccg agcacgacta ggccagcctt gttcagccag aaatgaaaac    180
ctcctcgaag cagattatga cccccagaa cccatcgtcc taagaaacac cactgccacg    240
cacactcact cacactcagt ctctccctcc ctgtataatt ctgattctcc ccagcctttg    300
aagcatcttg gagccgtgtc agctgcagag actggagtcc ggggcatgat ggggatgtac    360
ctgaaaccta gtgagagtcc attcctgact ctggggaaga gccgctcaaa gatggggatc    420
ctctag                                                              426


        <210> 236
        <211> 3204
        <212> DNA
        <213> Homo sapiens
```

```
<400> 236
atgtgcgaac tcgatatttt.acacgactct ctttaccaat tctgccccga attacactta    60
aaacgactca acagcttaac gttggcttgc cacgccttac ttgactgtaa aactctcact   120
cttaccgaac ttggccgtaa cctgccaacc aaagcgagaa caaaacataa catcaaacga   180
atcgaccgat tgttaggtaa tcgtcacctc cacaaagagc gactcgctgt ataccgttgg   240
catgctagct ttatctgttc gggcaatacg atgcccattg tacttgttga ctggtctgat   300
atccgtgagc aaaaacggct tatggtattg cgagcttcag tcgcactaca cggtcgttct   360
gttactcttt atgagaaagc gttcccgctt tcagagcaat gttcaaagaa agctcatgac   420
caatttctag ccgaccttgc gagcattcta ccgagtaaca ccacaccgct cattgtcagt   480
gatgctggct ttaaagtgcc atggtataaa tccgttgaga agctgggttg gtactggtta   540
agtcgagtaa gaggaaaagt acaatatgca gacctaggag cggaaaactg gaaacctatc   600
agcaacttac atgatatgtc atctagtcac tcaaagactt taggctataa gaggctgact   660
aaaagcaatc caatctcatg ccaaattcta ttgtataaat ctcgctctaa aggccgaaaa   720
aatcagcgct cgacacggac tcattgtcac cacccgtcac ctaaaatcta ctcagcgtcg   780
gcaaaggagc catggattct agcaactaac ttacctgttg aaattcgaac acccaaacaa   840
cttgttaata tctattcgaa gcgaatgcag attgaagaaa ccttccgaga cttgaaaagt   900
cctgcctacg gactaggcct acgccatagc cgaacgagca gctcagagcg ttttgatatc   960
atgctgctaa tcgccctgat gcttcaacta acatgttggc ttgcgggcgt tcatgctcag  1020
aaacaaggtt gggacaagca cttccaggct aacacagtca gaaatcgaaa cctcaaaatt  1080
tattcacaca tggttacgct ttggggaaat tatgagggga tctctcagac tcaagccttc  1140
gcgaaagaaa ataaccaaaa agcatacaaa gaaacgtacg gcgtctctca tattacacgc  1200
catgatatgc tgcagatccc taaacagcag caaaacgaaa aataccaagt gcctcaattc  1260
gatcaatcaa cgattaaaaa tattgagtct gcaaaaggac ttgatgtgtg ggacagctgg  1320
ccgctgcaaa acgctgacgg aacagtagct gaatacaacg gctatcacgt tgtgtttgct  1380
cttgcgggaa gcccgaaaga cgctgatgac acatcaatct acatgtttta tcaaaaggtc  1440
ggcgacaact caatcgacag ctggaaaaac gcgggccgtg tctttaaaga cagcgataag  1500
ttcgacgcca acgatccgat cctgaaagat cagacgcaag aatggtccgg ttctgcaacc  1560
tttacatctg acggaaaaat ccgtttattc tacactgact attccggtaa acattacggc  1620
aaacaaagcc tgacaacagc gcagaaagca taccggcttg aaattgtcag cttggaaatg  1680
cagaaaaatg gagccgcaga tgcagcaccg taccgacaaa ttgagtactg ggctctgggg  1740
catggtgacg acattaaaaa agctgttgcc ttctggtcct ctgggtggcc agtcggcttc  1800
tccaaaatgg agaaggcagg gaaaatactc aggtcccaag tgaagtttcc agaatatatg  1860
gaagaatcct cctgtctagg tagagggtca ctgatgtctc tcaacaacac aagttctagc  1920
aatggcagtt ttattttgt gttgcccctg aagttgctga gagttgggga cacctacaat  1980
tcttccgatc agtcaagaat ggcctggcgg ctcaccatag agtttgggg ttctgagttg  2040
catctggggg tgagggagga agcaggccac cagaaagggc tagtccatga gtccgggaat  2100
cccgcccgaa gctctggcag tgacccgcaa catgccaggc accggcagcc ctcggctacc  2160
agggctgctg ctgctgctgc tgctgctgct gctgctctgc ctgcgccgct gtcacttcca  2220
gttcctactt ctgcgatcca ggtccgggtc actgcttacc cgctgctggc ccagtgcctc  2280
caggccgctt tccctccgct gctcggctcc ggctgcgggc aggaggggac cggcgcggga  2340
ggcggcggcg gcgcggctgg agtgagggag cagctggagg acaggcgggc agcggccgag  2400
ccaggtgacc tgcctggggg caaaagggtc aggggaaggg gagcgcgcga gggcccgggg  2460
gtgggtgccg aaggaccccc tttggagagg aaccgccctt cttccccact gccgtggctc  2520
gcagccccag ctgcgggggc ctcacagttc gctgagatcc agggtgccgg gaaggggag  2580
atgagggcca aggacgcaga gcgaggacgc gccaaactta ggggcgagtt gtccagctct  2640
ggccgcaaga tatttgatcc tgatgacctt tattcagggg tcaatttctc caaggtactg  2700
agtactcttt tagctgtcaa caaagcaaca gaagatcagc tatcagaaag accatgtgga  2760
cgttcctctt ctcttagtgc tgctaatact tctcagacaa acccacaggg agcagtttct  2820
agcacagttt cagggctgca aaggcagtca aagacagtgg agatgacgga aaatggaagt  2880
catcagttga tagtaaaagc aagattcaac tttaagcaga ctaatgagga tgaactgtca  2940
gtttgtaagg gggacatcat ttacgtcaca cgagttgaag aaggaggctg tgggaaggc  3000
acattaaatg ggagaacagg ctggttcccc agtaattatg tccgtgaaat taaatccagt  3060
gagagacctc tctccccaaa agccgtcaaa ggatttgaaa ctgctccact taccaagaat  3120
tattatactg tgatgtctag aagtcttaca tctactgtgc tgaaaaattc aaaggtagca  3180
cggattcaca gcaagcccta ttaa                                         3204
```

<210> 237
<211> 1353
<212> DNA
<213> Homo sapiens

```
<220>
<221> misc_feature
<222> (1)...(1353)
<223> n = a,t,c or g


    <400> 237
tcatgcagca gaagaggaag agtgtgcaag cagaaaatgg aagtcctgtg atactgagga      60
gtcagaggta tctggagctg tcacagcagc tagaatatga ggagaaaaat tcttgcagta     120
tcctgtgcca ttgtggtagg taacacacat tccttcattt acacagggtt catagccatc     180
tcgacactgc aatgctgtaa acccgacttg acaggtgcac tcataggtat cccggctgag     240
catatggcat gtgccgccat tcaggcaggg tcgagacaca aagcatggat gagatgttga     300
gtactggcag tcctctcctg taaaccctga ggcacatcgg cacgtggctt tccccagcat     360
ggcctgggcc acacaagtcc caccattctg gcagcggttc ttctcacagg ggtctcgatg     420
ttgacaatat tcccccaaga agccttctgg acatcttatc agaatccctg ggtgctgagt     480
ccaagatcca ccccaacaga tttttgatgta gccaggacac agagtttttt ctaccataat     540
gggagaggta gggaggagga tcacatgcgc gggggccgcc cagcacagcc angacggcca     600
gcagcgccca cagcagagcg ggacgcaggg ggggcatctt ctcggtcgcc tcctcctcct     660
ccgccgccgc cgccgccgcc gccgccgcct gggcagatcc acatggggag ggggtcccga     720
tagaggagcc ccactctctc ctcccctcct cctgcttcaa aggctcaggc cctggcgcta     780
cgctccgaag cccaggcgca aatgcctcga ctcccgcgc cccgagtccg ccgctcctcg     840
gccgccgcct cagccgccgc ccgaagtttg gctgaaactt tctcgggtaa ggagtgccaa     900
tggacggatg cctgcctgtc tcatccctgt gcaaatggaa gtacctgtac cactgtggcc     960
aaccagttct cctgcaaatg cctcacaggc ttcacagggc agaaatgtga gactgatgtc    1020
aatgagtgtg acattccagg acactgccag catggtggca cctgcctcaa cctgcctggt    1080
tcctaccagt gccagtgcct tcagggcttc acaggccagt actgtgacag cctgtatgtg    1140
ccctgtgcac cctcgccttg tgtcaatgga ggcacctgtc ggcagactgg tgacttcact    1200
tttgagtgca actgccttcc agaaacagtg agaagaggaa cagagctctg ggaaagagac    1260
agggaagtct ggaatggaaa agaacccgat gagaattaga ccctggaaaa tatgtatgtg    1320
tggttaataa agtgctttaa actgaattga aaa                                 1353



    <210> 238
    <211> 362
    <212> DNA
    <213> Homo sapiens



    <400> 238
gaaaagagtt gttgactttc agggagccca aacctagggc ctccccaagc cagggttgtg      60
agacctttga ggctctatgg ttcctagcat ttccaagctt ctgggcacaa ctgcattacc     120
cggtacccat agtggaagcc acttgcagta tgcctggtcc agctgcagcc tcacacagag     180
ctagcaccta tgttagcact tggagttgcc cacctcacca cagctggcat gcctggcagt     240
gcacagtggc cagacctcac ttgcagacct ctcattgctg cacatctggc ttgcccttgg     300
cagacatgga atccaggctg gttgcttcac caagtgagtg gaacaagctc acttgggccc     360
ag                                                                     362



    <210> 239
    <211> 1350
    <212> DNA
    <213> Homo sapiens



    <400> 239
tcactgaaag agagagctac tcaaatccaa atccaaaacg cttccaccag cattctcttt      60
tcccaataag ccacaggcag aacagccatg gcctacagaa agcagccaaa tgcctgcagc     120
tgtgagcagg tgtaagatgg ctgtaagggc catccctcca tctccagagg cttccggagc     180
cttggagccg tggatggcaa gcagacactg ataccggatg agctgtgtga tcatgggcac     240
atcacgtctc tgaaccttgg tgttcttcct gtgagatggg ccattaacac caggcacctc     300
ataggatgga tgtgaagact tccaggctgt tgacaccagg ctcagattac tttgtctatt     360
aattcctggt aaacagtact ttctagtact gccaaagatg cttacagttc ccttcttgct     420
```

```
catatgaaca ccaaaatagg tgttcctgaa gggcagaggc tgttctccaa gcagcgtctg    480
aagcaccagg ctagttccat cttctggctt caccatttcc aacacagagt tcccaaggtc    540
agtaagttcg tctgcatgga ggcaatagca agagaagaag agagcgagaa gactcacttg    600
ctccttaacc acttctgcct ggaagtgatg cgtatcactt ctgcttacac tccactggca    660
aggacccatc acatggtccc atctactctt ctccatggag aaccagatgg cccaggtatg    720
agtggttgag gggctggtgc cccgatgagg tgggggcaaa gatgacctct ctccagggtg    780
atgtgaggaa atggagctcc ggaaggtaag aggcttgctc cccatcacac agctggcgtg    840
cgtggccaag agcagggcct cgctgtgttt tctgggctgt ctccaccgca gtgctgactc    900
tcctcctcct acttgccact gataggcctg gacttgcaca atttcaatct caccaaaaat    960
cacattcaat tcagtgaccc tgattatctt cagtgtgtgt gtgtgttttt ctataggctc   1020
attacgatca ctaggtccca caataggctc aataggctct ctgcaagtgg tcacagtaaa   1080
agcaagttga taaaggtggc cagtggggga acagagctta tgtgcctcct gagaaagcca   1140
gtcgctggaa actggactga gagccctgat ttggagcacg aggaaacctg gtgggcctgt   1200
gctgggtggc ctggtgttga taaaatgggc ttgggccagc cgctcaccag cttctccctc   1260
agacccatcc ccaggcccca acctctgctg cagccctacc agccccgcca caaagcccag   1320
ggtggacgga cccttcgtca tcagaaacat                                     1350
```

```
        <210> 240
        <211> 618
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 240
atgaattggg tgttacaaaa atttatcact gcatggaagt ttatgggcta cagaaagtcc     60
tccaacagcg caagaggaag caccataaaa gagcacattg agttggatgc acagagacct    120
gtcaggagaa gtgggccaat acaagcatca ggcgctcatc ccaagaaggg aaggggtgtg    180
agttgctcag tggaagagcc aagtgaccag cagagtccgt caccaccctc ccctcttacc    240
tttcagccca aagacggaga aatcaacttt tcagtaattg gtcagtatgt ggattatctt    300
gtgaaagaac agggagtgaa gaacatttt ggtaagtcaa ctctggggat gtcgctgcat    360
gtctccagct cagtctttag aaggtatatc ttacctggtt accagccaag aggtcacaca    420
gtcatggtgt cacaggtaaa cattgacttc cagacccgag aagccacgga gaagaacctg    480
caggagccat ccctgacttg ctttgaccaa gcccaaggaa aagtacacag cctcatggag    540
aaagactctt accccaggtt cctgaggtcc aaaatgtact tagatctgct gtcccaaagc    600
cagaggaggc tcagttag                                                  618
```

```
        <210> 241
        <211> 669
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 241
atggtgatgt cattcgtcaa gccaggagta aaggagaagg agcaggttaa gaagagagat     60
ggtgagttca attctgaaca tgcagaattg gatgtgcctg ccagggacac caagaggaaa    120
ttctggggagc ccaccaggct cagcagtacc ctgcggacat cgagcgaccc tttattttct    180
gtccccatca gcattacgat ggtttgtgag ccaggctcca agtccctgca aagctgctgt    240
ctgacagcag ggggcgccaa tgtctgggaa aaatctacct gccgcaaaaa atccagacaa    300
ttggtgctga ggaatgtaaa ggttccaggg aaaagcccat gtggtgaact gctgcccatc    360
ctcaaaaaaa accagttaaa catccttctc ttgcaaccag tggacacaga gactttggaa    420
gggcctccag gccttggcct ggatgcagag ggccctgaga agagacacag ctggatcctc    480
ctgccctgcc ctgggattga ccacacctct ggcttggagg ttatgtctga tctttatcac    540
aggaagggaa actcgctcca tccccaagga aagagaacca aggatgccag aaaggaaagc    600
ttcccccaga agatgggaca atttcccctta caaagtctgg cagtcatcta ccccgaagca    660
gggacctag                                                            669
```

```
        <210> 242
        <211> 2043
```

143

```
      <212> DNA
      <213> Homo sapiens


         <400> 242
atggaagaac attccatgct catgggtagg aagaatcaat atcgtgaaaa tggccgtatt     60
gcccaagaat tggaaaaaac tactttaaag ttcatatgga accaaaaaag agcctgcatc    120
accaagtcaa acctaagcca aaagaacaaa gctgaggca tcacgctacc tgacttcaaa    180
ctatactaca aggctacagt aaccaaaaca gcatggtact ggtaccaaaa cagagatata    240
gatcaatgga acagaacaga gccctcagaa ataatgccgc atatctacaa ctatctgatc    300
tttgacaaac ctgagaaaaa caagcaatgg ggaaaggatt ccctatttaa taaacggttc    360
tgggaaaact ggctagccat atttagaaag ctgaaactgg atcccttcct tacaccttat    420
acaaaaatta attcaagatg gattaaagac ttacatgtta gacctaaaac cataaaaacc    480
ctagaagaaa acccaggcat taccattcag gacacaggca tgggcaagga cttcacgtct    540
aaaacaccaa aagcaatggc aacaaaagcc aaaattgata aatgggatct aattaaacta    600
aagagcttct gcacagcaaa agaaactacc atcagagtga acaggcaacc tacaaaatgg    660
gagaaaattt tcgcaaccta ctcatctgac aaagggctaa catccagaat ctacaatgaa    720
ctcaaacaaa ttcacaagaa aaaaacaaac aaccccatca gaaagtgggc gaaggatatg    780
aacagacact tctcaaaaga agacatttat gcagccaaaa aacacatgaa aaaatgctca    840
ccatcactgg ccatcagaga aatgcaaatc aaaaccacaa tgagatacca tctcacatca    900
gttagaatgg caatcattca aaagtcagga aacaacagag ttttacccct tgcacctctg    960
gctctggctg ccctctggat ggatcctgtg atgccaggca tggatggcct gctaggggac   1020
tcagagagct tccagggcct ttctgctact ttctttgcct ctgtatttca ctcagctctc   1080
cacattgact cagctccagg gccctgcatc ggccctggag actcctctgc tgattcctct   1140
ccaacatttc ttcctccaga agccaaaagg aaaaactacc tcctcctttg gaggaaaaac   1200
ctaaaaaagt tctcagatga ccccaaaagg ctcatagagg gcttccccaa attggctctt   1260
acatttagat taatttggaa ggacataaat gtactcctgg gacaagccct tttacaagag   1320
gaaagacaga ccatctgcgg agcagcaatc cactgtcgaa atgacttaca cctggaaaat   1380
gccaactacc ctggaggggc tacagctgtt ccccagctgg accccaatca ggactacaat   1440
gccaaagcgg gaatatgggc caggaaccat aggctcttgt gtctaataga gacaacgacg   1500
caacaaccga ccaacgcaca cagtccacaa acacaacgac aacaacacga cacagacaaa   1560
ccacaaccga acccaccagc caaaacaacc ggtgttcctg tatcttttct ggcttttcta   1620
tatcagtatc tgtgtgggca catatccata agctggcccg tggtaattct taagtacgct   1680
gcgagcgtct atggtatttc tctagcagac cgtaagcgac aatatgacag atactttcga   1740
tatgaacgtt tacgcaccat aaagcctaat ttcttgccat tccaaatatt taagtctggg   1800
agtgtggtaa agctaaaagc tggcttcaca atcggaaaag ttcacaatac agaagtaaca   1860
gctttaaagg tttctgacac tcgaagagcg cagcatttgc agacaggatg ttggagtgca   1920
gttgtgaccc acccaaacaa cttggaaaat gtagtacggc atccgccaga ggctctggct   1980
gcttcttaca acaaaccctt catctgctcc ctggtcacac ttcaaggtgc atttgtgact   2040
tag                                                               . 2043



      <210> 243
      <211> 1116
      <212> DNA
      <213> Homo sapiens


         <400> 243
atgctcatgg tctatccccg gaccaacaag cagaatcaga agaagaaatg gaaagtggag     60
cccccacac cgcaggagcc tgggcctgcc aaggtggctg ttaccaccag cagcagcagc    120
agcagcagca tccccagtgc tgagaaagtc cccaccacca gtccacact ctggcaggaa    180
gaaatgagga ccaaggacca gccagatggc agcagtctga gtccagctca gagtcccagc    240
cagagccagc ctcctgctgc cagctcccctg cgggaacctg ggctggagag caaagaagag    300
gagagcgcca tgagtagcga ccgcatggac tgtggccgca tccccagcac ccccaaccac    360
aggaggtccc aggtgattga aaagtttgag gccttggaca ttgagaaggc agagcacatg    420
gagaccaatg cagtggggcc ctcgccatcc agtgacacac gccagggccg cagcgagaaa    480
agggcgttcc ctagcaagca ggacttcacc aatgaagccc ccccaagc tcctctccca    540
gacgcctcgg cttcccccgt ctccacaccg aagagccaag tcactggaca ggagggtcag    600
aacatatcct gggatatggc ggtagtcctg aaagcaactc aggaggcacc tgctgcttca    660
acccttggca gctactcatt accaggact ctggccagga gtgagatact ggagactcat    720
gggaccatga actttctaga cagcagtcct caggtccgtt accatccaag gaatcttggg    780
acagcctgta accaggcggg actcgaccgc tactacccgg aaggcccact gcctaggagc    840
```

```
ggggacgaca cagtgctgtc accacggcca gcctggtcca agctagcagc tacgaggagt      900
cagagactgg acccaagaca aaggggcagc actgaacgag agaaagggga ggcccacaac      960
gaccccttgg ctgccgcgcc catctcagca gcgggcagcc gcagaggagc cctggcctcc     1020
tggcttgcgt ctcccacacg ctcccagaac ccggcccgac cccccacgcc agactgtaga     1080
gcacccctca ccgaaagcgc cagacccaca tcttga                              1116
```

```
        <210> 244
        <211> 413
        <212> DNA
        <213> Homo sapiens


        <400> 244
atggggaagt gggatggagg ttttaatttc atggtctttt gtgttttgga aaatacctgc       60
agtttgaaca ggtctttgct ggaaaacctc atctttgcta cactcaagat cagctggggt      120
ggtgcaggga ttaagggctg gaatcatatg aaggctcagt tgctcacatg tgtggtgttt      180
gatgctggct ttcagttaag tccacagggt tctctagagc aaaaagcacct catcctttac      240
cctgaactca caggacctat agagttggac ccaatttgtt accaccacca tctttcaaat      300
ctgctctcac aaacacccaa agcatccttt gaagtttttac accagaatca ctgaaaagca      360
tccagcagat tttctactgg cagctttcaa ggagcagctg tagctgaaaa gac            413
```

```
        <210> 245
        <211> 975
        <212> DNA
        <213> Homo sapiens


        <400> 245
cccatatggg ccaccagatg ttacgggggg tggagggggt ctttgttctt agagctccca       60
agatgcgacg ggccgctctc aagatggggg tgggctgctc ccaagatggc tgcaagcctt      120
ttgttctctg accaggggtt cttggcctca tggattccaa ggaatggaac cttgggccat      180
gcgatgagtg gtatagctct attagaagct gtgggtcatg aagagaact gtggaaccca       240
gcgactagtg ctgcttctgt tatctcaaat acatcatcag atgccaatca atttccaaag      300
ttaccattag gagaaatcag tccagataaa gaaaaatctt actggtcaag taatccaact     ·360
aaaaacaatc ccaaagagac aacacgcgtg gctgttttttg cgagaatttt ggatgttaat      420
gacaatgccc cacactttgc tgtgttctat gacactttttg tatgtgaaaa tgccagacca      480
gggcagaggg atgcctgtgg aaggcttggt gattgggact cagagaaaca ggaagggaga      540
aaaggtttca cctccacgaa ttcagtcatt ctacataaaa aaagaacaaa aaggagtgtg      600
ttgggagggg acaagttttg gcaaaaaaaa tctccagaaa gtccacaagg ggacttccag      660
gacagtagga gcctcaggtc cacagtgaag tttcacaagt ccacaaggaa gttgcaaggg      720
gaagtggaaa agagcagtgt tgccagaaat tatggatttg atcctcttta atgcctgtga      780
agatacacaa aaacatgaaa tttctttttca atatttttgg gctgaaccac ttgggtggtg      840
gctgaaatga gaccatacat acagcacaat gcatgtctgt tatattgcaa agtgtattac      900
ctaggtctca tacatccccc tagtcatcag cattaatgca tgttgggacc ccgacccaca      960
caagcagaag taatg                                                      975
```

```
        <210> 246
        <211> 349
        <212> DNA
        <213> Homo sapiens


        <400> 246
gcccacgcaa tcattgattt cccttggtgg cccattgtcc cagggctgtc tggagcatga       60
ggccagcagt gcctacgaat ggctgtggag tctttgcgcg ctgcttgaca tgtacactgc      120
cgggccgacc aagacgcaga cgctccagcc catgggccaa cctaacctga aaggagatgg      180
aggcttcacc agagaatcaa ccggtttcat gcaacttcct gctgacttca tctccagcct      240
catttgtcat gaaacatggg ttccaggaaa gcccagtact gctatgcaca gaggccgata      300
```

```
ctgggcagag ccgattatgc ttccaaaggg tagcggcttt cggaaggag                    349
```

```
        <210> 247
        <211> 431
        <212> DNA
        <213> Homo sapiens


        <400> 247
caatgtcgga gaaaaatacc cctcttgttt tgagtggaga aaatcagaag aaagggagag        60
agatcggggt gtgccgaaag caaagccaat gtgatcatca agataataat agccatacat       120
taagattcag ctcctactcc tcctcctctg gtccagtcac tctggtctcc ttccattccc       180
acaactatcc aagcaaagtc ctgcttcagg gaaatttgga cacagagaca tgtacagaga       240
gaagacaaag agaaatttgg acacagagac atgaagggaa atgtggacac agagacatgt       300
acagagagaa gacgaagaga aaatacagag agaaggccat ctacaagcta agaaaaggac       360
ctgaaacaga tccttcctca cagccctcgg aaagaaccaa ccctgccaac accttgatct       420
cagactccta g                                                            431
```

```
        <210> 248
        <211> 1272
        <212> DNA
        <213> Homo sapiens


        <400> 248
atgaacaata agctggagac agggcagggg cggcgaggcg gggaggcgtt tatggcatac        60
gccaccgcag gtgaagcatc tggaacctgg gcatccaggc aacaggctcg caaggcccag       120
attcaggggc agccacctgc gccaggctgg gacctgacac agggtgagca ggctgggaaa       180
ttcaccagca ctgcggacag agcaggggat aacagcagca tcagaaagac ccataaggcc       240
ataggtttgc agagggaatg cagtccctca gcaaggagct tcagtcggac taaaccagca       300
gaaaaggcgg tttccgagta ccatgctcgc acaacaggga gccgccgacc aggcctggag       360
atccctgtga cagtcacggc aggactgggg ctgcaggagt gcagagccag gtacaggcct       420
gggaagccct catctcaccg cgaggacagt cgcgtgcgac aggcctgtaa ggtggcatcc       480
gagtccctcc cgcaattaag gacgccgggc tccaggccag cgccagggac agacccagca       540
ccagggcggc ccccggagcc ggcctctggc ggcctcgggt cttttgccaa attccccacc       600
ggcgccagga taccgagggg ccacccccac cacgcggctc caacagacac gtttcccaca       660
ctggctgcgg aggcccgccg gacgggggc cccgtgctga ccgcagccgc ggagcccgca       720
gcgcacatcc cggagcacag gacaaaacct gtgcctgcac cggagccccc atccggctcc       780
cgcaacactg accccctgg gcagcctcgg gcacggggca cctggaaagc cagccccgga       840
caccgcgcgg attctgcctc ccggagagct tccttcctgt tccgatgttt ggcgaacctg       900
cagcgctccc tgaagcagat gagagggaag ctgcactccc agaaagcgca gttttggttc       960
atattgaatg gatttattgg gggtgtcatc ggcaggcgga tgacagattg tcaggcctgt      1020
gaacctaggc taagaagcat ccagtgtcaa ctacctgaat cttacaccag cctttgccac      1080
ccagcagcac tgacccaaag tggacccaag aatgtccttg aaagagacca accatctgcc      1140
tgcagcctca agacacctgc tcagacctgc ctgcctcagt gctccctaca ctggacatta      1200
agagacgatc agacgcagcc actcacagcc ccgagcagta caatgaatgg agcctatcgc      1260
atgaaatgct ga                                                          1272
```

```
        <210> 249
        <211> 380
        <212> DNA
        <213> Homo sapiens


        <400> 249
gctccttctc cctggcctca atcatcttgg ccaatttcca agacagtaca gcacttgcta        60
ggaacagtgg agtaagggcc aaaataacgg ttgtaaggaa gccatagggg tcctttgcag       120
cccattccac aacatactca gcccaagcct ttaaaactgg ggcttatgct tgagtagtga       180
```

```
tcccttaact ttgtcctggt gttattagtg acccaatcac gacttcagat gacccttggt    240
agtctgtctt cttgagttct actgtacaca tctgagagac ggtttaaatt ctgtacaatt    300
ggcctatcgg ggctgcagac ccacggaggc cacgttcact cctgcccgtc ggccttggca    360
agcgcgggcc ccttgtcgcg                                                380
```

```
        <210> 250
        <211> 560
        <212> DNA
        <213> Homo sapiens


        <400> 250
ctacaaatag agggatctgt ttccgtcact cgcgccctaa cgcaaagggt gggacaaccc     60
gcgcgcatgc gtcgttgtcc tctgctctcc agggtaaacc ccgccccttt ctttaggcca    120
gttttaccac agcacatgcg cagtacagga tctgtctgtt cgtttgtcgg cgctaccaat    180
aaagttttag tgagcacaga ctcccttttc tttggcaaga tggcggagta cgacttgact    240
actcgcatcg cgcacttttt ggatcggcat ctagtctttc cgcttcttga atttctctct    300
gtaaaggagg tgaggggtc tttgggcgca aggaaggcgt gggggcggat gaggtgctga    360
gcaaggccga aaggtggtgt ctgtagtcct aggcctgaca cgtgcgaggc ggtcgcgagt    420
ttggttcctg gacggacact aaggatcttc tggtagttta gcgtcgtctc agttaagaag    480
caccgcaaaa tgcagttagc tctctgttct gcatctgtgg attcagccaa ctgcagattg    540
aaaatattca gggaaagaaa                                                560
```

```
        <210> 251
        <211> 1092
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(1092)
        <223> n = a,t,c or g


        <400> 251
cagtacgacg tttaaacacg gccatgcaag caaaattacc ccactaaagg aataagttcg     60
gcccatcttt ttttttttt ttttgctgct ggaacgtttt attaagttaa gaggttcagg    120
gagcagaaga gaaacacctt ttgggtggct tctggcggtt ctgcacccaa gcacagcctc    180
gaaggaggct gtgggccat ggaggcccag ctgctagctc cctctgtcct gagccccatg    240
gtacgggtcc aaatggggca ggaagtgtta gtaggaggta gggcaggaag agggtgngca    300
ggctcccgcc tctccctgt agagacaccg ccgccatggc ttgctgcctg ggcctccgcc    360
agacctctgg gccagggcca ccagctcaga agcccaagca cagcggtggc tggagacaga    420
ggggaccag ggttggaggc acacagccac caggaattgc ttttttttt ttttttttta    480
aagtataaag tgttttggaa aaaaaggaaa aaatctata taaaaatctc ttcacatata    540
aaatcctgaa gaaggtgcaa ggtgagaccc cagntgcgag gggcgcgcat cagatatgca    600
gtgtgtgtgt gtgtgtgtgt gtgtgtgtat ccgtgtgtac atgtgtgcac gtgtgtgcgt    660
atgtgtctgt gtgtctgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgg tgggtgcaag    720
tgcacgtgtg gcccaacaga gggtgggggag aaagcttggc tttttacttc catccaggag    780
ggaaggaggt gcggctggtc ctccagcctg agagggtctg cagctgggcg ggacctctac    840
tcagccaggc tgtttgcgca tcgactcctt ctcctggagg gccggccatg gcaagacgca    900
ggtgctcctt cagctgctcg aatctcccgc tcagagccgt ggtcttgatg gtggctcagc    960
tccacataga acgtcctggt actttcccga ggtgaagcgc ttgtccttct gcatcatctg   1020
gagctcgtcc cggaggcacc tgccctactt tcttaagtac tggagttccg tttctttaa   1080
ccgaaaccac ac                                                      1092
```

```
        <210> 252
        <211> 246
        <212> PRT
```

<213> Homo sapiens

<400> 252

```
Arg Gln Ser Ser Gly Asn Leu Thr Met Ala Trp Thr Pro Leu Leu Leu
1               5                   10                  15
Pro Leu Leu Thr Phe Cys Thr Val Ser Glu Ala Ser Tyr Glu Leu Thr
            20                  25                  30
Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Thr Ile Thr
        35                  40                  45
Cys Ser Gly Asp Ala Leu Pro Lys Lys His Pro Tyr Trp Tyr Gln Gln
    50                  55                  60
Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg
65                  70                  75                  80
Pro Ser Gly Ile Pro Glu Arg Phe Ser Ala Ser Ser Ser Gly Thr Met
            85                  90                  95
Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr
            100                 105                 110
Tyr Cys Tyr Ser Thr Asp Ser Ser Gly Asn His Arg Gly Val Phe Gly
        115                 120                 125
Gly Gly Thr Arg Leu Thr Val Leu Ser Gln Pro Lys Ala Ala Pro Ser
    130                 135                 140
Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
145                 150                 155                 160
Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
            165                 170                 175
Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
            180                 185                 190
Thr Pro Gly Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
    195                 200                 205
Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln
    210                 215                 220
Val Thr His Glu Gly Ser Thr Val Glu Glu Thr Gly Ala Pro Thr Glu
225                 230                 235                 240
Tyr Leu Leu Arg Val Tyr
            245
```


<210> 253
<211> 539
<212> PRT
<213> Homo sapiens

<400> 253

```
Met Glu Lys Gly Ser Gly Phe Ile Lys Tyr Ser Thr Tyr Lys Gln Gly
1               5                   10                  15
Thr Ile Arg Val Ala Glu Glu Ala Glu Thr Ala His Ser Ser Val Leu
            20                  25                  30
Ile Gly Pro Glu Lys Gly Val Val His Leu Ala Thr Ala Ala Val Leu
        35                  40                  45
Asn Ala Val Trp Asp Leu Trp Ala Lys Gln Glu Gly Lys Val Leu Ala
    50                  55                  60
Val Gly Arg Glu Leu Gln Glu Glu Glu Lys Glu Glu Thr Gly Trp Arg
65                  70                  75                  80
Lys Ala Gln Ala Ala Val Glu Gly Gly Val Gly Thr Trp Trp Leu Thr
            85                  90                  95
Ala Ser Ile Arg Ala Ala Asn Ala Phe Thr Val Arg Lys Lys Trp Gly
            100                 105                 110
Leu Tyr Thr Tyr Val Leu Gln Ile Leu Ser Phe Leu Leu Gln Ala Cys
        115                 120                 125
Leu Glu Val Thr Cys Gly His Asp Leu Ile Met Gly Cys Ile Lys Ser
    130                 135                 140
```

```
Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro
145                 150                 155                 160
Glu Pro Val Ser Thr Ser Val Ser His Tyr Gly Ala Glu Pro Thr Thr
            165                 170                 175
Val Ser Pro Cys Pro Ser Ser Ser Ala Lys Gly Thr Ala Val Asn Phe
            180                 185                 190
Ser Ser Leu Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro
            195                 200                 205
Phe Gly Gly Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro
    210                 215                 220
Ala Gly Leu Thr Gly Gly Val Thr Ile Phe Val Ala Leu Tyr Asp Tyr
225                 230                 235                 240
Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe Lys Lys Gly Glu Arg Phe
            245                 250                 255
Gln Ile Ile Asn Asn Thr Pro Met Val Leu Asn Leu Gly Gln Asn His
            260                 265                 270
Pro Gly Asp Ile Trp Gln Tyr Leu Glu Thr Phe Leu Val Val Thr Val
    275                 280                 285
Gly Val Leu Pro Leu Ser Ser Ser Ala Ser Thr Pro Val Phe Asp Arg
    290                 295                 300
Val Thr Asn Gly Val Thr Pro Thr Ile Lys Asp Leu Thr Gly Cys Cys
305                 310                 315                 320
Val Glu Asn Arg Leu Leu Thr Ser Asn Ser Ser Asp Phe Phe Thr Leu
            325                 330                 335
Ile Asn His Ser Asn Ser Ser Lys Thr Pro Phe Gln Asn Thr Arg Leu
            340                 345                 350
Val Val Ser Arg Gly Asn Ser Ser Glu Lys Gln Phe Ala Ile Arg Phe
    355                 360                 365
Gln Asp Gly Lys Thr Asp His Ala Ile Gln Leu Ser Ser Gly Lys Lys
    370                 375                 380
Thr Ala Leu Gly Arg Glu Ala Leu Glu His Pro Glu Ser Leu Asp Ser
385                 390                 395                 400
Arg Lys Val Gly Gln Arg Ser Arg Trp Ser Ser Gln Ala Ala Ser Pro
            405                 410                 415
Ile Ser Gly Pro Ile Gln Ala Glu Thr Ala Leu Leu Cys Pro Gly Asp
            420                 425                 430
Gln Trp Thr Gln Glu Phe His Thr Ser Pro Leu Leu Thr Val Pro His
            435                 440                 445
Leu Pro Asp Ile Tyr Thr Leu Asp Cys Cys Arg Lys Asp Phe Ser Ile
    450                 455                 460
Tyr Ile His Ser Phe Gly Asp Ile Thr Gln Ser Tyr Ile Phe Lys Tyr
465                 470                 475                 480
His Leu Gln Ile Asp Asp Tyr Gln Leu Cys Ala Gln Ala Leu Lys Asp
            485                 490                 495
Gly Trp Thr Arg Pro Pro Pro Phe His Thr Ala His Leu His Phe Ser
            500                 505                 510
Leu Leu Thr Leu Ala Cys Ala Glu Thr Val Thr Ser Ala Glu Thr Pro
            515                 520                 525
Asp Ala Leu Ala Lys Ser Arg Phe Lys Val Lys
    530                 535
```

```
<210> 254
<211> 236
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(236)
<223> Xaa = X or * as defined in Table 6
```

<400> 254

```
Gly Thr Arg Asp Ala Thr Ala Glu Glu Asn Arg Val Leu Leu Ala Met
1               5                   10                  15
Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro Leu
            20                  25                  30
Gly Arg Val Ser Phe Glu Val Arg Gly Leu Asp Thr Lys Lys Xaa Leu
        35                  40                  45
Leu Ile Xaa Ser Ile Lys Leu Cys Xaa Gln Ile Gly Gly Ser Ser Ile
        50                  55                  60
Phe Ile Thr Ser Asp Xaa Lys Asn Ser Cys Leu Pro Leu Ile Val Gln
65                  70                  75                  80
Gln Cys Leu Leu Phe Leu Arg Ile Leu Pro Leu Phe Ala Asp Lys Val
            85                  90                  95
Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly
            100                 105                 110
Phe Gly Leu Xaa Gly Val Pro Cys Phe His Arg Ile Ile Pro Gly Phe
        115                 120                 125
Met Cys Gln Gly Gly Asp Cys Glu Arg His His Asn Gly Thr Gly Gly
130                 135                 140
Lys Ser Ile Tyr Thr Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys
145                 150                 155                 160
Ala Tyr Gly Val Leu Gly Ser Leu Ser Met Ala Asn Ala Gly Pro Asn
            165                 170                 175
Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu
            180                 185                 190
Asp Gly Lys Pro Val Val Phe Gly Lys Val Lys Glu Gly Met Asn Ile
        195                 200                 205
Val Glu Ala Met Glu Arg Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys
210                 215                     220
Lys Ile Ile Ser Ile Ala Asp Cys Gly Gln Leu Glu
225                 230                 235
```

<210> 255
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(105)
<223> Xaa = X or * as defined in Table 6

<400> 255

```
Ile Cys His Gln Pro Thr Ser Leu Ser His Gln Xaa Glu Arg Asn Gly
1               5                   10                  15
Trp Pro Gly Arg Trp His Ser Gln Pro Arg Ser Lys Phe Cys Arg Leu
            20                  25                  30
Arg Val Leu Ser Gln Gly Asp His Glu Lys Lys Ser Leu Pro Ser Gly
        35                  40                  45
Gln Arg Pro His Arg Thr Gly Cys Ala Ser Ser Ser Gly Ser Ser Lys
    50                  55                  60
Gly Leu Leu Leu Leu Pro Leu Asp Gly Leu Gly Val Ile Val Leu Ile
65                  70                  75                  80
Asn Pro His Leu Val Val Phe Pro Gly Met Arg Ala Pro Xaa Leu Leu
            85                  90                  95
Pro Arg Leu Trp Leu Arg Arg Trp Ser
            100                 105
```

<210> 256

```
        <211> 128
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(128)
        <223> Xaa = X or * as defined in Table 6


        <400> 256
Val Arg Asp Tyr Asn Leu Thr Glu Glu Gln Lys Ala Ile Lys Ala Lys
 1               5                  10                  15
Tyr Pro Pro Val Asn Arg Lys Tyr Glu Tyr Leu Asp His Thr Ala Asp
            20                  25                  30
Val Gln Trp Ile Val Leu His Arg Ala Xaa Ile Tyr Phe Phe Arg Leu
        35                  40                  45
His Ala Trp Gly Asp Thr Leu Glu Glu Ala Phe Glu Gln Cys Ala Met
    50                  55                  60
Ala Met Phe Gly Tyr Met Thr Asp Thr Gly Thr Val Glu Pro Leu Gln
65                  70                  75                  80
Thr Val Glu Val Glu Thr Gln Gly Trp Gly Glu Glu Phe Ser Leu Ser
                85                  90                  95
Lys His Pro Gln Gly Thr Glu Val Lys Ala Ile Thr Tyr Ser Ala Met
           100                 105                 110
Gln Val Tyr Asn Glu Glu Asn Pro Glu Val Phe Val Ile Ile Asp Ile
           115                 120                 125



        <210> 257
        <211> 111
        <212> PRT
        <213> Homo sapiens


        <400> 257
Val Thr Ser Ser Cys Pro Arg Lys Lys Arg Arg Phe Gly Gly Asp Arg
 1               5                  10                  15
Pro Ser Ser Ser Phe Ser Pro Pro Ser Lys Glu Leu Leu Ala Val Lys
            20                  25                  30
Ala Pro Arg Glu Gly Arg Arg Gly Pro Gly Asn Glu Ser Arg Ser Glu
        35                  40                  45
Pro Ser Gln Pro Leu Asp Ser His Gly Pro Gly Leu Arg Arg Thr Phe
    50                  55                  60
Leu Pro Pro Ser Pro Arg His Pro Thr Lys Asp Arg Arg Thr Ala Ala
65                  70                  75                  80
Arg Ser Gly Pro Arg Arg Lys Arg Gly Gln Thr Asn Glu Ile Arg Gly
                85                  90                  95
Cys Lys Glu Glu Glu Gly Glu Lys Tyr Leu Val Pro Ala Gln Gly
           100                 105                 110



        <210> 258
        <211> 224
        <212> PRT
        <213> Homo sapiens


        <400> 258
Phe Tyr Phe Val Pro Ser Gln Glu Ser Val Pro Ser Ala Ser Pro Thr
```

```
     1                   5                   10                  15
Gly Ile Pro Lys His Ser Leu Arg Lys Thr Thr Ser Thr Glu Glu Pro
             20                  25                  30
Arg Gly Thr His Ser Gln Gly Gln Phe Thr Met Pro Leu Ala Gly Met
         35                  40                  45
Ser Leu Gly Ser Leu Lys Ser Glu Phe Val Pro Leu Phe Ser Ala Thr
     50                  55                  60
Pro Phe Trp Val Pro Phe Ser Ser Leu Pro Leu Phe Pro Trp Val Leu
65                  70                  75                  80
Val Glu Asp His Val Cys Leu Leu Asp Cys Val Val Val Asp Leu Gln
                 85                  90                  95
Asp Met Asp Ile Phe Ala Ala Glu Arg His Pro Arg Asp Tyr Ser Lys
            100                 105                 110
Ala Pro Glu Asp Ser Ser Gly Asp Leu Ile Phe Pro Ser Tyr Phe Val
        115                 120                 125
Arg Gln Thr Gly Gly Ser Leu Leu Thr Glu Pro Cys Arg Leu Lys Leu
    130                 135                 140
Gln Val Glu Arg Asn Leu Asp Lys Glu Ile Ser His Thr Val Pro Asp
145                 150                 155                 160
Ile Ser Ile His Gly Asn Leu Ser Ser Val His Cys Ser Leu Asp Leu
                165                 170                 175
Tyr Lys Tyr Lys Leu Ile Arg Gly Leu Leu Glu Asn Asn Leu Gly Glu
            180                 185                 190
Pro Ile Glu Glu Phe Met Arg Pro Tyr Asp Leu Gln Arg Ser Lys Asn
        195                 200                 205
Ser Tyr Cys Pro Glu Trp Arg Ser Val His Leu Tyr Val Leu Pro His
    210                 215                 220
```

```
<210> 259
<211> 164
<212> PRT
<213> Homo sapiens
```

```
<400> 259
Met Ile Val Asn Leu Phe Asn Met Phe Ile Thr Tyr Gly Asp Thr Phe
1                   5                   10                  15
Leu Pro Thr Pro Ser Ser Tyr Asp Glu Leu Tyr Tyr Glu Ile Ile Arg
             20                  25                  30
Met His Gln Ser Phe Asp Asn Leu Tyr Ser Met Val Leu Arg Leu Ser
         35                  40                  45
Thr Asn Ala Gly Gln Trp Lys Glu Ala Ala Ser Lys Val Thr His Ala
     50                  55                  60
Leu Val Asn Ile Arg Ala Ile Ile Asn His Phe Asn Pro Lys Ile Glu
65                  70                  75                  80
Ser Tyr Ala Ala Val Asn His Ile Ser Gln Leu Ser Glu Glu Gln Val
                 85                  90                  95
Leu Glu Val Val Arg Ala Asn Tyr Asp Thr Leu Thr Leu Lys Leu Gln
            100                 105                 110
Asp Gly Leu Asp Gln Tyr Glu Arg Tyr Ser Glu Gln His Lys Glu Ala
        115                 120                 125
Ala Phe Phe Lys Glu Leu Val Arg Ser Ile Ser Thr Asn Val Arg Arg
    130                 135                 140
Asn Leu Ala Phe His Thr Leu Ser Gln Glu Val Leu Leu Lys Glu Phe
145                 150                 155                 160
Ser Thr Ile Ser
```

```
<210> 260
<211> 815
<212> PRT
<213> Homo sapiens


<400> 260
Met Thr Pro Gly Gln Leu Ser Asn Val Arg Ala Pro Gly Ser Ala Glu
 1               5                  10                  15
Lys Gly Ser Gly Asp Thr Gly Asp Ala Arg Pro Pro Ser Ala Ala Pro
                20                  25                  30
Pro Gly Gly Ser Ala Gly Glu Ala Arg Thr Ala Gly Ala Arg Tyr Leu
            35                  40                  45
Cys Pro Arg Ser Ser Leu Ser Gly Gly Ala Ala Ala Thr Arg Thr Cys
        50                  55                  60
Gly Leu Ala Asn Pro Glu Glu Glu Gly Pro Ser Ala Lys Cys Gly Glu
65                  70                  75                  80
Asn Gly Ser Ala Glu Arg Thr Asp Leu Gly Gly Asn Lys Tyr Asn Gln
                85                  90                  95
Glu Arg Ile Gln Ile Glu Tyr Val Glu Val Leu Phe Ala Asp Phe Phe
            100                 105                 110
Arg Glu Val Phe Ala Ile Cys Gly Ser Cys Asp Ala Leu Gly Asn Trp
        115                 120                 125
Asn Pro Gln Asn Ala Val Ala Leu Leu Pro Glu Asn Asp Thr Gly Glu
    130                 135                 140
Ser Met Leu Trp Lys Ala Thr Ile Val Leu Ser Arg Gly Val Ser Val
145                 150                 155                 160
Gln Tyr Arg Tyr Phe Lys Gly Tyr Phe Leu Glu Pro Lys Glu Asn Ile
                165                 170                 175
His His Arg Gly Asp Phe Leu Val Thr Phe Pro Ser Ser Ser Arg Ser
            180                 185                 190
Ser Phe Val Gln Thr Gly Gln Phe Ser Gly Arg Asp Ile Asp Lys Asp
        195                 200                 205
Pro Lys Leu Ser Pro Val Gly Arg Gly Trp Gly Phe Glu Trp Ala Ile
    210                 215                 220
Glu Leu Cys Met Ala Val Lys Glu Asp Val Arg Gln Glu Val Gly Ser
225                 230                 235                 240
His Ile Gly Leu Leu Pro Asp Val Ala Met Ala Phe Val Asn Cys Arg
                245                 250                 255
Gly Thr Asp Gly Ser Val Ala Val Arg Met Thr Arg Gly His Ser His
            260                 265                 270
Cys His Leu Gly Phe Ala Tyr Cys Ala Ser Gly Phe Ser Leu Glu Pro
        275                 280                 285
Cys Val Glu Asn Asp Cys Gly Ala Ser Ser Ala Glu Val Gln Gln Gly
    290                 295                 300
Phe Val Phe Ile Thr Ser Ala Ser Ser Ser Ser Tyr Cys Thr Glu
305                 310                 315                 320
Ala Lys Arg Val Lys Leu Thr Leu Glu Gly Leu Glu Glu Asp Asp Asp
                325                 330                 335
Asp Arg Val Ser Pro Thr Val Leu His Lys Met Ser Asn Ser Leu Glu
            340                 345                 350
Ile Ser Leu Ile Ser Asp Asn Glu Phe Lys Cys Arg His Ser Gln Pro
        355                 360                 365
Glu Cys Gly Tyr Gly Leu Gln Pro Asp Arg Trp Thr Glu Tyr Ser Ile
    370                 375                 380
Gln Thr Met Glu Pro Asp Asn Leu Glu Leu Ile Phe Asp Phe Phe Glu
385                 390                 395                 400
Glu Asp Leu Ser Glu His Val Val Gln Gly Asp Ala Leu Pro Gly His
            405                 410                 415
Val Gly Thr Ala Cys Leu Leu Ser Ser Thr Ile Ala Glu Ser Gly Lys
            420                 425                 430
Ser Ala Gly Ile Leu Thr Leu Pro Ile Met Ser Arg Asn Ser Arg Lys
        435                 440                 445
Thr Ile Gly Lys Val Arg Val Asp Tyr Ile Ile Ile Lys Pro Leu Pro
```

```
        450                    455                      460
Gly Tyr Ser Cys Asp Met Lys Ser Ser Phe Ser Lys Tyr Trp Lys Pro
465                     470                    475                  480
Arg Ile Pro Leu Asp Val Gly His Arg Gly Ala Gly Asn Ser Thr Thr
                    485             490                    495
Thr Ala Gln Leu Ala Lys Val Gln Glu Asn Thr Ile Ala Ser Leu Arg
                500                     505                    510
Asn Ala Ala Ser His Gly Ala Ala Phe Val Glu Phe Asp Val His Leu
            515                     520                    525
Ser Lys Asp Phe Val Pro Val Val Tyr His Asp Leu Thr Cys Cys Leu
        530                     535                    540
Thr Met Lys Lys Lys Phe Asp Ala Asp Pro Val Glu Leu Phe Glu Ile
545                     550                    555                  560
Pro Val Lys Glu Leu Thr Phe Asp Gln Leu Gln Leu Leu Lys Leu Thr
                565                     570                    575
His Val Thr Ala Leu Lys Ser Lys Asp Arg Lys Glu Ser Val Val Gln
            580                     585                    590
Glu Glu Asn Ser Phe Ser Glu Asn Gln Pro Phe Pro Ser Leu Lys Met
        595                     600                    605
Asp Gly Met Trp Asp Gly Asn Leu Ser Thr Tyr Phe Asp Met Asn Leu
        610                     615                    620
Phe Leu Asp Ile Ile Leu Lys Thr Val Leu Glu Asn Ser Gly Lys Arg
625                     630                    635                  640
Arg Ile Val Phe Ser Ser Phe Asp Ala Asp Ile Cys Thr Met Val Arg
                645                     650                    655
Gln Lys Gln Asn Lys Tyr Pro Ile Leu Phe Leu Thr Gln Gly Lys Ser
            660                     665                    670
Glu Ile Tyr Pro Glu Leu Met Asp Leu Arg Ser Arg Thr Thr Pro Ile
        675                     680                    685
Ala Met Ser Phe Ala Gln Phe Glu Asn Leu Leu Gly Ile Asn Val His
        690                     695                    700
Thr Glu Asp Leu Leu Arg Asn Pro Ser Tyr Ile Gln Glu Ala Lys Ala
705                     710                    715                  720
Lys Gly Leu Val Ile Phe Cys Trp Gly Asp Asp Thr Asn Asp Pro Glu
                725                     730                    735
Asn Arg Arg Lys Leu Lys Glu Leu Gly Val Asn Gly Leu Ile Tyr Asp
            740                     745                    750
Arg Ile Tyr Asp Trp Met Pro Glu Gln Pro Asn Ile Phe Gln Val Glu
        755                     760           ,        765
Gln Leu Glu Arg Leu Lys Gln Glu Leu Pro Glu Leu Lys Ser Cys Leu
        770                     775                    780
Cys Pro Thr Val Ser Arg Phe Val Pro Ser Ser Leu Cys Gly Glu Ser
785                     790                    795                  800
Asp Ile His Val Asp Ala Asn Gly Ile Asp Asn Val Glu Asn Ala
                805             810       .            815
```

```
        <210> 261
        <211> 1083
        <212> PRT
        <213> Homo sapiens


        <400> 261
Met Glu Pro Ile Glu Gly Lys Arg Ser Ser Cys His Lys Thr Gly Glu
 1               5                    10                    15
Ala Thr Ala Val Val His Cys Pro Pro Gly Trp Asn Ile Thr Met Gly
                20                    25                    30
Val Glu Ala Ser Cys Ala Phe Val Gly Arg Ala Gly Ser Gln Asp Thr
            35                    40                    45
Val Arg Thr Gly Arg Ala Leu Lys Ala Leu Thr Gln Leu Arg Ala Ala
        50                    55                    60
Gln Gly Arg Gly Ser Gln Gly Ala Ala Ala Ala Glu Thr Gly Leu Gly
```

154

```
     65                      70                      75                      80
Gly Arg Arg Leu Arg Arg Ala Pro Gly Gly Gly Pro Cys Val Gly Pro
                 85                      90                      95
Arg Ala Ala Ala Ala Thr Thr Leu Ser Gly Pro Arg Gly Thr Ala Gln
             100                     105                     110
Gly His Gly Gly Gly Arg Ser Ser Gly Lys Gly Asp Gln Arg Ala
             115                     120                     125
His Glu Leu Ala Ala Trp Ile Pro Arg Ala Thr Arg Ala Arg His Thr
    130                     135                     140
Gly Ala Ala Gly Ala Glu Pro Tyr Tyr Arg Ala Trp Gly Ser Gly Glu
145                     150                     155                     160
Gln Gly Arg Gly Val Cys Arg Gly Leu Leu Arg Leu Pro Ala Gly Pro
                 165                     170                     175
Pro Thr Pro Gly Arg Ala Arg Ala Leu Ala Glu Arg Leu Ser Pro Pro
             180                     185                     190
Arg Ala Ala Pro Arg Gln Asp Ser Trp Pro Leu Arg Gly Phe Leu Pro
             195                     200                     205
Pro Pro Gln Pro Leu Asn Pro Thr Ser Ala Ser Pro His Pro Arg Leu
    210                     215                     220
Phe Ser Leu Leu Gly Ala Arg Pro Ile Ser Pro Trp Thr Met Ala Ala
225                     230                     235                     240
Thr Ile Gln Ala Met Glu Arg Lys Ile Glu Ser Gln Ala Ala His Leu
             245                     250                     255
Leu Ser Leu Glu Gly Gln Thr Gly Met Ala Glu Lys Lys Leu Ala Asp
             260                     265                     270
Cys Glu Lys Thr Ala Val Glu Phe Gly Asn Gln Leu Glu Gly Lys Trp
         275                     280                     285
Ala Val Leu Gly Thr Leu Leu Gln Glu Tyr Gly Leu Leu Gln Arg Arg
    290                     295                     300
Leu Glu Asn Val Glu Asn Leu Leu His Asn Arg Asn Phe Trp Ile Leu
305                     310                     315                     320
Arg Leu Pro Pro Gly Ser Lys Gly Glu Ser Pro Lys Val Ala Leu Gly
                 325                     330                     335
Arg Pro Gly Val Gly Glu Ala Ala Ala Lys Pro Val Ser Val Trp Phe
             340                     345                     350
Ser Glu Gln Val Trp Gly Lys Leu Glu Asp Trp Gln Lys Glu Leu Cys
         355                     360                     365
Lys His Val Met Arg Gly Asn Cys Glu Met Leu Val Ser Leu Asp Tyr
    370                     375                     380
Ala Ile Ser Lys Ser Glu Val Leu Ser Gln Ile Glu Gln Gly Lys Glu
385                     390                     395                     400
Pro Cys Asn Trp Arg Arg Pro Gly Pro Lys Ile Pro Asp Val Pro Val
             405                     410                     415
Asp Pro Ser Pro Ala Pro Val Pro Leu Pro Leu Phe Cys Ser Leu Tyr
             420                     425                     430
Pro Pro Gly Glu Ile His Gln Cys Ser Val Pro Ala Ala Lys Gln Leu
         435                     440                     445
His Val Val Gln Arg Thr Ser Pro Val Thr Ala Lys Leu Ser Thr Leu
    450                     455                     460
Gln Pro Lys Pro His Phe His Leu Val Leu His Pro Thr Pro Cys Gln
465                     470                     475                     480
Leu Leu Lys Gly Asn Thr Val Asn Pro Thr Leu Thr Ser Thr Pro Thr
             485                     490                     495
Ala Thr Ala Cys Phe Ser Ala Pro Leu Arg Gly Arg Ala Pro Trp Ile
         500                     505                     510
Tyr Thr Met Glu Gly Asn Arg Leu Asn Gln Cys Phe Gln Thr Gly Cys
         515                     520                     525
Trp Arg Ala Pro Gly His Ile Gln Ala Gly Glu Glu Ala Pro Gly Ser
    530                     535                     540
Arg Val Val Phe Thr Arg Ile Thr Gly Ser Gly Glu Cys Arg Arg Gly
545                     550                     555                     560
Pro Glu Lys Ser Cys Gly Phe Gly His Ser Arg Glu Ala Leu Gly Glu
                 565                     570                     575
Glu Trp Met Ile Arg Lys Val Lys Val Glu Asp Glu Asp Gln Glu Ala
```

155

```
                580                        585                        590
Glu Glu Glu Val Glu Trp Pro Gln His Leu Ser Leu Leu Pro Ser Pro
        595                        600                        605
Phe Pro Ala Pro Asp Leu Gly His Leu Ala Ala Ala Tyr Lys Leu Glu
        610                        615                        620
Pro Gly Ala Pro Gly Ala Leu Ser Gly Leu Ala Leu Ser Gly Trp Gly
625                        630                        635                        640
Pro Met Pro Glu Lys Pro Tyr Gly Cys Gly Glu Cys Glu Arg Arg Phe
                645                        650                        655
Arg Asp Gln Leu Thr Leu Arg Leu His Gln Arg Leu His Arg Gly Glu
                660                        665                        670
Gly Pro Cys Ala Cys Pro Asp Cys Gly Arg Ser Phe Thr Gln Arg Ala
        675                        680                        685
His Met Leu Leu His Gln Arg Ser His Arg Gly Glu Arg Pro Phe Pro
        690                        695                        700
Cys Ser Glu Cys Asp Lys Arg Phe Ser Lys Lys Ala His Leu Thr Arg
705                        710                        715                        720
His Leu Arg Thr His Thr Gly Glu Arg Pro Tyr Pro Cys Ala Glu Cys
                725                        730                        735
Gly Lys Arg Phe Ser Gln Lys Ile His Leu Gly Ser His Gln Lys Thr
                740                        745                        750
His Thr Gly Glu Arg Pro Phe Pro Cys Thr Glu Cys Glu Lys Arg Phe
        755                        760                        765
Arg Lys Lys Thr His Leu Ile Arg His Gln Arg Ile His Thr Gly Glu
        770                        775                        780
Arg Pro Tyr Gln Cys Ala Gln Cys Ala Arg Ser Phe Thr His Lys Gln
785                        790                        795                        800
His Leu Val Arg His Gln Arg Val His Gln Thr Ala Gly Pro Ala Arg
                805                        810                        815
Pro Ser Pro Asp Ser Ser Ala Ser Pro His Ser Thr Ala Pro Ser Pro
                820                        825                        830
Thr Pro Ser Phe Pro Gly Pro Lys Pro Phe Ala Cys Ser Asp Cys Gly
        835                        840                        845
Leu Ser Phe Gly Trp Lys Lys Asn Leu Ala Thr His Gln Cys Leu His
.       850                        855                        860
Arg Ser Glu Gly Arg Pro Phe Gly Cys Asp Glu Cys Ala Leu Gly Ala
865                        870                        875                        880
Thr Val Asp Ala Pro Ala Ala Lys Pro Leu Ala Ser Ala Pro Gly Gly
                885                        890                        895
Pro Gly Cys Gly Pro Gly Ser Asp Pro Val Val Pro Gln Arg Ala Pro
                900                        905                        910
Ser Gly Glu Arg Ser Phe Phe Cys Pro Asp Cys Gly Arg Gly Phe Ser
        915                        920                        925
His Gly Gln His Leu Ala Arg His Pro Arg Val His Thr Gly Glu Arg
        930                        935                        940
Pro Phe Ala Cys Thr Gln Cys Asp Arg Arg Phe Gly Ser Arg Pro Asn
945                        950                        955                        960
Leu Val Ala His Ser Arg Ala His Ser Gly Ala Arg Pro Phe Ala Cys
                965                        970                        975
Ala Gln Cys Gly Arg Arg Phe Ser Arg Lys Ser His Leu Gly Arg His
        980                        985                        990
Gln Ala Val His Thr Gly Ser Arg Pro His Ala Cys Ala Val Cys Ala
        995                        1000                       1005
Arg Ser Ser Phe Ser Ser Lys Thr Asn Leu Val Arg His Gln Gly Ile
        1010                       1015                       1020
His Thr Gly Ser Arg Pro Phe Ser Cys Pro Gln Cys Gly Lys Ser Phe
1025                       1030                       1035                       1040
Ser Arg Lys Thr His Leu Val Arg His Gln Leu Ile His Gly Glu Ala
                1045                       1050                       1055
Ala His Ala Ala Pro Asp Ala Ala Leu Ala Ala Pro Ala Trp Ser Ala
        1060                       1065                       1070
Pro Pro Glu Val Ala Pro Pro Pro Leu Phe Phe
        1075                       1080
```

```
<210> 262
<211> 738
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(738)
<223> Xaa = X or * as defined in Table 6


<400> 262
Ile Thr Met Gly Ser Ser Gly Leu Gly Lys Ala Ala Thr Leu Asp Glu
1               5                   10                  15
Leu Leu Cys Thr Cys Ile Glu Met Phe Asp Asp Asn Gly Glu Leu Asp
                20                  25                  30
Asn Ser Tyr Leu Pro Arg Ile Val Leu Leu Met His Arg Trp Tyr Leu
        35                  40                  45
Ser Ser Thr Glu Leu Ala Glu Lys Leu Leu Cys Met Tyr Arg Asn Ala
    50                  55                  60
Thr Gly Glu Ser Cys Asn Glu Phe Arg Leu Lys Ile Cys Tyr Phe Met
65                  70                  75                  80
Arg Tyr Trp Ile Leu Lys Phe Pro Ala Glu Phe Asn Leu Asp Leu Gly
                85                  90                  95
Leu Ile Arg Met Thr Glu Glu Phe Arg Glu Val Ala Ser Gln Leu Gly
            100                 105                 110
Tyr Glu Lys His Val Ser Leu Ile Asp Ile Ser Ser Ile Pro Ser Tyr
        115                 120                 125
Asp Trp Met Arg Arg Val Thr Gln Arg Lys Lys Val Ser Lys Lys Gly
    130                 135                 140
Lys Ala Cys Leu Leu Phe Asp His Leu Glu Pro Ile Glu Leu Ala Glu
145                 150                 155                 160
His Leu Thr Phe Leu Glu His Lys Ser Phe Arg Arg Ile Ser Phe Thr
                165                 170                 175
Asp Tyr Gln Ser Tyr Val Ile His Gly Cys Leu Glu Asn Asn Pro Thr
            180                 185                 190
Leu Glu Arg Ser Ile Ala Leu Phe Asn Gly Ile Ser Lys Trp Val Gln
        195                 200                 205
Leu Met Val Leu Ser Lys Pro Thr Pro Gln Gln Arg Ala Glu Val Ile
    210                 215                 220
Thr Lys Phe Ile Asn Val Ala Lys Lys Leu Leu Gln Leu Lys Asn Phe
225                 230                 235                 240
Asn Asn Leu Ile Ala Ile Val Gly Ala Leu Ser His Arg Ser Ile Ser
                245                 250                 255
Gly Phe Lys Gly Thr His Ser His Leu Ser Ser Glu Val Thr Lys Asn
            260                 265                 270
Trp Asn Val Lys Xaa Gln Lys Trp Val Ser Ser Asn Gly Asn Tyr Cys
        275                 280                 285
Asn Tyr Arg Lys Pro Phe Ala Asp Cys Asp Gly Phe Lys Ile Pro Ile
    290                 295                 300
Leu Gly Val His Leu Lys Asp Leu Ile Ala Val His Val Ile Phe Pro
305                 310                 315                 320
Asp Trp Thr Glu Glu Asn Lys Val Asn Ile Val Lys Met His Gln Leu
                325                 330                 335
Ser Val Thr Leu Ser Glu Leu Val Ser Leu Gln Asn Ala Ser His His
            340                 345                 350
Leu Glu Pro Asn Met Asp Leu Ile Asn Leu Leu Thr Leu Ser Leu Asp
        355                 360                 365
Leu Tyr His Thr Glu Asp Asp Ile Tyr Lys Leu Ser Leu Val Leu Glu
    370                 375                 380
Pro Arg Asn Ser Lys Ser Gln Pro Thr Ser Pro Thr Thr Pro Asn Lys
385                 390                 395                 400
```

```
Pro Val Val Pro Leu Glu Trp Ala Leu Gly Val Met Pro Lys Pro Asp
              405                     410             415
Pro Thr Val Ile Asn Lys His Ile Arg Lys Leu Val Glu Ser Val Phe
              420                 425                 430
Arg Asn Tyr Asp His Asp His Asp Gly Tyr Ile Ser Gln Glu Asp Phe
          435             440                 445
Glu Ser Ile Ala Ala Asn Phe Pro Phe Leu Asp Ser Phe Cys Val Leu
    450             455                 460
Asp Lys Asp Gln Asp Gly Leu Ile Ser Lys Asp Glu Met Met Ala Tyr
465             470                 475                 480
Phe Leu Arg Ala Lys Ser Gln Leu His Cys Gln Ile Gly Ala Pro Gly
              485                 490                 495
Phe Ile His Asn Phe Gln Glu Met Thr Tyr Leu Lys Pro Thr Phe Cys
          500                 505                 510
Glu His Cys Ala Gly Phe Ile Leu Gly Ile Ile Lys Gln Gly Tyr Lys
          515                 520                 525
Cys Lys Asp Cys Gly Ala Asn Cys His Lys Gln Cys Lys Asp Leu Leu
    530                 535                 540
Val Leu Ala Cys Arg Arg Phe Ala Arg Ala Pro Ser Leu Ser Ser Gly
545                 550                 555                 560
His Gly Ser Leu Pro Gly Ser Pro Ser Leu Pro Pro Ala Gln Asp Xaa
              565                 570                 575
Val Phe Lys Phe Pro Gly Val Thr Ala Asp Asn Ser Asp Leu Asp Ser
          580                 585                 590
Arg Ala Ile Thr Leu Val Thr Gly Ser Ser Arg Lys Thr Ser Val Arg
          595                 600                 605
Leu Gln Arg Ala Thr Thr Ser Gln Ala Thr Gln Thr Glu Pro Val Trp
    610                 615                 620
Ser Glu Ala Gly Trp Gly Asp Ser Gly Ser His Thr Leu Pro Tyr Asn
625                 630                 635                 640
Arg Tyr Ser Gly Ser Leu His Lys Pro Ala Lys Arg His Lys Gly Phe
              645                 650                 655
Ala Ile Trp Glu Lys Xaa Lys Ser Pro Gly Trp His Ala Gly Gly Asp
          660                 665                 670
Val Xaa Asn Pro Gly Thr Glu Phe Glu Leu Ala Pro Asp Glu Gly Glu
    675                 680                 685
Lys Thr Thr Gln Asp Gly Glu Asp Gly Leu Thr Ser Arg Leu Ala Glu
    690                 695                 700
Asn Leu Lys Ala Asn Asn Gly Trp Leu Leu Gly Gly Gly Lys Asn Lys
705                 710                 715                 720
Lys Leu Leu Arg Lys Ala Leu Ala Ser Gln Glu Val Ile Leu Glu Arg
              725                 730                 735
Thr Pro
```

```
        <210> 263
        <211> 80
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(80)
        <223> Xaa = X or * as defined in Table 6


        <400> 263
Arg Pro Lys Met Gly Arg Arg Ser Lys His Lys Pro Pro Ala Ser Phe
 1               5                   10                  15
Gln Val Ser Ser Leu Ser Asn Pro Gly Phe Phe Phe Ile Xaa His
              20                  25                  30
Cys Phe Phe Xaa Leu Tyr Phe Ser Tyr Lys Arg Asn Val Ser Leu Xaa
```

```
            35                       40                       45
Lys Ile Thr His Tyr Arg Lys Ile Leu Arg Arg Lys Thr Phe Thr Ser
      50                       55                       60
Glu Thr Lys Phe Phe Pro Met Lys Thr Glu Pro Lys Arg Val Ser Gly
65                       70                       75                       80
```

```
        <210> 264
        <211> 644
        <212> PRT
        <213> Homo sapiens


        <400> 264
Met Pro Ala Pro Arg Ala Arg Glu Gln Pro Arg Val Pro Gly Glu Arg
 1               5                       10                      15
Gln Pro Leu Leu Pro Arg Gly Ala Arg Gly Pro Arg Arg Trp Arg Arg
              20                       25                      30
Ala Ala Gly Ala Ala Val Leu Leu Val Glu Met Leu Glu Arg Ala Ala
              35                       40                      45
Phe Phe Gly Val Thr Ala Asn Leu Val Leu Tyr Leu Asn Ser Thr Asn
      50                       55                       60
Phe Asn Trp Thr Gly Glu Gln Ala Thr Arg Ala Ala Leu Val Phe Leu
65                       70                       75                      80
Gly Ala Ser Tyr Leu Leu Ala Pro Val Gly Gly Trp Leu Ala Asp Val
              85                       90                      95
Tyr Leu Gly Arg Tyr Arg Ala Val Ala Leu Ser Leu Leu Leu Tyr Leu
             100                      105                     110
Ala Ala Ser Gly Leu Leu Pro Ala Thr Ala Phe Pro Asp Gly Arg Ser
             115                      120                     125
Ser Phe Cys Gly Glu Met Pro Ala Ser Pro Leu Gly Pro Ala Cys Pro
     130                      135                      140
Ser Ala Gly Cys Pro Arg Ser Ser Pro Ser Pro Tyr Cys Ala Pro Val
145                      150                      155                     160
Leu Tyr Ala Gly Leu Leu Leu Leu Gly Leu Ala Ala Ser Ser Val Arg
             165                      170                     175
Ser Asn Leu Thr Ser Phe Gly Ala Asp Gln Val Met Asp Leu Gly Arg
             180                      185                     190
Asp Ala Thr Arg Arg Phe Phe Asn Trp Phe Tyr Trp Ser Ile Asn Leu
             195                      200                     205
Gly Ala Val Leu Ser Leu Leu Val Val Ala Phe Ile Gln Gln Asn Ile
     210                      215                      220
Ser Phe Leu Leu Gly Tyr Ser Ile Pro Val Gly Cys Val Gly Leu Ala
225                      230                      235                     240
Phe Phe Ile Phe Leu Phe Ala Thr Pro Val Phe Ile Thr Lys Pro Pro
             245                      250                     255
Met Gly Ser Gln Val Ser Ser Met Leu Lys Leu Ala Leu Gln Asn Cys
             260                      265                     270
Cys Pro Gln Leu Trp Gln Arg His Ser Ala Arg Ser Lys Leu Ser Gln
     275                      280                      285
Gly Gln Gln Gly Asn Asn Gly Ser Glu Ser Lys Leu His Leu Leu Val
     290                      295                      300
Ala Lys Trp Gln His Thr Leu Gly Arg Val Glu Leu Thr Val Ala Val
305                      310                      315                     320
Phe Gly Asp Asp Tyr Thr Asn Ile Val Pro Phe Gly Ile Ser Lys Asp
             325                      330                     335
Ser Ala Arg Leu Leu Asp Lys Lys Arg Asp Arg Gln Cys Ala Arg Val
             340                      345                     350
Leu Ala Asp Glu Arg Ser Pro Gln Pro Gly Ala Ser Pro Gln Glu Asp
             355                      360                     365
Ile Ala Asn Phe Gln Val Leu Val Lys Ile Leu Pro Val Met Val Thr
```

```
         370                      375                      380
Leu Val Pro Tyr Trp Met Val Tyr Phe Gln Met Gln Ser Thr Tyr Val
385                      390                      395                  400
Leu Gln Gly Leu His Leu His Ile Pro Asn Ile Phe Pro Ala Asn Pro
                    405                      410                  415
Ala Asn Ile Ser Val Ala Leu Arg Ala Gln Gly Ser Ser Tyr Thr Ile
                420                      425                  430
Pro Glu Ala Trp Leu Leu Leu Ala Asn Val Val Val Val Leu Ile Leu
            435                      440                  445
Val Pro Leu Lys Asp Arg Leu Ile Asp Pro Leu Leu Leu Arg Cys Lys
        450                      455                  460
Leu Leu Pro Ser Ala Leu Gln Lys Met Ala Leu Gly Met Phe Phe Gly
465                      470                      475                  480
Phe Thr Ser Val Ile Val Ala Gly Val Leu Glu Met Glu Arg Leu His
                    485                      490                  495
Tyr Ile His His Asn Glu Thr Val Ser Gln Gln Ile Gly Glu Val Leu
                500                      505                  510
Tyr Asn Ala Ala Pro Leu Ser Ile Trp Trp Gln Ile Pro Gln Tyr Leu
            515                      520                  525
Leu Ile Gly Ile Ser Glu Ile Phe Ala Ser Ile Pro Gly Leu Glu Phe
        530                      535                  540
Ala Tyr Ser Glu Ala Pro Arg Ser Met Gln Gly Ala Ile Met Gly Ile
545                      550                      555                  560
Phe Phe Cys Leu Ser Gly Val Gly Ser Leu Leu Gly Ser Ser Leu Val
                565                      570                  575
Gly Thr Ala Val Pro Leu Pro Gly Gly Trp Leu His Cys Pro Lys Asp
            580                      585                  590
Phe Gly Asn Ile Asn Asn Cys Arg Met Asp Leu Tyr Phe Phe Leu Leu
        595                      600                  605
Ala Gly Ile Gln Ala Val Thr Ala Leu Leu Phe Val Trp Ile Ala Gly
        610                      615                  620
Arg Tyr Glu Arg Ala Ser Gln Gly Pro Ala Ser His Ser Arg Phe Ser
625                      630                      635                  640
Arg Asp Arg Gly
```

```
    <210> 265
    <211> 99
    <212> PRT
    <213> Homo sapiens

    <220>
    <221> misc_feature
    <222> (1)...(99)
    <223> Xaa = X or * as defined in Table 6


    <400> 265
Xaa Ala Cys Ser Gly Val Pro Gly Thr Lys Cys Ser Pro Pro Ser Gly
1                   5                       10                  15
Ser Gly Tyr Pro Asn Pro Tyr Ser Lys His Val Leu Thr Glu Asp Ile
                20                      25                  30
Val His Arg Glu Val Thr Pro Asp Gln Lys Leu Leu Ser Arg Ala Thr
            35                      40                  45
Leu Thr Lys Thr Asn Arg Asn Ala His Ala Gly Pro Glu Arg Leu Phe
        50                      55                  60
Pro Ala Asn Val Ala His Ser Val Tyr Val Leu Glu Asp Ser Ile Val
65                      70                      75                  80
Asp Pro Gln Asn Gln Thr Leu Thr Thr Phe Asn Trp Asn Ile Asn Pro
                85                      90                  95
Arg Pro Gly
```

<210> 266
<211> 840
<212> PRT
<213> Homo sapiens

<400> 266

Ser	Ser	Leu	Thr	Ser	Ser	Met	Glu	Asp	Pro	Ala	Ala	Pro	Gly	Thr	Gly
1				5					10					15	
Gly	Pro	Pro	Ala	Asn	Gly	Asn	Gly	Asn	Gly	Gly	Gly	Lys	Gly	Lys	Gln
			20				25					30			
Ala	Ala	Pro	Lys	Gly	Arg	Glu	Ala	Phe	Arg	Ser	Gln	Arg	Arg	Glu	Ser
		35				40					45				
Glu	Gly	Ser	Val	Asp	Cys	Pro	Thr	Leu	Glu	Phe	Glu	Tyr	Gly	Asp	Ala
	50				55					60					
Asp	Gly	His	Ala	Ala	Glu	Leu	Ser	Glu	Leu	Tyr	Ser	Tyr	Thr	Glu	Asn
65					70					75					80
Leu	Glu	Phe	Thr	Asn	Asn	Arg	Arg	Cys	Phe	Glu	Glu	Asp	Phe	Lys	Thr
				85					90					95	
Gln	Val	Gln	Gly	Lys	Glu	Trp	Leu	Glu	Leu	Glu	Glu	Asp	Ala	Gln	Lys
			100				105					110			
Ala	Tyr	Ile	Met	Gly	Leu	Leu	Asp	Arg	Leu	Glu	Val	Val	Ser	Arg	Glu
		115				120					125				
Arg	Arg	Leu	Lys	Ala	Ala	Arg	Ala	Val	Leu	Tyr	Leu	Ala	Gln	Gly	Thr
	130				135					140					
Phe	Gly	Glu	Cys	Asp	Ser	Glu	Val	Asp	Val	Leu	His	Trp	Ser	Arg	Tyr
145					150					155					160
Asn	Cys	Phe	Leu	Leu	Tyr	Gln	Met	Gly	Thr	Phe	Ser	Thr	Phe	Leu	Glu
				165					170					175	
Leu	Leu	His	Met	Glu	Ile	Asp	Asn	Ser	Gln	Ala	Cys	Ser	Ser	Ala	Leu
			180				185					190			
Arg	Lys	Pro	Ala	Val	Ser	Ile	Ala	Asp	Ser	Thr	Glu	Leu	Arg	Val	Leu
		195				200					205				
Leu	Ser	Val	Met	Tyr	Leu	Met	Val	Glu	Asn	Ile	Arg	Leu	Glu	Arg	Glu
	210				215					220					
Thr	Asp	Pro	Cys	Gly	Trp	Arg	Thr	Ala	Arg	Glu	Thr	Phe	Arg	Thr	Glu
225					230					235					240
Leu	Ser	Phe	Ser	Met	His	Asn	Glu	Glu	Pro	Phe	Ala	Leu	Leu	Leu	Phe
				245					250					255	
Ser	Met	Val	Thr	Lys	Phe	Cys	Ser	Gly	Leu	Ala	Pro	His	Phe	Pro	Ile
			260				265					270			
Lys	Lys	Val	Leu	Leu	Leu	Leu	Trp	Lys	Val	Val	Met	Phe	Thr	Leu	Gly
		275				280					285				
Gly	Phe	Glu	His	Leu	Gln	Thr	Leu	Lys	Val	Gln	Lys	Arg	Ala	Glu	Leu
	290				295					300					
Gly	Leu	Pro	Pro	Leu	Ala	Glu	Asp	Ser	Ile	Gln	Val	Val	Lys	Ser	Met
305					310					315					320
Arg	Ala	Ala	Ser	Pro	Pro	Ser	Tyr	Thr	Leu	Asp	Leu	Gly	Glu	Ser	Gln
				325					330					335	
Leu	Ala	Pro	Pro	Pro	Ser	Lys	Leu	Arg	Gly	Arg	Arg	Gly	Ser	Arg	Arg
			340				345					350			
Gln	Leu	Leu	Thr	Lys	Gln	Asp	Ser	Leu	Asp	Ile	Tyr	Asn	Glu	Arg	Asp
		355				360					365				
Leu	Phe	Lys	Thr	Glu	Glu	Pro	Ala	Thr	Glu	Glu	Glu	Glu	Glu	Ser	Ala
	370				375					380					
Gly	Asp	Gly	Glu	Arg	Thr	Leu	Asp	Gly	Glu	Leu	Asp	Leu	Leu	Glu	Gln
385					390					395					400
Asp	Pro	Leu	Val	Pro	Pro	Pro	Ser	Gln	Ala	Pro	Leu	Ser	Ala	Glu
				405					410					415	
Arg	Val	Ala	Phe	Pro	Lys	Gly	Leu	Pro	Trp	Ala	Pro	Lys	Val	Arg	Gln
		420				425					430				

```
Lys Asp Ile Glu His Phe Leu Glu Met Ser Arg Asn Lys Phe Ile Gly
        435                 440                 445
Phe Thr Leu Gly Gln Asp Thr Asp Thr Leu Val Gly Leu Pro Arg Pro
    450             455                 460
Ile His Glu Ser Val Lys Thr Leu Lys Gln His Lys Tyr Ile Ser Ile
465             470             475                 480
Ala Asp Val Gln Ile Lys Asn Glu Glu Glu Leu Glu Lys Cys Pro Met
            485             490                 495
Ser Leu Gly Glu Glu Val Val Pro Glu Thr Pro Cys Glu Ile Leu Tyr
        500             505             510
Gln Gly Met Leu Tyr Ser Leu Pro Gln Tyr Met Ile Ala Leu Leu Lys
        515             520             525
Ile Leu Leu Ala Ala Ala Pro Thr Ser Lys Ala Lys Thr Asp Ser Ile
    530             535             540
Asn Ile Leu Ala Asp Val Leu Pro Glu Glu Met Pro Ile Thr Val Leu
545             550             555                 560
Gln Ser Met Lys Leu Gly Ile Asp Val Asn Arg His Lys Glu Ile Ile
            565             570             575
Val Lys Ser Ile Ser Thr Leu Leu Leu Leu Leu Leu Lys His Phe Lys
        580             585             590
Leu Asn His Ile Tyr Gln Phe Glu Tyr Val Ser Gln His Leu Val Phe
    595             600             605
Ala Asn Cys Ile Pro Leu Ile Leu Lys Phe Phe Asn Gln Asn Ile Leu
    610             615             620
Ser Tyr Ile Thr Ala Lys Asn Ser Ile Ser Val Leu Asp Tyr Pro Cys
625             630             635                 640
Cys Thr Ile Gln Asp Leu Pro Glu Leu Thr Thr Glu Ser Leu Glu Ala
            645             650             655
Gly Asp Asn Ser Gln Phe Cys Trp Arg Asn Leu Phe Ser Cys Ile Asn
        660             665             670
Leu Leu Arg Leu Leu Asn Lys Leu Thr Lys Trp Lys His Ser Arg Thr
    675             680             685
Met Met Leu Val Val Phe Lys Ser Ala Pro Ile Leu Lys Arg Ala Leu
    690             695             700
Lys Val Lys Gln Ala Met Leu Gln Leu Tyr Val Leu Lys Leu Leu Lys
705             710             715                 720
Leu Gln Thr Lys Tyr Leu Gly Arg Gln Trp Arg Lys Ser Asn Met Lys
            725             730             735
Thr Met Ser Ala Ile Tyr Gln Lys Val Arg His Arg Met Asn Asp Asp
            740             745             750
Trp Ala Tyr Gly Asn Asp Ile Asp Ala Arg Pro Trp Asp Phe Gln Ala
    755             760             765
Glu Glu Cys Thr Leu Arg Ala Asn Ile Glu Ala Phe Asn Ser Arg Arg
    770             775             780
Tyr Asp Arg Pro Gln Asp Ser Glu Phe Ser Pro Val Asp Asn Cys Leu
785             790             795                 800
Gln Ser Val Leu Gly Gln Arg Leu Asp Leu Pro Glu Asp Phe His Tyr
            805             810             815
Ser Tyr Glu Leu Trp Leu Glu Arg Glu Val Phe Ser Gln Pro Ile Cys
        820             825             830
Trp Glu Glu Leu Leu Gln Asn His
        835             840
```

```
        <210> 267
        <211> 308
        <212> PRT
        <213> Homo sapiens


        <400> 267
Pro Ala Trp Asn Ala Arg Pro Arg Gln Val Asp Leu Lys Leu Thr His
  1               5                   10                  15
```

```
Lys Lys Gln Arg Ala Leu Leu Glu Arg Phe Asp Ile Tyr Arg Lys Val
            20                      25                      30
Pro Lys Asp Leu Thr Gln Pro Thr Tyr Thr Gly Ala Ile Ile Ser Ile
        35                      40                      45
Cys Cys Cys Leu Phe Ile Leu Phe Leu Phe Leu Ser Glu Leu Thr Gly
    50                      55                      60
Phe Ile Thr Thr Glu Val Val Asn Glu Leu Tyr Val Asp Asp Pro Asp
65                  70                      75                  80
Lys Asp Ser Gly Gly Lys Ile Asp Val Ser Leu Asn Ile Ser Leu Pro
                85                      90                      95
Asn Leu His Cys Glu Leu Val Gly Leu Asp Ile Gln Asp Glu Met Gly
            100                     105                     110
Arg His Glu Val Gly His Ile Asp Asn Ser Met Lys Ile Pro Leu Asn
        115                     120                     125
Asn Gly Ala Gly Cys Arg Phe Glu Gly Gln Phe Ser Ile Asn Lys Val
    130                     135                     140
Pro Gly Asn Phe His Val Ser Thr His Ser Ala Thr Ala Gln Pro Gln
145                     150                     155                 160
Asn Pro Asp Met Thr His Val Ile His Lys Leu Ser Phe Gly Asp Thr
                165                     170                     175
Leu Gln Val Gln Asn Ile His Gly Ala Phe Asn Ala Leu Gly Gly Ala
            180                     185                     190
Asp Arg Leu Thr Ser Asn Pro Leu Ala Ser His Asp Tyr Ile Leu Lys
        195                     200                     205
Ile Val Pro Thr Val Tyr Glu Asp Lys Ser Gly Lys Gln Arg Tyr Ser
    210                     215                     220
Tyr Gln Tyr Thr Val Ala Asn Lys Glu Tyr Val Ala Tyr Ser His Thr
225                     230                     235                 240
Gly Arg Ile Ile Pro Ala Ile Trp Phe Arg Tyr Asp Leu Ser Pro Ile
                245                     250                     255
Thr Val Lys Tyr Thr Glu Arg Arg Gln Pro Leu Tyr Arg Phe Ile Thr
                260                     265                     270
Thr Ile Cys Ala Ile Ile Gly Gly Thr Phe Thr Val Ala Gly Ile Leu
            275                     280                     285
Asp Ser Cys Ile Phe Thr Ala Ser Glu Ala Trp Lys Lys Ile Gln Leu
        290                     295                     300
Gly Lys Met His
305
```

```
        <210> 268
        <211> 162
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 268
Met Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg Glu Thr Ser Val
1               5                       10                      15
Thr Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu Gly Val Ser Ile
            20                      25                      30
Arg Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val Trp His Val Leu
        35                      40                      45
Glu Val Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His
    50                      55                      60
Ser Asp Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp
65                  70                      75                  80
Leu Phe Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr
                85                      90                      95
Val Tyr Asn Thr Asp Thr Val Tyr Thr Gly Asn Ser Thr Trp Lys Thr
                100                     105                     110
Cys Val Lys Ser Ser Tyr Ser Gly Ala Leu Val Asn Leu Asn Arg Leu
        115                     120                     125
```

163

```
Phe Ser Ser Ala Tyr Thr Arg Ile Pro Cys Phe Gly Ala Leu Arg Ile
130                 135                 140
Asn Ser Asp Lys His Phe Val Asn Gly Cys Trp Leu Leu Ser Thr Tyr
145                 150                 155                 160
Thr Leu
```


```
<210> 269
<211> 280
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(280)
<223> Xaa = X or * as defined in Table 6


<400> 269
Asn Leu Leu Leu Gly Gly Gly Gly Lys Lys Lys Lys Pro Pro Arg Thr
1               5                   10                  15
Arg Gly Pro Phe Pro Gly Leu Ser Gln Pro Gly Leu Leu Trp Leu Phe
            20                  25                  30
Pro Lys Arg Pro Gly Cys Ser His Leu Pro Ser Thr Pro Ile Lys Glu
        35                  40                  45
Met Gly Leu Pro Lys Ile His His Arg Val Gly Trp Glu Ser Phe Ser
    50                  55                  60
Gly Val Phe Leu Glu Val Asp Phe Lys Ile Tyr Lys Lys Lys Met Asn
65                  70                  75                  80
Glu Phe Phe Ser Val Asp Asp Asn Asn Glu Glu Glu Asp Val Glu
                85                  90                  95
Met Lys Glu Asp Ser Asp Glu Asn Gly Pro Glu Glu Lys Gln Ser Val
            100                 105                 110
Glu Glu Met Glu Glu Gln Ser Gln Asp Ala Asp Gly Val Asn Thr Val
    115                 120                 125
Thr Val Pro Gly Pro Ala Ser Glu Glu Ala Val Glu Asp Cys Lys Asp
    130                 135                 140
Glu Asp Phe Ala Lys Asp Glu Asn Ile Thr Lys Gly Gly Glu Val Thr
145                 150                 155                 160
Asp His Ser Val Arg Asp Gln Asp His Pro Asp Gly Gln Glu Asn Asp
            165                 170                 175
Ser Thr Lys Asn Glu Ile Lys Ile Glu Thr Glu Ser Gln Ser Ser Tyr
            180                 185                 190
Met Glu Thr Glu Glu Leu Ser Ser Asn Gln Glu Asp Ala Val Ile Val
    195                 200                 205
Glu Gln Pro Glu Val Ile Pro Leu Thr Glu Asp Gln Glu Glu Lys Glu
    210                 215                 220
Gly Glu Lys Ala Pro Gly Glu Asp Thr Pro Arg Met Pro Gly Lys Ser
225                 230                 235                 240
Glu Gly Ser Ser Asp Leu Glu Asn Thr Pro Gly Pro Asp Val Glu Met
            245                 250                 255
Asn Ser Gln Val Asp Lys Val Asn Asp Pro Thr Glu Ser Gln Pro Ser
            260                 265                 270
Cys Gln Ala Xaa Arg Ser Arg Gly
    275                 280


<210> 270
<211> 160
<212> PRT
<213> Homo sapiens
```

<220>
<221> misc_feature
<222> (1)...(160)
<223> Xaa = X or * as defined in Table 6

<400> 270

| Glu | Arg | Arg | Glu | Arg | Ser | Pro | Asp | Gln | Ser | Ser | Gly | Arg | Ala | Ser | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| Gly | Pro | Pro | Glu | Arg | Gln | Ser | Leu | Arg | Met | Ser | Pro | Ser | Arg | Ala | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| Trp | Thr | Ser | Ser | Pro | Cys | Arg | Ser | Cys | Ala | Ser | Gln | Gly | Val | Cys | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| Trp | Pro | Leu | Asn | Leu | Arg | Arg | Ile | Ala | Ser | Thr | Ser | Trp | Cys | Xaa | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |

| Met | Ser | Ala | Gly | Ile | Gly | Pro | Met | Ala | Trp | Trp | Pro | Ser | Thr | Thr | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

| Pro | Cys | Met | Met | Ser | Thr | Val | Ser | Thr | Met | Ala | Lys | Pro | His | Arg | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |

| Cys | Pro | Gly | Cys | Phe | Val | Pro | Phe | Ala | Val | Cys | Val | Val | Ser | Arg | Phe |
| | | | 100 | | | | | 105 | | | | | 110 | | |

| Pro | Tyr | Tyr | Asn | Ser | Leu | Lys | Asp | Cys | Leu | Ser | Trp | His | Tyr | Arg | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |

| Pro | Gly | Ala | Thr | Leu | Leu | Ser | Pro | Ser | Ser | Leu | Val | Thr | Leu | Leu | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |

| Val | Lys | Gly | Pro | Gly | Ala | Ala | Ala | Ala | Asp | Ala | Gly | Glu | Ile | Pro | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

<210> 271
<211> 132
<212> PRT
<213> Homo sapiens

<400> 271

| Ala | Ser | Ala | Pro | Val | Gly | Cys | Leu | Thr | Arg | Ala | Val | Cys | Gly | Arg | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| Pro | Trp | Arg | Thr | Asn | Thr | Val | Val | Glu | Pro | Arg | Glu | Gly | Thr | Arg | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| Leu | Glu | Phe | Gly | His | Leu | Lys | Leu | Ala | His | Val | Pro | Pro | Leu | Glu | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| Leu | Val | Asn | Gln | His | Gln | Pro | Glu | Asp | His | Val | Leu | Ile | Lys | Arg | Trp |
| | 50 | | | | | 55 | | | | | 60 | | | | |

| Lys | Glu | Glu | Lys | Leu | Glu | Pro | Ala | Trp | Glu | Gly | Pro | Tyr | Pro | Val | Leu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

| Leu | Thr | Thr | Lys | Thr | Ala | Val | Arg | Thr | Asp | Lys | Lys | Lys | Lys | Lys | Lys |
| | | | 85 | | | | | 90 | | | | | 95 | | |

| Lys | Lys | Arg | Trp | Thr | His | His | Thr | Gln | Val | Lys | Lys | Val | Pro | Pro | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |

| Pro | Glu | Ser | Trp | Ala | Ile | Val | Pro | Gly | Glu | Asn | Pro | Thr | Lys | Leu | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |

| Leu | Arg | Lys | Met |
| | 130 | | |

<210> 272
<211> 1262
<212> PRT

```
<213> Homo sapiens


      <400> 272
Met Arg Arg Gly Gly Trp Arg Lys Arg Ala Glu Asn Asp Gly Trp Glu
1               5                   10                  15
Thr Trp Gly Gly Tyr Met Ala Ala Lys Val Gln Lys Leu Glu Glu Gln
            20                  25                  30
Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
        35                  40                  45
Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
    50                  55                  60
Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
65                  70                  75                  80
Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
                85                  90                  95
Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
            100                 105                 110
Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
        115                 120                 125
Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
    130                 135                 140
Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
145                 150                 155                 160
Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
                165                 170                 175
Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
            180                 185                 190
Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
        195                 200                 205
Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
    210                 215                 220
Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
225                 230                 235                 240
Cys Leu Val Pro Met Val Asn Ser Val Ala Ser Arg Leu Ser Pro Ala
                245                 250                 255
Phe Ser Gln Glu Glu Asp Lys Ala Glu Lys Ser Ser Thr Asp Phe Arg
            260                 265                 270
Asp Cys Thr Leu Gln Gln Leu Gln Gln Ser Thr Arg Asn Thr Asp Ala
        275                 280                 285
Leu Arg Asn Pro His Arg Thr Asn Ser Phe Ser Leu Ser Pro Leu His
    290                 295                 300
Ser Asn Thr Lys Ile Asn Gly Ala His His Ser Thr Val Gln Gly Pro
305                 310                 315                 320
Ser Ser Thr Lys Ser Thr Ser Ser Val Ser Thr Phe Ser Lys Ala Ala
                325                 330                 335
Pro Ser Val Pro Ser Lys Pro Ser Asp Cys Asn Phe Ile Ser Asn Phe
            340                 345                 350
Tyr Ser His Ser Arg Leu His His Ile Ser Met Trp Lys Cys Glu Leu
        355                 360                 365
Thr Glu Phe Val Asn Thr Leu Gln Arg Gln Ser Asn Gly Ile Phe Pro
    370                 375                 380
Gly Arg Glu Lys Leu Lys Lys Met Lys Thr Gly Arg Ser Ala Leu Val
385                 390                 395                 400
Val Thr Asp Thr Gly Asp Met Ser Val Leu Asn Ser Pro Arg His Gln
                405                 410                 415
Ser Cys Ile Met His Val Asp Met Asp Cys Phe Phe Val Ser Val Gly
            420                 425                 430
Ile Arg Asn Arg Pro Asp Leu Lys Gly Lys Pro Val Ala Val Thr Ser
        435                 440                 445
Asn Arg Gly Thr Gly Arg Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln
    450                 455                 460
Leu Glu Trp Gln Tyr Tyr Gln Asn Lys Ile Leu Lys Gly Lys Ala Ala
465                 470                 475                 480
```

166

```
Asp Ile Pro Asp Ser Ser Leu Trp Glu Asn Pro Asp Ser Ala Gln Ala
             485                 490                 495
Asn Gly Ile Asp Ser Val Leu Ser Arg Ala Glu Ile Ala Ser Cys Ser
             500                 505                 510
Tyr Glu Ala Arg Gln Leu Gly Ile Lys Asn Gly Met Phe Phe Gly His
         515             520                 525
Ala Lys Gln Leu Cys Pro Asn Leu Gln Ala Val Pro Tyr Asp Phe His
     530             535                 540
Ala Tyr Lys Glu Val Ala Gln Thr Leu Tyr Glu Thr Leu Ala Ser Tyr
545             550                 555                 560
Thr His Asn Ile Glu Ala Val Ser Cys Asp Glu Ala Leu Val Asp Ile
             565                 570                 575
Thr Glu Ile Leu Ala Glu Thr Lys Leu Thr Pro Asp Glu Phe Ala Asn
             580                 585                 590
Ala Val Arg Met Glu Ile Lys Asp Gln Thr Lys Cys Ala Ala Ser Val
         595             600                 605
Gly Ile Gly Ser Asn Ile Leu Leu Ala Arg Met Ala Thr Arg Lys Ala
     610             615                 620
Lys Pro Asp Gly Gln Tyr His Leu Lys Pro Glu Glu Val Asp Asp Phe
625             630                 635                 640
Ile Arg Gly Gln Leu Val Thr Asn Leu Pro Gly Val Gly His Ser Met
             645                 650                 655
Glu Ser Lys Leu Ala Ser Leu Gly Ile Lys Thr Cys Gly Asp Leu Gln
             660                 665                 670
Tyr Met Thr Met Ala Lys Leu Gln Lys Glu Phe Gly Pro Lys Thr Gly
         675             680                 685
Gln Met Leu Tyr Arg Phe Cys Arg Gly Leu Asp Asp Arg Pro Val Arg
     690             695                 700
Thr Glu Lys Glu Arg Lys Ser Val Ser Ala Glu Ile Asn Tyr Gly Ile
705             710                 715                 720
Arg Phe Thr Gln Pro Lys Glu Ala Glu Ala Phe Leu Leu Ser Leu Ser
             725                 730                 735
Glu Glu Ile Gln Arg Arg Leu Glu Ala Thr Gly Met Lys Gly Lys Arg
             740                 745                 750
Leu Thr Leu Lys Ile Met Val Arg Lys Pro Gly Ala Pro Val Glu Thr
         755             760                 765
Ala Lys Phe Gly Gly His Gly Ile Cys Asp Asn Ile Ala Arg Thr Val
     770             775                 780
Thr Leu Asp Gln Ala Thr Asp Asn Ala Lys Ile Ile Gly Lys Ala Met
785             790                 795                 800
Leu Asn Met Phe His Thr Met Lys Leu Asn Ile Ser Asp Met Arg Gly
             805                 810                 815
Val Gly Ile His Val Asn Gln Leu Val Pro Thr Asn Leu Asn Pro Ser
             820                 825                 830
Thr Cys Pro Ser Arg Pro Ser Val Gln Ser Ser His Phe Pro Ser Gly
         835             840                 845
Ser Tyr Ser Val Arg Asp Val Phe Gln Val Gln Lys Ala Lys Lys Ser
     850             855                 860
Thr Glu Glu Glu His Lys Glu Val Phe Arg Ala Ala Val Asp Leu Glu
865             870                 875                 880
Ile Ser Ser Ala Ser Arg Thr Cys Thr Phe Leu Pro Pro Phe Pro Ala
             885                 890                 895
His Leu Pro Thr Ser Pro Asp Thr Asn Lys Ala Glu Ser Ser Gly Lys
         900                 905                 910
Trp Asn Gly Leu His Thr Pro Val Ser Val Gln Ser Arg Leu Asn Leu
         915                 920                 925
Ser Ile Glu Val Pro Ser Pro Ser Gln Leu Asp Gln Ser Val Leu Glu
     930                 935                 940
Ala Leu Pro Pro Asp Leu Arg Glu Gln Val Glu Gln Val Cys Ala Val
945                 950                 955                 960
Gln Gln Ala Glu Ser His Gly Asp Lys Lys Lys Glu Pro Val Asn Gly
             965                 970                 975
Cys Asn Thr Gly Ile Leu Pro Gln Pro Val Gly Thr Met Ser Leu Leu
             980                 985                 990
```

167

```
Gln Ile Pro Glu Pro Gln Glu Ser Asn Ser Asp Ala Gly Ile Asn Leu
        995                 1000                1005
Ile Ala Leu Pro Ala Phe Ser Gln Val Asp Pro Glu Val Phe Ala Ala
    1010                1015                1020
Leu Ser Ala Glu Leu Gln Arg Glu Leu Lys Ala Ala Tyr Asp Gln Arg
1025                1030                1035                1040
Gln Arg Gln Gly Glu Asn Ser Thr His Gln Gln Ser Ala Ser Ala Ser
                1045                1050                1055
Val Pro Lys Asn Pro Leu Ile His Leu Lys Ala Ala Val Lys Glu Lys
                1060                1065                1070
Lys Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro Lys Arg Ile Gln
        1075                1080                1085
Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala Lys Thr Leu Pro
        1090                1095                1100
Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly Phe Leu Lys His
1105                1110                1115                1120
Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Lys Asn Ser Ser Gly Phe
                1125                1130                1135
Leu Leu Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp Pro Ser
                1140                1145                1150
Leu Gly Cys Val Arg Pro Pro Pro Asn Leu Ala Gly Ala Val Glu
        1155                1160                1165
Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Val Thr Thr Ile Ser
    1170                1175                1180
Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr Asp
1185                1190                1195                1200
Leu Ile Glu Asp Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys Tyr
                1205                1210                1215
Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp Asn Met Ala
        1220                1225                1230
Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr Tyr
        1235                1240                1245
Gly Ser His Ile Lys Ser Tyr Ile Asn Ile Thr Gln Arg Ala
1250                1255                1260
```

```
        <210> 273
        <211> 260
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(260)
        <223> Xaa = X or * as defined in Table 6


        <400> 273
Met Ala Glu Thr Glu Glu Arg Ser Leu Asp Asn Phe Phe Ala Lys Arg
1               5                   10                  15
Asp Lys Lys Lys Lys Glu Arg Ser Asn Arg Ala Ala Ser Ala Ala
            20                  25                  30
Gly Ala Ala Gly Ser Ala Gly Gly Ser Ser Gly Ala Ala Gly Ala Ala
        35                  40                  45
Gly Gly Gly Ala Gly Ala Gly Thr Arg Pro Gly Asp Gly Gly Thr Ala
    50                  55                  60
Ser Ala Gly Ala Ala Gly Pro Gly Ala Ala Thr Lys Ala Val Thr Lys
65                  70                  75                  80
Asp Glu Asp Glu Trp Lys Glu Leu Glu Gln Lys Glu Val Asp Tyr Ser
                85                  90                  95
Gly Leu Arg Val Gln Ala Met Gln Ile Ser Ser Glu Lys Glu Glu Asp
            100                 105                 110
Asp Asn Glu Lys Arg Gln Asp Pro Gly Asp Asn Trp Glu Glu Gly Gly
```

```
          115                    120                    125
Gly Gly Gly Gly Gly Met Glu Lys Ser Ser Gly Pro Trp Asn Lys Thr
    130                    135                    140
Ala Pro Val Gln Ala Pro Ala Pro Val Ile Val Thr Glu Thr Pro
145                    150                    155                    160
Glu Pro Ala Met Thr Ser Gly Val Tyr Arg Pro Pro Gly Ala Arg Leu
                165                    170                    175
Thr Thr Thr Arg Lys Thr Pro Gln Gly Pro Pro Glu Ile Tyr Gln Xaa
                180                    185                    190
Tyr His Ser Ser His Pro Leu Ala Val Asn Leu Pro Lys His Val Glu
        195                    200                    205
Ser Arg Lys Asp Lys Glu Met Glu Lys Ser Phe Glu Val Val Arg His
        210                    215                    220
Lys Asn Arg Gly Arg Asp Glu Val Ser Lys Asn Gln Ala Leu Lys Leu
225                    230                    235                    240
Gln Leu Asp Asn Gln Tyr Ala Val Leu Glu Asn Gln Lys Ser Ser His
                245                    250                    255
Ser Gln Tyr Asn
            260
```

```
        <210> 274
        <211> 122
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(122)
        <223> Xaa = X or * as defined in Table 6


        <400> 274
His Leu Arg Ile Leu Arg Asp Ser Arg Thr His Ser Tyr Phe Leu Thr
 1               5                   10                  15
Ser Leu Arg Gly Glu Asn Asn Pro Trp Thr Asp Gln Ser Pro Cys Ala
            20                  25                  30
Ala Ala Ser Arg Ala Gln His Leu His Pro Ala Ala Val Ala Ala Ala
        35                  40                  45
Thr Met Pro Lys Thr Lys Ala Glu Gly Asp Ala Lys Gly Asp Lys Ala
    50                  55                  60
Lys Val Lys Asp Glu Pro Gln Val Thr Arg Ala Ala Ile Gln Thr Asn
65                  70                  75                  80
Thr Phe Ile Phe Lys Cys Xaa Ile Glu Pro Gln Lys Gln Ile Tyr Ile
                85                  90                  95
Leu Tyr Ile Gln Asn Ser Cys Gln Ile Ser Leu Leu Ile Leu Pro Lys
            100                 105                 110
Ser Thr Leu Met Lys Trp Met Gln Thr Leu
        115                 120
```

```
        <210> 275
        <211> 630
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(630)
        <223> Xaa = X or * as defined in Table 6
```

<400> 275

Ser	Ser	Val	Glu	Gln	Ala	Ser	Val	Glu	Val	Pro	Asp	Gly	Pro	Thr	Leu
1				5					10					15	
His	Asp	Pro	Asp	Leu	Tyr	Ile	Glu	Ile	Val	Lys	Asn	Thr	Lys	Ser	Val
			20					25					30		
Pro	Glu	Tyr	Ser	Glu	Val	Ala	Tyr	Pro	Asp	Tyr	Phe	Gly	His	Ile	Pro
		35					40					45			
Pro	Pro	Phe	Lys	Glu	Pro	Ile	Leu	Glu	Arg	Pro	Tyr	Gly	Val	Gln	Arg
	50					55					60				
Thr	Lys	Ile	Ala	Gln	Asp	Ile	Glu	Arg	Leu	Ile	His	Gln	Ser	Asp	Ile
65					70					75					80
Ile	Asp	Arg	Val	Val	Tyr	Asp	Leu	Asp	Asn	Pro	Asn	Tyr	Thr	Ile	Pro
				85					90					95	
Glu	Glu	Gly	Asp	Ile	Leu	Lys	Phe	Asn	Ser	Lys	Phe	Glu	Ser	Gly	Asn
			100					105					110		
Leu	Arg	Arg	Val	Ile	Gln	Ile	Arg	Lys	Asn	Glu	Tyr	Asp	Leu	Ile	Leu
		115					120					125			
Asn	Ser	Asp	Ile	Asn	Ser	Asn	His	Tyr	His	Gln	Trp	Phe	Tyr	Phe	Glu
	130					135					140				
Val	Ser	Gly	Met	Arg	Pro	Gly	Val	Ala	Tyr	Arg	Phe	Asn	Ile	Ile	Asn
145					150					155					160
Cys	Glu	Arg	Cys	Asn	Arg	Leu	Phe	Asn	Tyr	Gly	Met	Gln	Pro	Leu	Met
			165					170					175		
Tyr	Ser	Val	Gln	Glu	Ala	Leu	Asn	Ala	Arg	Pro	Trp	Trp	Ile	Arg	Met
			180					185					190		
Gly	Thr	Asp	Ile	Arg	Tyr	Tyr	Ile	Asn	His	Phe	Ser	Arg	Ser	Ser	Val
		195					200					205			
Ala	Ala	Gly	Gly	Ala	Gln	Arg	Gly	Lys	Ser	Tyr	Tyr	Thr	Ile	Thr	Phe
	210					215					220				
Thr	Val	Gln	Phe	Ser	Thr	Xaa	Arg	Met	Asp	Val	Cys	Tyr	Phe	Ala	Tyr
225					230					235					240
Ile	His	Tyr	Pro	Tyr	Thr	Tyr	Ser	Thr	Leu	Gln	Met	His	Leu	Gln	Lys
				245					250					255	
Leu	Glu	Ser	Ala	His	Asn	Pro	Gln	Gln	Ile	Tyr	Phe	Arg	Lys	Asp	Val
			260					265					270		
Leu	Cys	Glu	Thr	Leu	Ser	Gly	Asn	Ser	Cys	Pro	Leu	Val	Thr	Ile	Thr
		275					280					285			
Ala	Met	Pro	Glu	Ser	Asn	Tyr	Tyr	Glu	His	Ile	Cys	His	Phe	Arg	Asn
	290					295					300				
Arg	Pro	Tyr	Val	Leu	Met	Tyr	Ala	Arg	Val	His	Pro	Gly	Glu	Thr	Asn
305					310					315					320
Ala	Ser	Trp	Gly	Tyr	Glu	Arg	Glu	Arg	Trp	Glu	Tyr	Leu	His	Glu	Ala
			325					330					335		
Ile	Asn	Pro	Thr	Gly	Phe	Arg	Ser	Leu	Arg	Arg	Asn	Leu	Tyr	Tyr	Ile
			340					345					350		
Phe	Lys	Ile	Val	Pro	Met	Leu	Asn	Pro	Asp	Gly	Val	Ile	Asn	Gly	Asn
		355					360					365			
His	Arg	Cys	Ser	Leu	Ser	Gly	Glu	Asp	Leu	Asn	Arg	Gln	Trp	Gln	Ser
		370					375					380			
Pro	Ser	Pro	Asp	Leu	His	Pro	Thr	Ile	Tyr	His	Ala	Lys	Gly	Leu	Leu
385					390					395					400
Gln	Tyr	Leu	Ala	Ala	Val	Lys	Arg	Leu	Pro	Leu	Val	Tyr	Cys	Asp	Tyr
			405					410					415		
His	Gly	His	Ser	Arg	Lys	Lys	Asn	Val	Phe	Met	Tyr	Gly	Cys	Ser	Ile
			420					425					430		
Lys	Glu	Thr	Val	Trp	His	Thr	Asn	Asp	Asn	Ala	Thr	Ser	Cys	Asp	Val
		435					440					445			
Val	Glu	Asp	Thr	Gly	Tyr	Arg	Thr	Leu	Pro	Lys	Ile	Leu	Ser	His	Ile
	450					455					460				
Ala	Pro	Ala	Phe	Cys	Met	Ser	Ser	Cys	Ser	Phe	Val	Val	Glu	Lys	Ser
465					470					475					480
Lys	Glu	Ser	Thr	Ala	Arg	Val	Val	Val	Xaa	Arg	Glu	Ile	Gly	Val	Gln
			485					490					495		
Arg	Ser	Tyr	Thr	Met	Glu	Ser	Thr	Leu	Cys	Gly	Cys	Asp	Gln	Gly	Lys

```
              500                       505                      510
Tyr Lys Gly Leu Gln Ile Gly Thr Arg Glu Leu Glu Glu Met Gly Ala
        515                       520                      525
Lys Phe Cys Val Gly Leu Leu Arg Leu Lys Arg Leu Thr Ser Pro Leu
        530                       535                      540
Glu Tyr Asn Pro Ala Leu Pro Ser Pro Ala Leu Thr Phe Glu Asn Asp
545                       550                       555                  560
Leu Asn Xaa Ile Gln Ala Cys Lys Val Thr Ser Pro Tyr Pro Leu Met
                     565                       570                      575
Ser Leu Asp Glu Asp Glu Pro Arg Phe Leu Glu Glu Val Asp Tyr Ser
                580                       585                      590
Ala Glu Ser Asn Asp Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly
            595                       600                      605
Asp Tyr Glu Pro Ser Ala Gln Glu Glu Val Leu Ser Asp Ser Glu Leu
        610                       615                      620
Ser Arg Thr Tyr Leu Pro
625                       630
```

```
        <210> 276
        <211> 812
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(812)
        <223> Xaa = X or * as defined in Table 6


        <400> 276
Ile Lys Ala Leu Ser Ser Ser Ala Glu Asp Ala Ser Leu Val Asn Ala
 1               5                      10                      15
Ser Ile Ser Ser Ser Val Lys Ala Thr Ser Pro Val Lys Ser Thr Thr
                20                      25                      30
Ser Ile Thr Asp Ala Lys Ser Cys Glu Gly Gln Asn Pro Glu Leu Leu
            35                      40                      45
Pro Lys Thr Pro Ile Ser Pro Leu Lys Thr Gly Val Ser Lys Pro Ile
        50                      55                      60
Val Lys Ser Thr Leu Ser Gln Thr Val Pro Ser Lys Gly Glu Leu Ser
65                      70                       75                      80
Arg Glu Ile Cys Leu Gln Ser Gln Ser Lys Asp Lys Ser Thr Thr Pro
                85                      90                      95
Gly Gly Thr Gly Ile Lys Pro Phe Leu Glu Arg Phe Gly Glu Arg Cys
            100                     105                     110
Gln Glu His Ser Lys Glu Ser Pro Ala Arg Ser Thr Pro His Arg Thr
        115                     120                     125
Pro Ile Ile Thr Pro Asn Thr Lys Ala Ile Gln Glu Arg Leu Phe Lys
    130                     135                     140
Gln Asp Thr Ser Ser Ser Thr Thr His Leu Ala Gln Gln Leu Lys Gln
145                     150                     155                     160
Glu Arg Gln Lys Glu Leu Ala Cys Leu Arg Gly Arg Phe Asp Lys Gly
                165                     170                     175
Asn Ile Trp Ser Ala Glu Lys Gly Gly Asn Ser Lys Ser Lys Gln Leu
                180                     185                     190
Glu Thr Lys Gln Glu Thr His Cys Gln Ser Thr Pro Leu Lys Lys His
            195                     200                     205
Gln Gly Val Ser Lys Thr Gln Ser Leu Pro Val Thr Glu Lys Val Thr
        210                     215                     220
Glu Asn Gln Ile Pro Ala Lys Asn Ser Ser Thr Glu Pro Lys Glu Val
225                     230                     235                     240
Ile Arg Glu Ile Glu Met Ser Val Asp Asp Asp Ile Asn Ser Ser
                245                     250                     255
```

Lys Val Ile Asn Asp Leu Phe Ser Asp Val Leu Glu Glu Gly Glu Leu
            260   265   270
Asp Met Glu Lys Ser Gln Ala Gly Asp Gly Ser Ser Ile Ser Arg Thr
        275   280   285
Ala Ala Lys Asn Arg Lys Met His Xaa Ile Ser Pro Gln Cys Leu Tyr
        290   295   300
Leu His His Trp His Lys Gln Leu Val Xaa Val Xaa Cys Pro His Leu
305   310   315   320
Asp Trp Asn Xaa Lys Thr Pro Ala Glu Val Met Lys Val Gln Asn Gln
                325   330   335
Glu Asn Ser Lys Glu Leu Val Ser Arg Arg Ala Glu Ser Gly Asp Ser
            340   345   350
Leu Gly Ser Glu Asp Arg Asp Leu Leu Tyr Arg Ser Gln Arg Phe Lys
        355   360   365
Glu Thr Glu Arg Pro Ser Ile Lys Gln Val Ile Val Arg Lys Glu Asp
    370   375   380
Val Thr Ser Lys Leu Asp Glu Lys Asn Asn Ala Phe Pro Cys Gln Val
385   390   395   400
Asn Ile Lys Gln Lys Met Gln Glu Leu Asn Asn Glu Ile Asn Met Gln
            405   410   415
Gln Thr Val Ile Tyr Gln Ala Ser Gln Ala Leu Asn Cys Cys Val Asp
            420   425   430
Glu Glu His Gly Lys Gly Ser Leu Glu Glu Ala Glu Ala Glu Arg Leu
        435   440   445
Leu Leu Ile Ala Thr Gly Lys Arg Thr Leu Leu Ile Asp Glu Leu Asn
    450   455   460
Lys Leu Lys Asn Glu Gly Pro Gln Arg Lys Asn Xaa Gly Xaa Ser Ala
465   470   475   480
Pro Ser Glu Phe Ile Ala Ile Pro Lys Asp Gln Phe Thr Leu Ser Glu
                485   490   495
Ile Arg Leu Pro Xaa Lys Ala Asp Phe Val Cys Ser Thr Val Gln Lys
            500   505   510
Pro Asp Ala Ala Asn Tyr Tyr Tyr Leu Ile Ile Leu Lys Ser Arg Ser
        515   520   525
Glu Asn Met Val Ala Thr Pro Leu Ala Ser Thr Ser Asn Ser Leu Asn
    530   535   540
Gly Asp Ala Leu Thr Phe Thr Thr Thr Phe Thr Leu Gln Asp Val Ser
545   550   555   560
Asn Asp Phe Glu Ile Asn Ile Glu Val Tyr Ser Leu Val Gln Lys Lys
                565   570   575
Asp Pro Ser Gly Leu Asp Lys Lys Lys Lys Thr Ser Lys Ser Lys Lys
        580   585   590
Ser Asn Ile His Ser Ser Val Met Ala Ser Pro Gly Gly Leu Ser Ala
    595   600   605
Val Arg Thr Ser Asn Phe Ala Leu Val Gly Ser Tyr Thr Leu Ser Leu
    610   615   620
Ser Ser Val Gly Asn Thr Lys Phe Val Leu Asp Lys Val Pro Phe Leu
625   630   635   640
Ser Ser Leu Glu Gly His Ile Tyr Leu Lys Ile Lys Cys Gln Val Asn
            645   650   655
Ser Ser Val Glu Glu Arg Gly Phe Leu Gly Cys Pro Gly Gly Gly Arg
        660   665   670
Leu Gln Pro Lys Arg Gln Thr Ile Phe Glu Asp Val Ser Gly Phe Gly
    675   680   685
Ala Trp His Arg Arg Trp Cys Val Leu Ser Gly Asn Cys Ile Ser Tyr
    690   695   700
Trp Thr Tyr Pro Asp Asp Glu Lys Arg Lys Asn Pro Ile Gly Arg Ile
705   710   715   720
Asn Leu Ala Asn Cys Thr Ser Arg Gln Ile Glu Pro Ala Asn Arg Glu
                725   730   735
Phe Cys Ala Arg Arg Asn Thr Phe Glu Leu Ile Thr Val Arg Pro Gln
            740   745   750
Arg Glu Asp Asp Arg Glu Thr Leu Val Thr Asn Ala Gly Thr His Ser
        755   760   765

172

```
Val Phe Thr Lys Asn Trp Leu Ser Ala Asp Thr Lys Glu Glu Arg Asp
    770                 775                 780
Leu Trp Met Gln Lys Leu Asn Gln Val Leu Cys Asp Ile Arg Leu Trp
785                 790                 795                 800
Gln Pro Asp Ala Cys Tyr Lys Pro Ile Gly Lys Pro
                805                 810
```

```
        <210> 277
        <211> 772
        <212> PRT
        <213> Homo sapiens


        <400> 277
Met Gln Ile Asn Glu Thr Ile Trp Asp Thr Val Gly Ala Ala Ser Arg
 1               5                  10                  15
His Gly Glu Gly Glu Arg Gln Ala Lys Ser Ser Thr Arg Gly Cys Thr
            20                  25                  30
His Leu Ala Glu Gly Gln Gly Ile Tyr Leu Gln Glu Glu Gln Ser Pro
        35                  40                  45
Pro Glu Met Cys Thr Arg Val Met Glu Lys Arg Glu Gly Leu Thr Ile
    50                  55                  60
Glu Arg Glu Arg Asp Pro Leu Leu Pro Val Trp Lys Ala Leu Gly Ile
65                  70                  75                  80
Gln Ala His Lys Cys Val Ala His Thr Thr Asn Pro Ser Lys Ala Thr
                85                  90                  95
Ala Val His Leu Pro His Leu Thr Met Gln Pro Gln Gly Cys Leu Met
            100                 105                 110
Ser Phe Phe Pro Thr Ala Ala Glu Phe Ser Thr Tyr Gly Gln Glu Leu
        115                 120                 125
Tyr Leu Glu Asn Asn Gln Ile Glu Glu Ile Thr Glu Ile Cys Phe Asn
    130                 135                 140
His Thr Arg Lys Ile Asn Val Ile Val Leu Arg Tyr Asn Lys Ile Glu
145                 150                 155                 160
Glu Asn Arg Ile Ala Pro Leu Ala Trp Ile Asn Gln Glu Asn Leu Glu
                165                 170                 175
Ser Ile Asp Leu Ser Tyr Asn Lys Leu Tyr His Val Pro Ser Tyr Leu
            180                 185                 190
Pro Lys Ser Leu Leu His Leu Val Leu Leu Gly Asn Gln Ile Glu Arg
        195                 200                 205
Ile Pro Gly Tyr Val Phe Gly His Met Glu Pro Gly Leu Glu Tyr Leu
    210                 215                 220
Tyr Leu Ser Phe Asn Lys Leu Ala Asp Asp Gly Met Asp Arg Val Ser
225                 230                 235                 240
Phe Tyr Gly Ala Tyr His Ser Leu Arg Glu Leu Phe Leu Asp His Asn
                245                 250                 255
Asp Leu Lys Ser Ile Pro Pro Gly Ile Gln Glu Met Lys Ala Leu His
            260                 265                 270
Phe Leu Arg Leu Asn Asn Asn Lys Ile Arg Gly Asn Lys Gln Glu Ile
        275                 280                 285
Lys Gln Thr Ser Lys Gln Ala Ser Ala Val Gln Ser Glu Lys Trp Val
    290                 295                 300
Thr Met Arg Arg Ala His Trp Gly Leu Arg Ala Ala Arg Arg Leu Arg
305                 310                 315                 320
Pro Pro Ser Thr Ala Trp Ile Asn Ser Arg Ser Arg Pro Val Pro Val
                325                 330                 335
Glu Gln Thr His Cys Gly Leu Ala Val Ala Glu Glu Arg Lys Asp Leu
            340                 345                 350
Phe Met Phe Phe Arg Ser Leu His Phe Phe Val Glu Trp Phe Glu Tyr
        355                 360                 365
Arg Lys Arg Thr Phe Lys His Leu Lys Trp Asp Glu Asp Tyr Asp Gln
    370                 375                 380
```

173

```
Glu Pro Asp Asp Asp Tyr Gln Thr Gly Phe Pro Phe Arg Gln Asn Val
385                 390                 395                 400
Asp Tyr Gly Val Pro Phe His Gln Tyr Thr Leu Gly Cys Val Ser Glu
                405                 410                 415
Cys Phe Cys Pro Thr Asn Phe Pro Ser Ser Met Tyr Cys Asp Asn Arg
                420                 425                 430
Lys Leu Lys Thr Ile Pro Asn Ile Pro Met His Ile Gln Gln Leu Tyr
                435                 440                 445
Leu Gln Phe Asn Glu Ile Glu Ala Val Thr Ala Asn Ser Phe Ile Asn
    450                 455                 460
Ala Thr His Leu Lys Glu Ile Asn Leu Ser His Asn Lys Ile Lys Ser
465                 470                 475                 480
Gln Lys Ile Asp Tyr Gly Val Phe Ala Lys Leu Pro Asn Leu Leu Gln
                485                 490                 495
Leu His Leu Glu His Asn Asn Leu Glu Glu Phe Pro Phe Pro Leu Pro
                500                 505                 510
Lys Ser Leu Glu Arg Leu Leu Leu Gly Tyr Asn Glu Ile Ser Lys Leu
    515                 520                 525
Gln Thr Asn Ala Met Asp Gly Leu Val Asn Leu Thr Met Leu Asp Leu
    530                 535                 540
Cys Tyr Asn Tyr Leu His Asp Ser Leu Leu Lys Asp Lys Ile Phe Ala
545                 550                 555                 560
Lys Met Glu Lys Leu Met Gln Leu Asn Leu Cys Ser Asn Arg Leu Glu
                565                 570                 575
Ser Met Pro Pro Gly Leu Pro Ser Ser Leu Met Tyr Leu Ser Leu Glu
                580                 585                 590
Asn Asn Ser Ile Ser Ser Ile Pro Glu Lys Tyr Phe Asp Lys Leu Pro
    595                 600                 605
Lys Leu His Thr Leu Arg Met Ser His Asn Lys Leu Gln Asp Ile Pro
    610                 615                 620
Tyr Asn Ile Phe Asn Leu Pro Asn Ile Val Glu Leu Ser Val Gly His
625                 630                 635                 640
Asn Lys Leu Lys Gln Ala Phe Tyr Ile Pro Arg Asn Leu Glu His Leu
                645                 650                 655
Tyr Leu Gln Asn Asn Glu Ile Glu Lys Met Asn Leu Thr Val Met Cys
                660                 665                 670
Pro Ser Ile Asp Pro Leu His Tyr His His Leu Thr Tyr Ile Arg Val
    675                 680                 685 .
Asp Gln Asn Lys Leu Lys Glu Pro Ile Ser Ser Tyr Ile Phe Phe Cys
    690                 695                 700
Phe Pro His Ile His Thr Ile Tyr Tyr Gly Glu Gln Arg Ser Thr Asn
705                 710                 715                 720
Gly Gln Thr Ile Gln Leu Lys Thr Gln Val Phe Arg Arg Phe Pro Asp
                725                 730                 735
Asp Asp Asp Glu Ser Glu Asp His Asp Asp Pro Asp Asn Ala His Glu
                740                 745                 750
Ser Pro Glu Gln Glu Gly Ala Glu Gly His Phe Asp Leu His Tyr Tyr
    755                 760                 765
Glu Asn Gln Glu
    770
```

```
<210> 278
<211> 65
<212> PRT
<213> Homo sapiens


.<400> 278
Ser Arg Arg Arg Gly Gly Val Ser Ala Pro Thr Ser Phe Tyr Gly Arg
  1           5                 10                  15
Asp Arg Arg Met Phe Pro Ala Gln Glu Glu Ala Asp Arg Thr Val Phe
              20                  25                  30
```

```
Val Gly Asn Leu Glu Ala Arg Val Arg Glu Glu Ile Leu Tyr Glu Leu
        35                      40                      45
Phe Leu Gln Val Leu Cys Pro Arg Glu Met Gly Ile Leu Ser Ile Ser
        50                      55                      60
Pro
65
```

```
<210> 279
<211> 294
<212> PRT
<213> Homo sapiens
```

```
<400> 279
Met Ser Arg Trp Gly Ala Ala Val Gly Gln Gly Ala Leu Arg Glu Glu
1               5                       10                      15
His Phe Ala His Ala His Ile Thr Glu Arg Thr Arg Arg Val Arg Glu
                20                      25                      30
Gly Arg Arg Lys Arg Arg Ser Ser Leu Leu Thr Thr Ser Pro Thr Ser
        35                      40                      45
Ala Asn Ala Gln Ala His Phe Leu Lys Leu Lys Val Ser Ile Asp Lys
        50                      55                      60
Gly Pro Gln Asn Arg Ala Gly Ala Ile Val Pro Trp Phe Ala Lys Met
65                      70                      75                      80
Ser Phe Pro Lys Tyr Lys Pro Ser Ser Leu Arg Thr Leu Pro Glu Thr
                85                      90                      95
Leu Asp Pro Ala Glu Tyr Asn Ile Ser Pro Glu Thr Arg Arg Ala Gln
            100                     105                     110
Ala Glu Arg Leu Ala His Arg Ala Gln Leu Lys Arg Glu Tyr Leu Leu
        115                     120                     125
Gln Tyr Asn Asp Pro Asn Arg Arg Gly Leu Ile Glu Asn Pro Ala Leu
        130                     135                     140
Leu Arg Trp Ala Tyr Ala Arg Thr Ile Asn Val Tyr Pro Asn Phe Lys
145                     150                     155                     160
Pro Thr Pro Lys Ser Ser Leu Met Gly Ala Phe Val Trp Asp Phe Gly
                165                     170                     175
Pro Leu Ile Phe Ile Tyr Tyr Ile Ile Lys Thr Glu Arg Trp Asp Pro
                180                     185                     190
Asn Gln Arg Trp Leu Thr Asp Ser Arg Ile Leu Lys Tyr Glu Ala Ile
            195                     200                     205
Leu Leu Glu Arg Asp Asp Leu Thr Leu Thr Thr Asp Asn Ser Leu Asn
        210                     215                     220
Pro Ala Ala Phe Leu Arg Gly Asn Pro Asn Pro Glu Glu Pro Glu His
225                     230                     235                     240
Lys Cys Leu Asp Leu Ile Ser Tyr Gln Thr Arg Val Arg Leu Asp Leu
                245                     250                     255
Ser Lys Thr Pro Phe Gln Thr Gly Arg His Leu Phe Ile Asp Gly Ser
                260                     265                     270
Ser Leu Val Ile Gly Gly Lys Gly His Asn Gly Tyr Ser Val Val Asp
        275                     280                     285
Gly Glu Thr Leu Thr Lys
        290
```

```
<210> 280
<211> 198
<212> PRT
<213> Homo sapiens
```

```
<400> 280
```

175

```
Met Gln Thr Phe Thr Thr Cys Ile Ser Tyr Ser Glu Tyr Ser Cys Met
1               5                   10                  15
Leu Leu Ala Asn Ala Ser Ser His Gly Thr Leu Tyr Cys Lys Leu Arg
            20                  25                  30
Val Gly Ile Cys Leu Leu Met Val Pro Ala Val Lys Asn Gln Ala Ser
            35                  40                  45
Gly Ser Ala Arg Gly Ala Thr Lys Val Arg Arg Lys Cys Gln Ala Gly
    50                  55                  60
Cys Gln Asn Glu His Leu Gly Glu Leu Asp Asp Gly Thr Asp Gly Lys
65                  70                  75                  80
Asn Gln Leu Asn Ile Arg Glu Asn Gly Gly Arg Gly Gln Asn Cys Glu
                85                  90                  95
Gln Glu Leu Glu Glu Ser Val Ala Glu Lys Asp Leu Ser Gln Thr Ser
            100                 105                 110
Arg Asp Leu Glu Lys Met Met Ser Lys His Ile Phe Leu Lys Pro Met
            115                 120                 125
Leu Ser Ile Ser Asp Leu Val Asn Phe Leu Met Gln Val Ser Lys Val
    130                 135                 140
Leu Val Lys Thr Ala Glu Gly Ile Val Leu Gln Gln Leu Pro Leu Ala
145                 150                 155                 160
Phe Pro Ala Leu His Phe His Ala Tyr Gly Asn Leu Phe Pro Val Cys
                165                 170                 175
Ser Phe Lys His Tyr Ile Tyr Met Ile Asp His Pro Ile Phe Ile Ser
            180                 185                 190
Ile Pro Asp Phe Leu Thr
    195
```

```
        <210> 281
        <211> 1352
        <212> PRT
        <213> Homo sapiens


        <400> 281
Met Pro Val Pro Ser Arg His Ile Asn Ile Gly Arg Ser Gln Ser Trp
1               5                   10                  15
Asp Ala Ala Gly Trp Tyr Glu Gly Pro Trp Glu Asn Ala Glu Ser Leu
            20                  25                  30
Arg Pro Leu Gly Arg Arg Ser Ser Leu Thr Tyr Gly Thr Ala Glu Gly
        35                  40                  45
Thr Trp Phe Glu Pro Asn His Arg Pro Gln Asp Ala Ala Leu Pro Val
    50                  55                  60
Ala Ala Glu Pro Tyr Leu Tyr Arg Glu Ala Val Tyr Asn Ser Val Ala
65                  70                  75                  80
Ala Arg Lys Gly Ser Thr Pro Asp Phe Thr Phe Tyr Asp Ser Arg Gln
                85                  90                  95
Ala Val Met Ser Gly Arg Ser Pro Leu Leu Pro Arg Glu Tyr Tyr Ser
            100                 105                 110
Asp Pro Ser Gly Ala Ala Arg Val Pro Lys Glu Pro Pro Leu Tyr Arg
    115                 120                 125
Asp Pro Gly Val Ser Arg Pro Val Pro Ser Tyr Gly Val Leu Gly Ser
    130                 135                 140
Arg Thr Ser Trp Asp Pro Met Gln Gly Arg Ser Pro Ala Leu Gln Asp
145                 150                 155                 160
Ala Gly His Leu Tyr Arg Asp Pro Gly Gly Lys Met Ile Pro Gln Gly
            165                 170                 175
Arg Gln Thr Gln Ser Arg Ala Ala Ser Pro Gly Arg Tyr Gly Arg Glu
            180                 185                 190
Gln Pro Asp Thr Arg Tyr Gly Ala Glu Val Pro Ala Tyr Pro Leu Ser
    195                 200                 205
Gln Val Phe Ser Asp Ile Ser Glu Arg Pro Ile Asp Pro Ala Pro Ala
    210                 215                 220
```

```
Arg Gln Val Ala Pro Thr Cys Leu Val Val Asp Pro Ser Ser Ala Ala
225             230             235             240
Ala Pro Glu Gly Ser Thr Gly Val Ala Pro Gly Ala Leu Asn Arg Gly
            245             250             255
Tyr Gly Pro Ala Arg Glu Ser Ile Pro Ser Lys Met Ala Tyr Glu Thr
            260             265             270
Tyr Glu Ala Asp Leu Ser Thr Phe Gln Gly Pro Gly Gly Lys Arg Thr
        275             280             285
Val Leu Pro Glu Phe Leu Ala Phe Leu Arg Ala Glu Gly Leu Ala Glu
        290             295             300
Ala Thr Leu Gly Ala Leu Leu Gln Gln Gly Phe Asp Ser Pro Ala Val
305             310             315             320
Leu Ala Thr Leu Glu Asp Ala Asp Ile Lys Ser Val Ala Pro Asn Leu
            325             330             335
Gly Gln Ala Arg Val Leu Ser Arg Leu Ala Asn Ser Cys Arg Thr Glu
            340             345             350
Met Gln Leu Arg Arg Gln Asp Arg Gly Gly Pro Leu Pro Arg Ala Arg
        355             360             365
Ser Ser Ser Phe Ser His Arg Ser Glu Leu Leu His Gly Asp Leu Ala
370             375             380
Ser Leu Gly Ala Ala Ala Pro Leu Gln Thr Ala Ser Pro Arg Ala Gly
385             390             395             400
Asp Pro Ala Arg Arg Pro Ser Ser Ala Pro Ser Gln His Leu Leu Glu
            405             410             415
Thr Ala Ala Thr Tyr Ser Ala Pro Gly Val Gly Thr His Ala Pro His
            420             425             430
Phe Pro Ser Asn Ser Gly Tyr Ser Ser Pro Thr Pro Cys Ala Leu Thr
            435             440             445
Ala Arg Leu Ser Pro Thr Tyr Pro Leu Gln Ala Gly Val Ala Leu Thr
450             455             460
Asn Pro Gly Pro Ser Asn Pro Leu His Pro Gly Pro Arg Thr Ala Tyr
465             470             475             480
Ser Thr Ala Tyr Thr Val Pro Met Glu Leu Leu Lys Arg Glu Arg Asn
            485             490             495
Val Ala Ala Ser Pro Leu Pro Ser Pro His Gly Ser Pro Gln Val Leu
            500             505             510
Arg Lys Pro Gly Ala Pro Leu Gly Pro Ser Thr Leu Pro Pro Ala Ser
        515             520             525
Gln Ser Leu His Thr Pro His Ser Pro Tyr Gln Lys Val Ala Arg Arg
        530             535             540
Thr Gly Ala Pro Ile Ile Val Ser Thr Met Leu Ala Pro Glu Pro Ile
545             550             555             560
Gln Phe Ala Gly Gln Ala Val Gln Ser Asp Asn Val Arg Lys Ala Tyr
            565             570             575
Ala Ala Gly Thr Pro Val Arg Pro Thr Ser Pro Gly Asp Thr Asp Lys
            580             585             590
Trp Gly Leu Gln Ala Arg Ala Pro Gly Arg Ala Val Asp Pro Arg Asn
        595             600             605
Met Ile Ser Ala Gln Glu His Lys Val Val Glu Cys Met Ala Arg Arg
610             615             620
Ser Ala Thr Cys Phe Val Phe Gly Gln Leu Cys Arg Leu His Ser Thr
625             630             635             640
Ser Ser Asp Pro Val Gly Val Asp Phe Ile Leu Ser Met Glu Asp Val
            645             650             655
Gly Arg Gly Lys Ser Arg Asn Pro Asp Ser Trp Ser Pro Asn Ala Val
            660             665             670
Val Trp Asp Ala Ser Gly Val Gly Gly Glu Arg Val Leu Gln Tyr Gln
        675             680             685
Leu Asp Met Asn Thr Val Pro Pro Gln Gly Trp Thr Thr Arg Lys Thr
        690             695             700
Arg Val Cys Cys Lys His Glu Ala Ser Pro Ser Pro Ile Ser Ala Leu
705             710             715             720
Ala Ala Ile Ala Lys Glu Glu Gly Val Ile Leu Leu Leu Trp Thr Phe
            725             730             735
```

177

```
Thr Leu Gly Asn Lys Arg Leu Gly Gly Ser Ala Thr Arg Val Gly Tyr
        740                     745                 750
Ala Glu Ala Gln Ala Glu Ala Pro Ser Cys Lys Ala Thr Thr Val Thr
        755             760                 765
Leu Ser Ser Gly Ser Ser His Glu Cys Asp Ser Ser Val Ser Ser Lys
        770             775                 780
Thr Ala Thr Cys Arg Asp Phe Met Gly Gln Pro Trp Gly His Ala Ser
785             790                 795                     800
Ile Pro Pro Thr Pro Asn Pro Pro Pro Ala Val Val Pro Gly Ile
                805                 810                 815
Phe Ser Gln His Glu Asn Pro Leu Ala Phe Leu Phe Ser Arg Leu Ala
            820             825             830
Met Lys Asp Leu Leu Pro Gly Phe Glu Pro Gln Thr Leu Asp Arg Ser
        835             840                 845
Arg Ala Ser Leu Ser His Val Leu Arg Ala Arg Pro Ser Gly Arg Val
    850             855                 860
Glu Gly Ile Arg Pro Gln Ile Met Asn Gly Pro Leu His Pro Arg Pro
865             870                 875                     880
Leu Val Ala Leu Leu Asp Gly Arg Asp Cys Thr Val Glu Met Pro Ile
            885                 890                 895
Leu Lys Asp Leu Ala Thr Val Ala Phe Cys Asp Ala Gln Ser Thr Gln
        900                 905                 910
Glu Ile His Glu Lys Val Leu Asn Glu Ala Val Gly Ala Met Met Tyr
        915  .            920                 925
His Thr Ile Thr Leu Thr Arg Glu Asp Leu Glu Lys Phe Lys Ala Leu
    930             935                 940
Arg Val Ile Val Arg Ile Gly Ser Gly Tyr Asp Asn Val Asp Ile Lys
945             950                 955                     960
Ala Ala Gly Glu Leu Gly Glu Cys Glu Ala Ala Leu Ala Ala Trp Ser
            965                 970                 975
Cys Pro Glu Leu Cys Gly Pro Cys Ser Gly Gly Leu Gly Glu Ala Ala
            980             985                 990
Gly Thr Gly Thr Thr Glu Gln Pro Leu Leu Ala Val Ala Arg Trp Leu
        995             1000                1005
Pro Pro Gly Arg Ala Val Glu His Leu Ala Ala Leu Pro Ser His Asp
    1010            1015                1020
Thr Gly Ile Ala Val Cys Asn Ile Pro Ser Ala Ala Val Glu Glu Thr
1025                1030                1035                1040
Ala Asp Ser Thr Ile Cys His Ile Leu Asn Leu Tyr Arg Arg Asn Thr
            1045                1050                1055
Trp Leu Tyr Gln Ala Leu Arg Glu Gly Thr Arg Val Gln Ser Val Glu
        1060                1065                1070
Gln Ile Arg Glu Val Ala Ser Gly Ala Ala Arg Ile Arg Gly Glu Thr
    1075                1080                1085
Leu Gly Leu Ile Gly Phe Gly Arg Thr Gly Gln Ala Val Ala Val Arg
    1090                1095                1100
Ala Lys Ala Phe Gly Phe Ser Val Ile Phe Tyr Asp Pro Tyr Leu Gln
1105                1110                1115                1120
Asp Gly Ile Glu Arg Ser Leu Gly Val Gln Arg Val Tyr Thr Leu Gln
            1125                1130                1135
Asp Leu Leu Tyr Gln Ser Asp Cys Val Ser Leu His Cys Asn Leu Asn
        1140                1145                1150
Glu His Asn His His Leu Ile Asn Asp Phe Thr Ile Lys Gln Met Arg
        1155                1160                1165
Ala Gly Ser Ile Pro Leu Trp Asn Ala Ala Arg Gly Gly Leu Val Asp
    1170                1175                1180
Glu Lys Ala Leu Ala Gln Ala Leu Lys Glu Gly Arg Ile Arg Gly Ala
1185                1190                1195                1200
Ala Leu Asp Val His Glu Ser Glu Pro Phe Ser Phe Ala Gln Gly Pro
            1205                1210                1215
Leu Lys Asp Ala Pro Asn Leu Ile Cys Thr Pro His Thr Ala Trp Tyr
        1220                1225                1230
Ser Glu Gln Ala Ser Leu Glu Met Arg Glu Ala Ala Ala Thr Glu Ile
        1235                1240                1245
```

178

```
Arg Arg Ala Ile Thr Gly Arg Ile Pro Glu Ser Leu Arg Asn Cys Val
    1250              1255              1260
Asn Lys Glu Phe Phe Val Thr Ser Ala Pro Trp Ser Val Ile Asp Gln
1265              1270              1275              1280
Gln Ala Ile His Pro Glu Leu Asn Gly Ala Thr Tyr Arg Tyr Pro Pro
              1285              1290              1295
Gly Ile Val Gly Val Ala Pro Gly Gly Leu Pro Ala Ala Met Glu Gly
              1300              1305              1310
Ile Ile Pro Gly Gly Ile Pro Val Thr His Asn Leu Pro Thr Val Ala
          1315              1320              1325
His Pro Ser Gln Ala Pro Ser Pro Asn Gln Pro Thr Lys His Gly Asp
    1330              1335              1340
Asn Arg Glu His Pro Asn Glu Gln
1345              1350
```

```
        <210> 282
        <211> 181
        <212> PRT
        <213> Homo sapiens


        <400> 282
Leu Leu Lys Ile Ser Gly Ile Ile Leu Lys Thr Gly Glu Ser Gln Asn
  1               5                  10                  15
Gln Leu Ala Val Asp Gln Ile Ala Phe Gln Lys Lys Leu Phe Gln Thr
              20                  25                  30
Leu Arg Arg His Pro Ser Tyr Pro Lys Ile Ile Glu Glu Phe Val Ser
      35                  40                  45
Gly Leu Glu Ser Tyr Ile Glu Asp Glu Asp Ser Phe Arg Asn Cys Leu
      50                  55                  60
Leu Ser Cys Glu Arg Leu Gln Asp Glu Glu Ala Ser Met Gly Ala Ser
 65               70                  75                  80
Tyr Ser Lys Ser Leu Ile Lys Leu Leu Leu Gly Ile Asp Ile Leu Gln
                  85                  90                  95
Pro Ala Ile Ile Lys Thr Leu Phe Glu Lys Leu Pro Glu Tyr Phe Phe
              100                 105                 110
Glu Asn Lys Asn Ser Asp Glu Ile Asn Ile Pro Arg Leu Ile Val Ser
              115                 120                 125
Gln Leu Lys Trp Leu Asp Arg Val Val Asp Gly Lys Asp Leu Thr Thr
      130                 135                 140
Lys Ile Met Gln Leu Ile Ser Ile Ala Pro Glu Asn Leu Gln His Asp
145                 150                 155                 160
Ile Ile Thr Ser Leu Pro Glu Ile Leu Gly Asp Ser Gln His Ala Asp
              165                 170                 175
Val Gly Lys Glu Leu
              180
```

```
        <210> 283
        <211> 1385
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(1385)
        <223> Xaa = X or * as defined in Table 6


        <400> 283
Lys Arg Lys Arg Arg Arg Thr Trp Lys Arg Tyr Arg Ser Ile Ile Asp
```

```
       1                       5                        10                        15
His  Leu  Gln  Glu  Lys  Arg  Arg  Glu  Val  Thr  Leu  Arg  Val  Asp  Thr  Tyr
                20                            25                        30
Thr  Leu  Val  Gln  Pro  Glu  Ala  Glu  Asp  His  Val  Glu  Ser  Tyr  Arg  Ser
                35                       40                            45
Met  Pro  Ile  Tyr  Pro  Thr  Tyr  Asn  Glu  Val  His  Leu  Asp  Glu  Arg  Pro
           50                       55                       60
Phe  Leu  Arg  Pro  Asn  Ile  Ile  Ser  Gly  Lys  Tyr  Asp  Ser  Thr  Ala  Ile
65                            70                       75                        80
Tyr  Leu  Asp  Thr  His  Phe  Arg  Leu  Leu  Arg  Glu  Glu  Ile  Val  Arg  Pro
                     85                       90                       95
Leu  Arg  Glu  Gly  Ile  Leu  Glu  Leu  Leu  Gln  Ser  Phe  Glu  Asp  Gln  Gly
                100                      105                      110
Leu  Arg  Lys  Arg  Lys  Phe  Asp  Asp  Ile  Arg  Ile  Tyr  Phe  Asp  Thr  Arg
                115                      120                      125
Ile  Ile  Thr  Pro  Met  Cys  Ser  Ser  Ser  Gly  Ile  Val  Tyr  Lys  Val  Gln
           130                      135                      140
Phe  Asp  Thr  Lys  Pro  Leu  Lys  Phe  Val  Arg  Trp  Gln  Asn  Ser  Lys  Arg
145                      150                      155                           160
Leu  Leu  Tyr  Gly  Ser  Leu  Val  Cys  Met  Ser  Lys  Asp  Asn  Phe  Glu  Thr
                165                      170                      175
Phe  Leu  Phe  Ala  Thr  Val  Ser  Asn  Arg  Glu  Gln  Glu  Asp  Leu  Cys  Arg
                180                      185                      190
Gly  Ile  Val  Gln  Leu  Cys  Phe  Asn  Glu  Gln  Ser  Gln  Gln  Leu  Leu  Ala
           195                      200                      205
Glu  Val  Gln  Pro  Ser  Asp  Ser  Phe  Leu  Met  Val  Glu  Thr  Thr  Ala  Tyr
           210                      215                      220
Phe  Glu  Ala  Tyr  Arg  His  Val  Leu  Glu  Gly  Leu  Gln  Glu  Val  Gln  Glu
225                      230                      235                           240
Glu  Asp  Val  Pro  Phe  Gln  Arg  Asn  Ile  Val  Glu  Cys  Asn  Ser  His  Val
                     245                      250                      255
Lys  Glu  Pro  Arg  Tyr  Leu  Leu  Met  Gly  Gly  Arg  Tyr  Asp  Phe  Thr  Pro
                260                      265                      270
Leu  Ile  Glu  Asn  Pro  Ser  Ala  Thr  Gly  Glu  Phe  Leu  Arg  Asn  Val  Glu
           275                      280                      285
Gly  Leu  Arg  His  Pro  Arg  Ile  Asn  Val  Leu  Asp  Pro  Gly  Gln  Trp  Pro
           290                      295                      300
Ser  Lys  Glu  Ala  Leu  Lys  Leu  Asp  Asp  Ser  Gln  Met  Glu  Ala  Leu  Gln
305                      310                      315                           320
Phe  Ala  Leu  Thr  Arg  Glu  Leu  Ala  Ile  Ile  Gln  Gly  Pro  Pro  Gly  Thr
                325                      330                      335
Gly  Lys  Thr  Tyr  Val  Gly  Leu  Lys  Ile  Val  Gln  Ala  Leu  Leu  Thr  Asn
                340                      345                      350
Glu  Ser  Val  Trp  Gln  Ile  Ser  Leu  Gln  Lys  Phe  Pro  Ile  Leu  Val  Val
           355                      360                      365
Cys  Tyr  Thr  Asn  His  Ala  Leu  Asp  Gln  Phe  Leu  Gly  Arg  His  Leu  Gln
           370                      375                      380
Leu  Ser  Gly  Arg  Pro  Gly  Ile  Val  Arg  Val  Gly  Trp  Lys  Gly  Ala  Thr
385                      390                      395                           400
Val  Glu  Ile  Pro  Glu  Gly  Ser  Phe  Thr  Leu  Arg  Glu  Leu  Arg  Asn  Lys
                405                      410                      415
Arg  Glu  Phe  Arg  Arg  Asn  Leu  Pro  Met  His  Leu  Arg  Arg  Ala  Tyr  Met
                420                      425                      430
Ser  Ile  Met  Thr  Gln  Met  Lys  Glu  Ser  Glu  Gln  Glu  Leu  His  Glu  Gly
                435                      440                      445
Ala  Lys  Thr  Leu  Glu  Cys  Thr  Met  Arg  Gly  Val  Leu  Arg  Glu  Gln  Tyr
           450                      455                      460
Leu  Gln  Lys  Tyr  Ile  Ser  Pro  Pro  Ala  Leu  Gly  Lys  Ser  His  Glu  Trp
465                      470                      475                           480
Pro  Gln  Cys  Arg  Ile  Val  Asn  Gly  Phe  Ser  Ser  Gln  His  Trp  Lys  His
                485                      490                      495
Ser  His  Asp  Ala  Gly  Val  Ala  Xaa  Val  Leu  Val  Ser  Val  Leu  Ser  Arg
           500                      505                      510
Lys  Val  Phe  Leu  Gln  Gln  Asp  Leu  Arg  Ile  Gln  Pro  Gln  Ala  Glu  Gly
```

180

```
                515                    520                    525
Asp Glu Glu Glu Gly Glu Arg Glu Phe Arg Leu Ile Arg Asp
    530                    535                    540
Ser Gln Arg Glu Ala Asp Pro Asp Phe Lys Gln Thr Gly Xaa Leu Arg
545                    550                    555                    560
Arg Lys Arg Trp Xaa Gly Pro Ser Gly Gly Arg Arg Lys Arg Val Glu
                565                    570                    575
Gln Thr Arg Ser Trp Leu Lys Cys Phe Trp Pro Xaa Gly Xaa Thr Ile
                580                    585                    590
Val Ala Leu Gly Gln Gln Leu Asp Arg Ser Lys Pro Gln Glu Ser Gly
            595                    600                    605
Arg Pro Ser Asp Asn Gln Lys Lys Lys Met Lys Lys Arg Val Lys Asp
    610                    615                    620
Glu Leu Arg Lys Leu Asn Thr Met Thr Ala Ala Glu Ala Asn Glu Ile
625                    630                    635                    640
Glu Asp Val Trp Gln Leu Asp Leu Ser Ser Arg Trp Gln Leu Tyr Arg
                645                    650                    655
Leu Trp Leu Gln Leu Tyr Gln Ala Asp Thr Arg Arg Lys Ile Leu Ser
                660                    665                    670
Tyr Glu Arg Gln Tyr Arg Thr Ser Ala Glu Arg Met Ala Glu Leu Arg
            675                    680                    685
Leu Gln Glu Asp Leu His Ile Leu Lys Asp Ala Gln Val Val Gly Met
    690                    695                    700
Thr Thr Thr Gly Ala Ala Lys Tyr Arg Gln Ile Leu Gln Lys Val Glu
705                    710                    715                    720
Pro Arg Ile Val Ile Val Glu Glu Ala Ala Glu Val Leu Glu Ala His
                725                    730                    735
Thr Ile Ala Thr Leu Ser Lys Ala Cys Gln His Leu Ile Leu Ile Gly
                740                    745                    750
Asp His Gln Gln Leu Arg Pro Ser Ala Asn Val Tyr Asp Leu Ala Lys
        755                    760                    765
Asn Phe Asn Leu Glu Val Ser Leu Phe Glu Arg Leu Val Lys Val Asn
    770                    775                    780
Ile Pro Phe Val Arg Leu Asn Tyr Gln His Arg Met Cys Pro Glu Ile
785                    790                    795                    800
Ala Arg Leu Leu Thr Pro His Ile Tyr Gln Asp Leu Glu Asn His Pro
            805                    810                    815
Ser Val Leu Lys Tyr Glu Lys Ile Lys Gly Val Ser Ser Asn Leu Phe
        820                    825                    830
Phe Val Glu His Asn Phe Pro Glu Gln Glu Ser Lys Arg Arg Lys Ser
    835                    840                    845
His Gln Asn Gln His Glu Ala His Asn Val Val Glu Leu Cys Lys Tyr
    850                    855                    860
Phe Leu Cys Gln Glu Tyr Leu Pro Ser Gln Ile Thr Ile Leu Thr Thr
865                    870                    875                    880
Tyr Thr Gly Gln Leu Phe Cys Leu Arg Lys Leu Met Pro Ala Lys Thr
                885                    890                    895
Phe Ala Gly Val Arg Val His Val Val Asp Lys Tyr Gln Gly Glu Glu
        900                    905                    910
Asn Asp Ile Ile Leu Leu Ser Leu Val Arg Ser Asn Gln Glu Gly Lys
    915                    920                    925
Val Gly Phe Leu Gln Ile Ser Asn Arg Ile Cys Val Ala Leu Ser Arg
    930                    935                    940
Ala Lys Lys Gly Met Tyr Cys Ile Gly Asn Met Gln Met Leu Ala Lys
945                    950                    955                    960
Val Pro Leu Trp Ser Lys Ile Ile His Thr Leu Arg Glu Asn Asn Gln
                965                    970                    975
Ile Gly Pro Met Leu Arg Leu Cys Cys Gln Asn His Pro Glu Thr His
            980                    985                    990
Thr Leu Val Ser Lys Ala Ser Asp Phe Gln Lys Val Pro Glu Gly Gly
    995                    1000                    1005
Cys Ser Leu Pro Cys Glu Phe Arg Leu Gly Cys Gly His Val Cys Thr
    1010                    1015                    1020
Arg Ala Cys His Pro Tyr Asp Ser Ser His Lys Glu Phe Gln Cys Met
```

```
1025                1030               1035                1040
Lys Pro Cys Gln Lys Val Ile Cys Gln Glu Gly His Arg Cys Pro Leu
              1045              .         1050              1055
Val Cys Phe Gln Glu Cys Gln Pro Cys Gln Val Lys Val Pro Lys Thr
          1060              1065              1070
Ile Pro Arg Cys Gly His Glu Gln Met Val Pro Cys Ser Val Pro Glu
      1075              1080              1085
Ser Asp Phe Cys Cys Gln Glu Pro Cys Ser Lys Ser Leu Arg Cys Gly
  1090              1095              1100
His Arg Cys Ser His Pro Cys Gly Glu Asp Cys Val Gln Leu Cys Ser
1105              1110              1115              1120
Glu Met Val Thr Ile Lys Leu Lys Cys Gly His Ser Gln Pro Val Lys
              1125              1130              1135
Cys Gly His Val Glu Gly Leu Leu Tyr Gly Gly Leu Leu Val Lys Cys
          1140              1145              1150
Thr Thr Lys Cys Gly Thr Ile Leu Asp Cys Gly His Pro Cys Pro Gly
          1155              1160              1165
Ser Cys His Ser Cys Phe Glu Gly Arg Phe His Glu Arg Cys Gln Gln
      1170              1175              1180
Pro Cys Lys Arg Leu Leu Ile Cys Ser His Lys Cys Gln Lys Pro Cys
1185              1190              1195              1200
Ile Gly Glu Cys Pro Pro Cys Gln Arg Thr Cys Gln Asn Arg Cys Val
              1205              1210              1215
His Ser Gln Cys Lys Lys Lys Cys Glu Glu Leu Cys Ser Pro Cys Val
          1220              1225              1230
Glu Pro Met Cys Ser Arg Cys Gln His Tyr Gln Cys Thr Lys Leu Cys
      1235              1240              1245
Ser Glu Pro Cys Asn Arg Pro Pro Cys Tyr Val Pro Cys Thr Lys Leu
  1250              1255              1260
Leu Val Cys Gly His Pro Cys Ile Gly Leu Cys Gly Glu Pro Cys Pro
1265              1270              1275              1280
Lys Lys Cys Arg Ile Cys His Met Asp Glu Val Thr Gln Ile Phe Phe
          .  1285              1290              1295
Gly Phe Glu Asp Glu Pro Asp Ala Arg Phe Val Gln Leu Glu Asp Cys
          1300              1305              1310
Ser His Ile Phe Glu Val Gln Ala Leu Asp Arg Tyr Met Asn Glu Gln
      1315              1320              1325
Lys Asp Asp Glu Val Ala Ile Arg Leu Lys Val Cys Pro Ile Cys Gln
  1330              1335              1340
Val Pro Ile Arg Lys Asn Leu Ser Tyr Gly Thr Ser Ile Lys Gln Arg
1345              1350              1355              1360
Leu Glu Glu Ile Glu Ile Ile Glu Glu Lys Tyr Pro Gly Leu Ile Arg
              1365              1370              1375
Gly Asn Gly Asn Gln Pro Gly Thr Ala
              1380              1385
```

```
        <210> 284
        <211> 552
        <212> PRT
        <213> Homo sapiens


        <400> 284
Ala Glu Arg Lys Leu Ser Glu Lys Ser Leu Val Val Ala Ala Val Ala
  1           5               10              15
Pro Asp Asn Arg Asn Pro Ala Phe Thr Thr Met Gly Trp Leu Phe Leu
          20              25              30
Lys Val Leu Leu Ala Gly Val Ser Phe Ser Gly Phe Leu Tyr Pro Leu
      35              40              45
Val Asp Phe Cys Ile Ser Gly Lys Thr Arg Gly Gln Lys Pro Asn Phe
  50              55              60
Val Ile Ile Leu Ala Asp Asp Met Gly Trp Gly Asp Leu Gly Ala Asn
```

```
 65                            70                        75                        80
Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu Asp Lys Met Ala Ser Glu
                     85                        90                        95
Gly Met Arg Phe Val Asp Phe His Ala Ala Ser Thr Cys Ser Pro
                100                       105                       110
Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu Gly Leu Arg Asn Gly Val
            115                       120                       125
Thr Arg Asn Phe Ala Val Thr Ser Val Gly Gly Leu Pro Leu Asn Glu
        130                       135                       140
Thr Thr Leu Ala Glu Val Leu Gln Gln Ala Gly Tyr Val Thr Gly Ile
145                       150                       155                       160
Ile Gly Lys Trp His Leu Gly His His Gly Ser Tyr His Pro Asn Phe
                165                       170                       175
Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro Tyr Ser His Asp Met Gly
                180                       185                       190
Cys Thr Asp Thr Pro Gly Tyr Asn His Pro Pro Cys Pro Ala Cys Pro
            195                       200                       205
Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln Arg Asp Cys Tyr Thr Asp
        210                       215                       220
Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn Ile Val Glu Gln Pro Val
225                       230                       235                       240
Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala Glu Lys Ala Thr Gln Phe
                245                       250                       255
Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro Phe Leu Leu Tyr Val Ala
            260                       265                       270
Leu Ala His Met His Val Pro Leu Pro Val Thr Gln Leu Pro Ala Ala .
            275                       280                       285
Pro Arg Gly Arg Lys Ser Leu Tyr Gly Ala Gly Leu Trp Glu Met Asp
        290                       295                       300
Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp His Thr Val Lys Glu
305                       310                       315                       320
Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly Pro Trp Ala Gln Lys
                325                       330                       335
Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr Gly Phe Trp Gln Thr
            340                       345                       350
Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr Trp Glu Gly Gly His
        355                       360                       365
Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg Val Pro Val Asn Val
    370                       375                       380
Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile Phe Pro Thr Val Val
385                       390                       395                       400
Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg Arg Phe Asp Gly Val
            405                       410                       415
Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln Pro Gly His Arg Val
        420                       425                       430
Leu Phe His Pro Asn Ser Gly Ala Ala Gly Asp Phe Gly Ala Leu Gln
        435                       440                       445
Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr Ile Thr Gly Gly Ala
    450                       455                       460
Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu Gln His Lys Phe Pro
465                       470                       475                       480
Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu Ala Val Pro Leu Glu
                485                       490                       495
Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro Glu Val Arg Lys Val
            500                       505                       510
Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp Asn Ile Ser Ser Pro
        515                       520                       525
Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys Cys Asn Pro Tyr Gln
    530                       535                       540
Ile Ala Cys Arg Cys Gln Ala Ala
545                 550
```

```
<210> 285
<211> 294
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(294)
<223> Xaa = X or * as defined in Table 6


<400> 285
Pro Val Ala Thr Thr Ile Ser Gln Pro Leu Ser Leu Glu Ala Asp Met
1               5                   10                  15
Trp Ser Ile Gly Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro
            20                  25                  30
Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
        35                  40                  45
Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Glu Thr Ser Glu Leu Ala
    50                  55                  60
Gln Asp Phe Ile Arg Lys Leu Leu Gly Xaa Glu Thr Arg Lys Arg Val
65                  70                  75                  80
Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Ser Lys Gly Glu
            85                  90                  95
Gly Arg Ala Pro Glu Gln Arg Lys Thr Glu Pro Thr Gln Leu Lys Thr
        100                 105                 110
Lys His Leu Arg Glu Tyr Thr Leu Lys Cys His Ser Ser Met Pro Pro
    115                 120                 125
Asn Asn Cys Tyr Val Asn Phe Glu Arg Phe Ala Cys Val Val Glu Asp
    130                 135                 140
Val Ala Arg Val Asp Leu Gly Cys Arg Ala Leu Val Glu Ala His Asp
145                 150                 155                 160
Thr Ile Gln Asp Asp Val Glu Ala Leu Val Ser Ile Phe Asn Glu Lys
            165                 170                 175
Glu Ala Trp Tyr Arg Asp Glu Asn Glu Ser Ala Arg His Asp Leu Ser
        180                 185                 190
Gln Leu Arg Tyr Glu Phe Arg Lys Val Glu Ser Leu Lys Lys Leu Leu
    195                 200                 205
Arg Glu Asp Ile Gln Ala Thr Gly Cys Ser Leu Gly Ser Met Ala Arg
    210                 215                 220
Lys Leu Asp His Leu Gln Ala Gln Phe Glu Ile Leu Arg Gln Glu Leu
225                 230                 235                 240
Ser Ala Asp Leu Gln Trp Ile Gln Glu Leu Val Gly Ser Phe Gln Leu
            245                 250                 255
Glu Ser Gly Ser Ser Glu Gly Leu Gly Ser Thr Phe Tyr Gln Asp Thr
        260                 265                 270
Ser Glu Ser Leu Ser Glu Leu Leu Ser Arg Ser Cys Thr Glu Glu Phe
    275                 280                 285
Leu Ala Gly Trp Lys Leu
290


<210> 286
<211> 51
<212> PRT
<213> Homo sapiens


<400> 286
Met Val Pro Val Phe Ser Val Glu Lys Asp Gly Glu Glu Leu Gly Ser
1               5                   10                  15
Phe Arg Pro Arg Trp Ala Asp Trp Leu Thr Gly Leu Leu Glu Trp Val
            20                  25                  30
```

```
Ser Val Glu Ser Leu Ser Ile Tyr Cys Ile Ser Gln Pro Val Tyr Met
         35                  40                  45
Trp Val Glu
    50
```

<210> 287
<211> 6
<212> PRT
<213> Homo sapiens

<400> 287
```
Met Trp His Leu Ser Val
 1               5
```


<210> 288
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(116)
<223> Xaa = X or * as defined in Table 6

<400> 288
```
His Pro His Ser Pro Asp Pro Gly Ser Ala Leu Gly Ser Ser Ser Gly
 1               5                  10                  15
Gly Trp Leu Pro Ala Pro Leu Ser Pro Cys Arg Gly Xaa Ala Gly Ala
             20                  25                  30
Gly Gly Gly Arg Arg Cys Arg Gly Arg Pro Trp Ser Arg Ala Gly Xaa
         35                  40                  45
Ala Cys Ser Gly His Ala Gly Ser Arg Cys Cys Pro Ala Xaa Ser Val
     50                  55                  60
Cys Gly Gly Leu Pro Gly Gly Ala Pro Gly Cys Leu Cys Lys Gly Gly
 65                  70                  75                  80
Ser Ala Gly Phe Cys Cys Gln Gly Pro Gly Cys Ser Cys Ser Gly Cys
                 85                  90                  95
Ser Gly Ser Gly His Gly Gly Tyr Arg His Arg Gln Gly Arg Pro Leu
             100                 105                 110
Ser Ala Ser Gln
         115
```


<210> 289
<211> 1654
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1654)
<223> Xaa = X or * as defined in Table 6

<400> 289
```
Ser Val Tyr Lys Ala Asp Leu Glu Trp Leu Arg Gly Ile Gly Trp Met
 1               5                  10                  15
```

```
Pro Glu Gly Ser Val Glu Met Asn Arg Val Lys Val Ala Gln Asp Leu
            20                  25                  30
Val Asn Glu Arg Leu Tyr Arg Thr Arg Pro Glu Ala Leu Ser Phe Thr
        35                  40                  45
Ser Ile Val Asp Thr Pro Glu Val Val Leu Ala Lys Ala Asn Ser Leu
    50                  55                  60
Gln Ile Ser Glu Lys Leu Tyr Gln Glu Ala Trp Asn Lys Asp Lys Ser
65                  70                  75                  80
Asn Ile Thr Ile Pro Ser Asp Thr Pro Glu Met Leu Gln Ala His Ile
                85                  90                  95
Asn Ala Leu Gln Ile Ser Asn Lys Leu Tyr Gln Lys Asp Trp Asn Asp
            100                 105                 110
Thr Lys Gln Lys Gly Tyr Asp Ile Arg Ala Asp Ala Ile Glu Ile Lys
        115                 120                 125
His Ala Lys Ala Ser Arg Glu Ile Ala Ser Glu Tyr Lys Tyr Lys Glu
    130                 135                 140
Gly Tyr Arg Lys Gln Leu Gly His His Met Gly Phe Arg Thr Leu Gln
145                 150                 155                 160
Asp Asp Pro Lys Ser Val Trp Ala Ile His Ala Ala Lys Ile Gln Ser
            165                 170                 175
Asp Arg Glu Tyr Lys Lys Ala Tyr Glu Lys Ser Lys Gly Ile His Asn
        180                 185                 190
Thr Pro Leu Asp Met Met Ser Ile Val Gln Ala Lys Lys Cys Gln Val
    195                 200                 205
Leu Val Ser Asp Ile Asp Tyr Arg Asn Tyr Leu His Gln Trp Thr Cys
210                 215                 220
Leu Pro Asp Gln Asn Asp Val Ile Gln Ala Lys Lys Ala Tyr Asp Leu
225                 230                 235                 240
Gln Ser Asp Pro Leu Tyr Arg Asn Ala Trp Glu Lys Glu Lys Ala Asn
            245                 250                 255
Val Asn Val Pro Ala Asp Thr Pro Leu Met Leu Gln Ser Lys Ile Asn
        260                 265                 270
Ala Leu Gln Ile Ser Asn Lys Arg Tyr Gln Gln Ala Trp Glu Asp Val
    275                 280                 285
Lys Met Thr Gly Tyr Asp Leu Arg Ala Asp Ala Ile Gly Ile Gln His
    290                 295                 300
Ala Lys Ala Ser Arg Asp Ile Ala Ser Asp Tyr Leu Tyr Lys Thr Ala
305                 310                 315                 320
Tyr Glu Lys Gln Lys Gly His Tyr Ile Gly Cys Arg Ser Ala Lys Glu
            325                 330                 335
Asp Pro Lys Leu Val Trp Ala Ala Asn Val Leu Lys Met Gln Asn Asp
            340                 345                 350
Arg Leu Tyr Lys Lys Ala Tyr Asn Asp His Lys Ala Lys Ile Ser Ile
        355                 360                 365
Pro Val Asp Met Val Ser Ile Ser Ala Ala Lys Glu Gly Gln Ala Leu
    370                 375                 380
Ala Ser Asp Val Asp Tyr Arg His Tyr Leu His His Trp Ser Cys Phe
385                 390                 395                 400
Pro Asp Gln Asn Asp Val Ile Gln Ala Arg Lys Ala Tyr Asp Leu Gln
            405                 410                     415
Ser Asp Thr Glu Pro Cys Ser Leu Ala Gln Ala Gly Val Gln Trp Val
        420                 425                 430
Ala Asp Met Thr Ala Arg Gly Gln Ser Pro Leu Ala Pro Leu Leu Glu
        435                 440                 445
Thr Leu Glu Asp Pro Ser Ala Ser His Gly Gly Gln Thr Asp Ala Tyr
    450                 455                 460
Leu Thr Leu Thr Ser Arg Met Thr Gly Glu Glu Gly Lys Glu Val Ile
465                 470                 475                 480
Thr Glu Ile Glu Lys Lys Leu Pro Arg Leu Tyr Lys Val Leu Lys Val
            485                 490                 495
Ser Ser Ile Ile Asp Ser Leu Glu Ile Leu Phe Asn Lys Gly Glu Thr
            500                 505                 510
His Ser Ala Val Val Asp Phe Glu Ala Leu Asn Val Ile Val Arg Leu
    515                 520                 525
```

186

```
Ile Glu Gln Ala Pro Ile Gln Met Gly Glu Glu Ala Val Arg Trp Ala
    530                 535                 540
Lys Leu Val Ile Pro Leu Val Val His Ser Ala Gln Lys Val His Leu
545                 550                 555                 560
Arg Gly Ala Thr Ala Leu Glu Met Gly Met Pro Leu Leu Leu Gln Lys
            565                 570                 575
Gln Gln Glu Ile Ala Ser Ile Thr Glu Gln Leu Met Thr Thr Thr Leu
            580                 585                 590
His Arg Ser Gly Ser Phe Ile Asn Ser Leu Leu Gln Leu Glu Glu Leu
        595                 600                 605
Gly Phe Arg Ser Gly Ala Pro Met Ile Lys Lys Ile Ala Phe Ile Ala
    610                 615                 620
Trp Lys Ser Leu Ile Asp Asn Phe Ala Leu Asn Pro Asp Ile Leu Cys
625                 630                 635                 640
Ser Ala Lys Arg Leu Lys Leu Leu Met Gln Pro Leu Ser Ser Ile His
            645                 650                 655
Val Arg Thr Glu Thr Leu Ala Leu Thr Lys Leu Glu Val Trp Trp Tyr
            660                 665                 670
Leu Leu Met Arg Leu Gly Pro His Leu Pro Ala Asn Phe Glu Gln Val
        675                 680                 685
Cys Val Pro Leu Ile Gln Ser Thr Ile Ser Ile Asp Ser Asn Ala Ser
    690                 ·695                700
Pro Gln Gly Asn Ser Cys His Val Ala Thr Ser Pro Gly Leu Asn Pro
705                 710                 715                 720
Met Thr Pro Val His Lys Gly Ala Ser Ser Pro Tyr Gly Ala Pro Gly
            725                 730                 735
Thr Pro Arg Met Asn Leu Ser Ser Asn Leu Gly Gly Met Ala Thr Ile
            740                 745                 750
Pro Ser Ile Gln Leu Leu Gly Leu Glu Met Leu Leu His Phe Leu Leu
        755                 760                 765
Gly Pro Glu Ala Leu Ser Phe Ala Lys Gln Asn Lys Leu Val Leu Ser
    770                 775                 780
Leu Glu Pro Leu Glu His Pro Leu Ile Ser Ser Pro Ser Phe Phe Ser
785                 790                 795                 800
Lys His Ala Asn Thr Leu Ile Thr Ala Val His Asp Ser Phe Val Ala
            805                 810                 815
Val Gly Lys Asp Ala Pro Gly Asn Lys Lys Glu Lys Pro Gly Ser Glu
            820                 825                 830
Val Leu Thr Leu Leu Leu Lys Ser Leu Glu Ser Ile Val Lys Ser Glu
            835                 840                 845
Val Phe Pro Val Ser Lys Thr Leu Gly Thr Pro Ala Leu Phe Leu Ile
    850                 855                 860
Gln Leu Ile Phe Asn Asn Phe Leu Glu Cys Gly Val Ser Asp Glu Arg
865                 870                 875                 880
Phe Phe Leu Ser Leu Glu Ser Leu Val Gly Cys Val Leu Ser Gly Pro
            885                 890                 895
Thr Ser Pro Leu Ala Phe Ser Asp Ser Val Leu Asn Val Ile Asn Gln
        900                 905                 910
Asn Ala Lys Gln Leu Glu Asn Lys Glu His Leu Trp Lys Met Trp Ser
    915                 920                 925
Val Ile Val Thr Pro Leu Thr Glu Leu Ile Asn Gln Thr Asn Glu Val
    930                 935                 940
Asn Gln Gly Asp Ala Leu Glu His Asn Phe Ser Ala Ile Tyr Gly Ala
945                 950                 955                 960
Leu Thr Leu Pro Val Asn His Ile Phe Ser Glu Gln Arg Phe Pro Val
            965                 970                 975
Ala Thr Met Lys Thr Leu Leu Arg Thr Trp Ser Glu Leu Tyr Arg Ala
        980                 985                 990
Phe Ala Arg Cys Ala Ala Leu Val Ala Thr Ala Glu Glu Asn Leu Cys
    995                 1000                1005
Cys Glu Glu Leu Ser Ser Lys Ile Met Ser Ser Leu Glu Asp Glu Gly
    1010                1015                1020
Phe Ser Asn Leu Leu Phe Val Asp Arg Ile Ile Tyr Ile Ile Thr Val
1025                1030                1035                1040
```

```
Met Val Asp Cys Ile Asp Phe Ser Pro Tyr Asn Ile Lys Tyr Gln Pro
          1045                1050                1055
Lys Val Lys Ser Pro Gln Arg Pro Ser Asp Trp Ser Lys Lys Lys Asn
          1060                1065                1070
Glu Pro Leu Gly Lys Leu Thr Ser Leu Phe Lys Leu Ile Val Lys Val
          1075                1080                1085
Ile Tyr Ser Phe His Thr Leu Ser Phe Lys Glu Ala His Ser Asp Thr
     1090                1095                1100
Leu Phe Thr Ile Gly Asn Ser Ile Thr Gly Ile Ile Ser Ser Val Leu
1105                1110                1115                1120
Gly His Ile Ser Leu Pro Ser Met Ile Arg Lys Ile Phe Ala Thr Leu
               1125                1130                1135
Thr Arg Pro Leu Ala Leu Phe Tyr Glu Asn Ser Lys Leu Asp Glu Val
          1140                1145                1150
Pro Lys Val Tyr Ser Cys Leu Asn Asn Lys Leu Glu Lys Leu Leu Gly
          1155                1160                1165
Glu Ile Ile Ala Cys Leu Gln Phe Ser Tyr Thr Gly Thr Tyr Asp Ser
     1170                1175                1180
Glu Leu Leu Glu Gln Leu Ser Pro Leu Leu Cys Ile Ile Phe Leu His
1185                1190                1195                1200
Lys Asn Lys Gln Ile Arg Lys Gln Ser Ala Gln Phe Trp Asn Ala Thr
               1205                1210                1215
Phe Ala Lys Val Met Met Leu Val Tyr Pro Glu Glu Leu Lys Pro Val
          1220                1225                1230
Leu Thr Gln Ala Lys Gln Lys Phe Leu Leu Leu Leu Pro Gly Leu Glu
          1235                1240                1245
Thr Val Glu Met Met Glu Glu Ser Ser Gly Pro Tyr Ser Asp Gly Leu
     1250                1255                1260
Lys Leu Glu Ser Ser Ser Leu Lys Val Lys Gly Glu Ile Leu Leu Glu
1265                1270                1275                1280
Glu Glu Lys Ser Thr Asp Phe Val Phe Ile Pro Pro Glu Gly Lys Asp
               1285                1290                1295
Ala Lys Glu Arg Ile Leu Thr Asp His Gln Lys Glu Val Leu Lys Thr
     1300                1305                1310
Lys Arg Phe Glu Glu Gln Met Asp Ser Asp Ile Val Ile Pro Gln Asp
     1315                1320                1325
Val Thr Glu Asp Cys Gly Met Ala Glu His Leu Glu Lys Ser Ser Leu
     1330                1335                1340
Ser Asn Asn Glu Cys Gly Ser Leu Asp Lys Thr Ser Pro Glu Met Ser
1345                1350                1355                1360
Asn Ser Asn Asn Asp Glu Arg Lys Lys Ala Leu Ile Ser Ser Arg Lys
               1365                1370                1375
Thr Ser Thr Glu Cys Ala Ser Ser Thr Glu Asn Ser Phe Val Val Ser
          1380                1385                1390
Ser Ser Ser Val Ser Asn Thr Thr Val Ala Gly Thr Pro Pro Tyr Pro
     1395                1400                1405
Thr Ser Arg Arg Gln Thr Phe Ile Thr Leu Glu Lys Phe Asp Gly Ser
     1410                1415                1420
Glu Asn Arg Pro Phe Ser Pro Ser Pro Leu Asn Asn Ile Ser Ser Thr
1425                1430                1435                1440
Val Thr Val Lys Asn Asn Gln Glu Thr Met Ile Lys Thr Asp Phe Leu
          1445                1450                1455
Pro Lys Ala Lys Gln Arg Glu Gly Thr Phe Ser Lys Ser Asp Ser Glu
          1460                1465                1470
Lys Ile Val Asn Gly Thr Lys Arg Ser Ser Arg Arg Ala Gly Lys Ala
     1475                1480                1485
Glu Gln Thr Gly Asn Lys Arg Ser Lys Pro Leu Met Arg Ser Glu Pro
     1490                1495                1500
Glu Lys Asn Thr Glu Glu Ser Val Glu Gly Ile Val Val Leu Glu Asn
1505                1510                1515                1520
Asn Pro Pro Gly Leu Leu Asn Gln Thr Glu Cys Val Ser Asp Asn Gln
               1525                1530                1535
Val His Leu Ser Glu Ser Thr Met Glu His Asp Asn Thr Lys Leu Lys
          1540                1545                1550
```

```
Ala Ala Thr Val Glu Asn Ala Val Leu Leu Glu Thr Asn Thr Val Glu
         1555                1560                1565
Glu Lys Asn Val Glu Ile Asn Leu Glu Ser Lys Glu Asn Thr Pro Pro
    1570                1575                1580
Val Val Ile Ser Ala Asp Gln Met Val Asn Glu Asp Ser Gln Val Gln
1585                1590                1595                1600
Ile Thr Pro Asn Gln Lys Thr Leu Arg Arg Ser Ser Arg Arg Arg Tyr
              1605                1610                1615
Arg Ser Ser Arg Val Tyr His Xaa Lys Pro Arg Xaa Gly Lys Xaa Ser
         1620                1625                1630
Ser Lys Lys Gly Thr Thr Xaa Gly Arg Arg Lys Thr Ser Ser Glu Glu
         1635                1640                1645
Ser Ile Ala Tyr Lys Arg
    1650
```


```
        <210> 290
        <211> 108
        <212> PRT
        <213> Homo sapiens


        <400> 290
Lys Asp Ala Tyr Met Phe Lys Lys Gly Leu Leu Ala Leu Ala Leu Val
 1               5                10                15
Phe Ser Met Pro Val Phe Ala Ala Glu His Trp Ile Asp Val Arg Val
             20                25                30
Pro Glu Gln Tyr Gln Gln Glu His Val Gln Gly Ala Ile Asn Ile Pro
    35                40                45
Leu Lys Glu Val Lys Glu Arg Ile Ala Thr Ala Val Pro Asp Lys Asn
    50                55                60
Asp Thr Val Lys Val Tyr Cys Asn Ala Gly Arg Gln Ser Gly Gln Ala
65                70                75                80
Lys Glu Ile Leu Ser Glu Met Gly Tyr Thr His Val Glu Asn Ala Gly
             85                90                95
Gly Leu Lys Asp Ile Ala Met Pro Lys Val Lys Gly
         100                105
```


```
        <210> 291
        <211> 119
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(119)
        <223> Xaa = X or * as defined in Table 6


        <400> 291
Ser Ser Pro Ser Cys His Leu Val Lys Lys Ile Lys Ile Lys Met Lys
 1               5                10                15
Ser Pro Ala Leu Arg Gly Leu Ser Arg Gln His Thr Lys Ser Pro Val
             20                25                30
Thr Phe Trp Trp Met Thr Phe Gly Asp Thr Ser Arg Pro Ser Gln Asp
             35                40                45
Thr Leu Pro Met Asp Leu Gln Gln Leu Leu Gly Val Thr Lys Val Cys
    50                55                60
Ser Lys Ala Thr Ser Pro Thr Ser Gln Arg Gly Gln Glu Val Ile Ser
65                70                75                80
Thr Pro Thr Ser Lys Ser Gly Pro Phe Ile Gly Arg Gly Ser Xaa Gly
```

```
                            85                    90                      95
Xaa Ser Gly Arg Trp Glu Arg Pro Ser Cys Cys Leu His Phe Ser Tyr
            100                    105                   110
Pro Gln Leu Arg Gly Leu Cys
        115



        <210> 292
        <211> 354
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(354)
        <223> Xaa = X or * as defined in Table 6



        <400> 292
Arg Glu Pro Ala Gly Ala Gly Ala Tyr Met Arg Ala Cys Ala Arg Val
 1               5                   10                  15
Arg Arg Arg Gly Asp Arg Arg Pro Arg Arg Ser Pro Arg Pro Arg Asp
            20                  25                  30
Pro Ala Val Arg Ala Arg Ala Arg Ser Ala Pro Pro Pro Leu Phe Ile
            35                  40                  45
Ala Ala Ala Gly Gly Gly Gly Ser Gly Trp Arg Leu Tyr Ala Asp Ser
    50                  55                  60
Gly Glu Glu Tyr Gly Ile Met Ala Phe Ala Leu Phe Val Leu Leu Gly
65                  70                  75                  80
Phe Ala Leu Leu Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val
            85                  90                  95
Phe Thr Thr Val Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser
            100                 105                 110
Leu Asn Asp Ser Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly
        115                 120                 125
Gly Val Val Leu Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Ser
        130                 135                 140
Phe Lys Val Asp Ser Asp Asp His Val Gly Met Lys Tyr Ser Cys Val
145                 150                 155                 160
Phe Leu Pro Glu Pro His Gly His Gly Pro Thr Ile Gln Ala Ser Thr
                165                 170                 175
.Gly Pro Pro Arg Val Glu Gly Leu Xaa Ser Ser Phe Arg Thr His Ser
            180                 185                 190
Thr Arg Gly Lys Thr Gly Leu Val Gly Ser Cys Lys Ser Glu Phe Val
        195                 200                 205
Pro Pro Val Thr Asp Trp Ala Pro Trp Tyr Lys Ile Thr Asp Ser Glu
    210                 215                 220
Pro Gln Gly Pro Ser Leu Asn Ala Gln Arg Thr Arg Phe Phe Val Gly
225                 230                 235                 240
Pro Ser Ala Gly Pro Val Lys Ser Tyr Gln His Xaa Glu Pro Glu His
                245                 250                 255
Ile Gly Pro Pro Ala Arg Asn Arg Cys Asn Gly Thr Ser Ser Lys
            260                 265                 270
Gly Leu Arg Pro Arg Pro Leu Gln Phe Leu Arg Val Arg Thr Ala Thr
        275                 280                 285
Xaa Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Gly Glu Val Leu Val
    290                 295                 300
Leu Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp
305                 310                 315                 320
Val Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Glu Ser Ala
                325                 330                 335
Gly Gln His Gln Asn Asp Lys Gly Lys Lys Arg Ser Ala Arg Gly Asn
            340                 345                 350
```

Phe Ser

```
        <210> 293
        <211> 312
        <212> PRT
        <213> Homo sapiens


        <400> 293
Met Lys Val Leu Leu Glu Ser Val Lys Glu Arg Ala Glu Glu Glu Lys
 1               5                   10                  15
Leu Ala Ala Ala His Leu Arg Ser Phe Ala Ala Lys Lys Ala Lys Lys
                20                  25                  30
Tyr Asp Ser Val Lys Lys Glu Lys Thr Leu Gln Asp Val Asp Leu Thr
            35                  40                  45
Gln His Gln His Lys Gln Thr Arg Ala Leu Ser Gly Gly Leu Lys Arg
        50                  55                  60
Lys Leu Ser Leu Gly Ile Ala Phe Met Gly Met Ser Arg Thr Val Val
 65                  70                  75                  80
Leu Asp Glu Pro Thr Ser Gly Val Asp Pro Cys Ser Arg His Ser Leu
                85                  90                  95
Trp Asp Ile Leu Leu Lys Tyr Arg Glu Gly Arg Thr Ile Ile Phe Thr
            100                 105                 110
Thr His His Leu Asp Glu Ala Glu Ala Leu Ser Asp Arg Val Ala Val
        115                 120                 125
Leu Gln His Gly Arg Leu Arg Cys Cys Gly Pro Pro Phe Cys Leu Lys
        130                 135                 140
Glu Ala Tyr Gly Gln Gly Leu Arg Leu Thr Leu Thr Arg Gln Pro Ser
145                 150                 155                 160
Val Leu Glu Ala His Asp Leu Lys Asp Met Ala Cys Val Thr Ser Leu
                165                 170                 175
Ile Lys Ile Tyr Ile Pro Gln Ala Phe Leu Lys Asp Ser Ser Gly Ser
            180                 185                 190
Glu Leu Thr Tyr Thr Ile Pro Lys Asp Thr Asp Lys Ala Cys Leu Lys
            195                 200                 205
Gly Leu Phe Gln Ala Leu Asp Glu Asn Leu His Gln Leu His Leu Thr
        210                 215                 220
Gly Tyr Gly Ile Ser Asp Thr Thr Leu Glu Glu Ala Glu Gly Arg Thr
225                 230                 235                 240
Ala Ala Pro Glu Pro Pro Met Leu Glu Asp Gly His Ala Val Thr Gln
            245                 250                 255
Arg Phe Ser Phe Ile Gln Val Val Gly Cys Glu Asp Asp Arg Thr Thr
            260                 265                 270
Trp Val Gln Ala Gln Gly Ala Ser Ala Pro Gly Gly Gln Arg Pro Gln
            275                     280                 285
Glu Asp Leu Pro Ser Phe Pro Gln Asp Gly Arg Ser Arg Ala Gln Phe
        290                 295                 300
Lys Asp Pro His Gln Phe Ser Asn
305                 310


        <210> 294
        <211> 581
        <212> PRT
        <213> Homo sapiens


        <400> 294
Met Ala Ser His Ala Tyr Asp Lys Asn Gln Asn Ala Asn Val Leu Val
 1               5                   10                  15
```

```
His Leu Cys Phe Tyr Asn Arg Ile Pro Lys Thr Gly Ala Tyr Tyr Leu
             20                      25                   30
Asp Ser Arg Ser Val Ser Ile Ser Tyr Leu Ile Gly His His Ile Asp
             35                      40                   45
Met Gly Leu Glu Thr Ala Thr Ser Lys Asn Glu Phe Ile Phe Asp Ser
     50                      55                   60
Ala Ser Thr Leu Leu Gly Met Leu Phe Arg Lys Pro Ser Gln His Ser
 65                      70                   75                   80
Leu Ser Leu Phe Ser Lys Lys Phe Gln Glu Asn Leu Ile Tyr Leu Glu
                     85                   90                   95
Ser Asp Asp Cys Leu Pro Pro Pro Pro Pro Pro Trp Ser Glu Pro
             100               105               110
Pro Ser Phe Leu Thr Trp Thr Ile Val Thr Val Phe Gln Trp Val Ser
             115               120               125
Leu Leu Leu Ser Leu Pro Asn Ile Gln Val Ile Leu Tyr Arg Ala Val
     130               135               140
Gly Val Val Pro Ser Gln Pro Lys Ser Asp Asn Leu Lys Gly Trp Gly
145               150               155               160
Ser Gly Arg Val Val Lys Glu Lys Leu Arg Ser Glu Ile Pro Asp Trp
             165               170               175
Lys Ile Lys Ser Ile His Ile Leu Glu Arg Thr Ala Ser Ser Ser Thr
             180               185               190
Glu Pro Ser Val Ser Arg Gln Leu Leu Glu Pro Glu Pro Val Pro Leu
             195               200               205
Ser Lys Glu Ala Asp Ser Trp Glu Ile Ile Glu Gly Leu Lys Ile Gly
     210               215               220
Gln Thr Asn Val Gln Lys Pro Asp Lys His Glu Gly Phe Met Leu Lys
225               230               235               240
Lys Arg Lys Trp Pro Leu Lys Gly Trp His Lys Ile Gln Lys Gly Lys
             245               250               255
Val His Gly Ser Ile Asp Val Gly Leu Ser Val Met Ser Ile Lys Lys
             260               265               270
Lys Ala Arg Arg Ile Asp Leu Asp Thr Glu Glu His Ile Tyr His Leu
             275               280               285
Lys Val Lys Ser Val Phe Asn Ser Phe Ser Ala Ile Ile Arg Gly Asn
     290               295               300
Asp Leu Pro Thr Pro Val Val Lys Ser Gln Asp Trp Phe Asp Ala Trp
305               310               315               320
Val Ser Lys Leu Arg His His Arg Leu Tyr Arg Gln Asn Glu Ile Val
             325               330               335
Arg Ser Pro Arg Asp Ala Ser Phe His Ile Phe Pro Ser Thr Ser Thr
             340               345               350
Ala Glu Ser Ser Pro Ala Ala Asn Val Ser Val Met Asp Gly Lys Met
             355               360               365
Gln Pro Asn Ser Phe Pro Trp Gln Ser Pro Leu Pro Cys Ser Asn Ser
     370               375               380
Leu Pro Ala Thr Cys Thr Thr Gly Gln Ser Lys Val Ala Ala Trp Leu
385               390               395               400
Gln Asp Ser Glu Glu Met Asp Arg Cys Ala Glu Asp Leu Ala His Cys
             405               410               415
Gln Ser Asn Leu Val Glu Leu Ser Lys Leu Leu Gln Asn Leu Glu Ile
             420               425               430
Leu Gln Arg Thr Gln Ser Ala Pro Asn Phe Thr Asp Met Gln Ala Asn
     435               440               445
Cys Val Asp Ile Ser Lys Lys Asp Lys Arg Val Thr Arg Arg Trp Arg
     450               455               460
Thr Lys Ser Val Ser Lys Asp Thr Lys Ile Gln Leu Gln Val Pro Phe
465               470               475               480
Ser Ala Thr Met Ser Pro Val Arg Leu His Ser Ser Asn Pro Asn Leu
             485               490               495
Cys Ala Asp Ile Glu Phe Gln Thr Pro Pro Ser His Leu Thr Asp Pro
             500               505               510
Leu Glu Ser Ser Thr Asp Tyr Thr Lys Leu Gln Glu Glu Phe Cys Leu
             515               520               525
```

192

```
Ile Ala Gln Lys Gly Lys Gly Ala Ser Lys Lys Gln Ala Lys Arg Asn
    530             535                 540
Ala Ala Glu Lys Phe Leu Ala Lys Phe Ser Asn Ile Ser Pro Glu Asn
545             550                 555                 560
His Ile Ser Leu Val Ser Asn Val Asp Ser Tyr Asp Val Asn Val Ile
                565                 570                 575
Lys His Phe Leu Gln
                580




    <210> 295
    <211> 416
    <212> PRT
    <213> Homo sapiens



    <400> 295
Met Leu Arg Thr Arg Lys Ala Pro His Ser Trp Val Lys Ser Ser Ser
1               5                   10                  15
Asn Thr Val His Tyr Arg Val Ser Val Val Cys Leu His Asp His Val
                20                  25                  30
Thr Asp Trp Glu Trp Gln Leu Thr Ala Thr Ala Arg His Pro Lys Arg
            35          ·       40                  45
Val Ser His Tyr Ile Leu Trp Asp Gln Glu Lys Thr Lys Ile Lys Ile
    50                  55                  60
Arg Lys Asp Ile Ile Arg Ile Leu Pro Ser Leu Asp Val Glu Val Lys
65                  70                  75                  80
Asp Ile Thr Asp Ser Tyr Asp Ala Asn Trp Phe Leu Gln Leu Leu Ser
                85                  90                  95
Thr Glu Asp Leu Phe Glu Met Thr Ser Lys Glu Phe Pro Ile Val Thr
                100                 105                 110
Glu Val Ile Glu Ala Pro Glu Gly Asn His Leu Pro Gln Ser Ile Leu
            115                 120                 125
Gln Pro Gly Lys Thr Ile Val Ile His Lys Lys Tyr Gln Ala Ser Arg
    130                 135                 140
Ile Leu Ala Ser Glu Ile Arg Ser Asn Phe Pro Lys Arg His Phe Leu
145                 150                 155                 160
Ile Pro Thr Ser Tyr Lys Gly Lys Phe Lys Arg Arg Pro Arg Glu Phe
                165                 170                 175
Pro Thr Ala Tyr Asp Leu Glu Ile Ala Lys Ser Glu Lys Glu Pro Leu
            180                 185                 190
His Val Val Ala Thr Lys Ala Phe His Ser Pro His Asp Lys Leu Ser
            195                 200                 205
Ser Val Ser Val Gly Asp Gln Phe Leu Val His Gln Ser Glu Thr Thr
    210                 215                 220
Glu Val Leu Cys Glu Gly Ile Lys Lys Val Val Asn Val Leu Ala Cys
225                 230                 235                 240
Glu Lys Ile Leu Lys Lys Ser Tyr Glu Ala Ala Leu Leu Pro Leu Tyr
                245                 250                 255
Met Glu Gly Gly Phe Val Glu Val Ile His Asp Lys Lys Gln Tyr Pro
            260                 265                 270
Ile Ser Glu Leu Cys Lys Gln Phe Arg Leu Pro Phe Asn Val Lys Val
            275                 280                 285
Ser Val Arg Asp Leu Ser Ile Glu Glu Asp Val Leu Ala Ala Thr Pro
    290                 295                 300
Gly Leu Gln Leu Glu Glu Asp Ile Thr Asp Ser Tyr Leu Leu Ile Ser
305                 310                 315                 320
Asp Phe Ala Asn Pro Thr Glu Cys Trp Glu Ile Pro Val Gly Arg Leu
                325                 330                 335
Asn Met Thr Val Gln Leu Val Ser Asn Phe Ser Arg Asp Ala Glu Pro
            340                 345                 350
Phe Leu Val Arg Thr Leu Val Glu Glu Ile Thr Glu Glu Gln Tyr Tyr
    355                 360                 365
```

```
Met Met Arg Arg Tyr Glu Ser Ser Ala Ser His Pro Pro Pro Arg Pro
    370                 375                 380
Pro Lys His Pro Ser Val Glu Glu Thr Lys Leu Thr Leu Leu Thr Leu
385                 390                 395                 400
Ala Glu Glu Arg Thr Val Asp Leu Pro Lys Ser Pro Lys Arg Arg Arg
                405                 410                 415
```

```
<210> 296
<211> 302
<212> PRT
<213> Homo sapiens
```

```
<400> 296
Met Phe Ala Phe Glu Pro Leu Gly Gly Cys Arg Pro Trp Arg Leu Ser
1               5                   10                  15
Leu Pro Gly Leu Gly Ser Arg Leu Phe Arg Thr Tyr Gly Ala Ala Asp
                20                  25                  30
Gly Arg Arg Gln Arg Arg Pro Gly Arg Glu Ala Ala Gln Trp Phe Pro
        35                  40                  45
Pro Gln Asp Arg Arg Arg Phe Phe Asn Ser Ser Gly Ser Ser Asp Ala
    50                  55                  60
Arg Met Gly Asp Pro Ser Gln Ser Asp Asp Pro Asp Asp Pro Asp Asp
65                  70                  75                  80
Pro Asp Phe Pro Gly Ser Pro Val Arg Arg Arg Arg Cys Pro Gly
                85                  90                  95
Gly Arg Val Pro Lys Asp Arg Pro Ser Leu Thr Val Thr Pro Lys Arg
            100                 105                 110
Trp Lys Leu Arg Ala Arg Pro Ser Leu Thr Val Thr Pro Arg Arg Leu
        115                 120                 125
Gly Leu Arg Ala Arg Pro Pro Gln Lys Cys Ser Thr Pro Cys Gly Pro
        130                 135                 140
Leu Arg Leu Pro Pro Phe Pro Ser Arg Asp Ser Gly Arg Leu Ser Pro
145                 150                 155                 160
Asp Leu Ser Val Cys Gly Gln Pro Arg Asp Gly Asp Glu Leu Gly Ile
                165                 170                 175
Ser Ala Ser Leu Phe Ser Ser Leu Ala Ser Pro Cys Pro Gly Ser Pro
                180                 185                 190
Thr Pro Arg Asp Ser Val Ile Ser Ile Gly Thr Ser Ala Cys Leu Val
        195                 200                 205
Ala Ala Ser Ala Val Pro Ser Gly Leu His Leu Pro Glu Val Ser Leu
    210                 215                 220
Asp Arg Ala Ser Leu Pro Cys Ser Gln Glu Glu Ala Thr Gly Gly Ala
225                 230                 235                 240
Lys Asp Thr Arg Met Gly Ser Val Arg Val Leu Arg Asp Pro Val Gly
                245                 250                 255
Val Asn Leu Tyr Glu His Ser Val Ser Lys Cys His Val Gly Gln Pro
                260                 265                 270
Asp Thr Asp Pro Arg Glu Lys Val Lys Ala Ala Pro Glu Glu Leu Cys
        275                 280                 285
Leu His Ala Leu Gln His Pro Arg Ser Glu Gln Ala Asp Cys
        290                 295                 300
```

```
<210> 297
<211> 98
<212> PRT
<213> Homo sapiens
```

<400> 297

```
Gln Gly Ala Phe Trp Leu Leu Phe Ser Ser Pro Arg Ser Phe Phe Leu
1               5                   10                  15
Leu Ser Val Pro Trp Trp Leu Pro Glu Ser Ser Arg Trp Leu Leu Leu
            20                  25                  30
His Gly Lys Ser Gln Leu Ala Val Gln Asn Leu Gln Lys Val Ala His
        35                  40                  45
Arg Gly Asp Trp Pro Gly Ser Gly His Pro Ala Pro Gln Ser Gln His
    50                  55                  60
Ser Ser Leu Arg Arg Ser Ala Ala Arg Ser Arg Pro Pro Cys Trp Ala
65                  70                  75                  80
Arg Arg Trp Arg Ala Pro Pro His Thr Pro Arg Val Ala Gly Gly Ser
                85                  90                  95
Gly Cys
```

<210> 298
<211> 175
<212> PRT
<213> Homo sapiens

<400> 298

```
Glu Ser Val Thr Phe Glu Asp Val Ala Val Glu Phe Ile Gln Glu Trp
1               5                   10                  15
Ala Leu Leu Asp Ser Ala Arg Arg Ser Leu Cys Lys Tyr Arg Met Leu
            20                  25                  30
Asp Gln Cys Arg Thr Leu Ala Ser Arg Gly Thr Pro Pro Cys Lys Pro
        35                  40                  45
Ser Cys Val Ser Gln Leu Gly Gln Arg Ala Glu Pro Lys Ala Thr Glu
    50                  55                  60
Arg Gly Ile Leu Arg Ala Thr Cys Val Ala Trp Glu Ser Gln Leu Lys
65                  70                  75                  80
Pro Glu Glu Leu Pro Ser Met Gln Asp Leu Leu Glu Glu Ala Ser Ser
                85                  90                  95
Arg Asp Met Gln Met Gly Pro Gly Leu Phe Leu Arg Met Gln Leu Val
            100                 105                 110
Pro Ser Ile Glu Glu Arg Glu Thr Pro Leu Thr Arg Glu Asp Arg Pro
        115                 120                 125
Ala Leu Gln Asp Pro Pro Trp Ser Leu Gly Cys Thr Gly Leu Lys Ala
    130                 135                 140
Ala Met Gln Ile Gln Arg Val Val Ile Pro Val Pro Thr Leu Gly His
145                 150                 155                 160
Arg Asn Pro Trp Val Ala Arg Asp Ser Gly Ala Ile Gly Asn Gly
                165                 170                 175
```

<210> 299
<211> 197
<212> PRT
<213> Homo sapiens

<400> 299

```
Pro Leu Pro Leu Asp Gln Arg Leu Leu Ala Ser Ile Thr Pro Ser Pro
1               5                   10                  15
Ser Gly Gln Ser Ile Ile Arg Thr Gln Pro Gly Ala Gly Val His Pro
            20                  25                  30
Lys Ala Asp Gly Ala Leu Lys Gly Glu Ala Glu Gln Ser Ala Gly His
        35                  40                  45
```

```
Pro Ser Glu His Leu Phe Ile Cys Glu Glu Cys Gly Arg Cys Lys Cys
    50                  55                  60
Val Pro Cys Thr Ala Ala Arg Pro Leu Pro Ser Cys Trp Leu Cys Asn
65              70                  75                      80
Gln Arg Cys Leu Cys Ser Ala Glu Ser Leu Leu Asp Tyr Gly Thr Cys
            85                  90                      95
Leu Cys Cys Val Lys Gly Leu Phe Tyr His Cys Ser Thr Asp Asp Glu
            100             105             110
Asp Asn Cys Ala Asp Glu Pro Cys Ser Cys Gly Pro Ser Ser Cys Phe
        115             120             125
Val Arg Trp Ala Ala Met Ser Leu Ile Ser Leu Phe Leu Pro Cys Leu
    130             135             140
Cys Cys Tyr Leu Pro Thr Arg Gly Cys Leu His Leu Cys Gln Gln Gly
145             150             155                     160
Tyr Asp Ser Leu Arg Arg Pro Gly Cys Arg Cys Lys Arg His Thr Asn
                165             170             175
Thr Val Cys Arg Lys Ile Ser Ser Gly Ser Ala Pro Phe Pro Lys Ala
            180             185 :             190
Gln Glu Lys Ser Val
        195
```

```
<210> 300
<211> 523
<212> PRT
<213> Homo sapiens
```

```
<400> 300
Met Lys Thr Cys Leu Ala Phe Pro Leu Ala Phe His His Asp Ser Asn
1               5               10                  15
Gly Ser Ala Val Leu Arg Leu Gln Ala Thr His Gly Ile Ser Ser Asp
            20                  25                  30
Ser Pro Leu Pro Ser Val Glu Lys Ala Ser His Ser Pro Asp Pro Ser
        35                  40                  45
Glu Tyr Phe Arg Lys His Pro Pro Val Arg Arg Ser Gly Leu Arg Thr
    50                  55                  60
Lys Arg Thr Ser Pro Gly Pro Gly Ala Arg Val Pro Gly Ser Gln Ser
65                  70                  75                      80
Phe Arg Ser Ala Glu Ala Cys Gly Val Ala Ala Leu Glu Cys Trp Arg
            85                  90                  95
Arg Arg Val Pro Val Pro Leu Ser Ser Pro Ala Glu Val Gln Val Leu
            100             105             110
Leu Lys Lys Ala Leu Arg Pro Glu Ser Arg Pro Phe Arg Asn Gln Ile
        115             120             125
Leu His Asn Cys Glu Arg Asn Trp Gly Asn Lys Gly Trp Lys Gly Leu
    130             135             140
Val Gly Arg Ser Glu Ser Gln Thr Gly Gln Ser Glu Lys Leu Ser Met
145             150             155                     160
Ser Ser His His Arg Gly Thr Val Arg Glu Glu Leu Val Val Glu Glu
                165             170             175
Tyr Ile Gly Gly Trp Cys Leu Cys Gly Ser Ala Trp Lys Leu Leu Val
                180             185             190
Thr Gly Leu Glu Gln Leu Leu Phe Ser Arg Thr Arg Pro Gln Glu Glu
        195             200             205
Ala Val Asp Lys Thr Trp Arg Thr Ala Arg Gln Leu Glu Ser Gly Thr
    210             215             220
Leu Leu Cys Arg His Cys Ile Thr Leu Pro Trp Pro Ser Glu Arg Asn
225             230             235                     240
Gly Gly Cys Phe Leu Ser Pro Ser Asn Met Leu Val Cys Glu Leu Arg
            245             250             255
Val Leu Ser Val Ile Val Ala Ser Pro Glu Pro Ser Thr Glu His Thr
            260             265             270
```

```
Gln Glu His Leu Ser Gly Asp Glu Phe Glu Lys Ser Gln Pro Ser Arg
        275                 280                 285
Lys Glu Lys Ser Leu Gly Leu Leu Cys His Lys Phe Leu Ala Arg Tyr
    290                 295                 300
Pro Asn Tyr Pro Asn Pro Ala Val Asn Asn Asp Ile Cys Leu Asp Glu
305                 310                 315                 320
Val Ala Glu Glu Leu Asn Val Glu Arg Arg Ile Tyr Asp Ile Val
                325                 330                 335
Asn Val Leu Glu Ser Leu His Met Val Ser Arg Leu Ala Lys Asn Arg
            340                 345                 350
Tyr Thr Trp His Gly Arg His Asn Leu Asn Lys Thr Leu Gly Thr Leu
        355                 360                 365
Lys Ser Ile Gly Glu Glu Asn Lys Tyr Ala Glu Gln Ile Met Met Ile
    370                 375                 380
Lys Lys Lys Glu Tyr Glu Gln Glu Phe Asp Phe Ile Lys Ser Tyr Thr
385                 390                 395                 400
Ser Val Asn Ser Arg Lys Asp Lys Ser Leu Arg Val Met Ser Gln Lys
                405                 410                 415
Phe Val Met Leu Phe Leu Val Ser Thr Pro Gln Ile Val Ser Leu Glu
            420                 425                 430
Val Ala Ala Lys Ile Leu Ile Gly Glu Asp His Val Glu Asp Leu Asp
        435                 440                 445
Lys Ser Lys Phe Lys Thr Gly Ser Leu Val Arg Leu Phe Ala Pro Cys
    450                 455                 460
Leu Ser Gly Ala Gly Ser Lys Leu Pro Gly Leu Val Glu Ala Leu Ala
465                 470                 475                 480
Phe Glu Val Ser Leu Ala Ala Phe Ser Val Val Ala Ser Val Glu Ser
                485                 490                 495
Phe Glu Pro Val Ala Leu Glu Glu Trp Val Val His Thr Val Gly Leu
            500                 505                 510
Arg Pro Trp Gly Gly Val Thr Leu Trp Trp Ala
        515                 520
```

```
<210> 301
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(81)
<223> Xaa = X or * as defined in Table 6


<400> 301
```
```
Met Asp Leu Ile Val Tyr His Lys Lys Ser Asp Ile Ser Asn Gln Pro
1               5                   10                  15
Ser Ile Pro Thr Cys Ala Leu Phe Phe Pro Cys Val Ser Leu Glu Pro
            20                  25                  30
Phe Gln Leu Phe Pro Val Lys Gln Thr Ala Arg Arg Pro Pro Pro Tyr
        35                  40                  45
Ser Ser Pro Gly Lys Ser Thr Gly Asn Val Ile Pro Phe Gly His Gly
    50                  55                  60
Phe Pro Thr Leu Gln Pro Lys Xaa Gln Ile Thr Pro Val Gly Gly Gln
65                  70                  75                  80
Tyr
```

```
<210> 302
<211> 585
```

```
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(585)
<223> Xaa = X or * as defined in Table 6


<400> 302
Met Arg Gln Thr Lys Thr Glu Tyr Ile Gln Glu Phe Asn Gln Glu Ala
1               5                   10                  15
Thr Val Ala Arg Ala Leu Glu Gly Gln Glu Lys Pro Thr Glu Gly Pro
            20                  25                  30
Arg Asn Thr Cys Leu Gly Ser Asn Asn Met Tyr Asp Ile Phe Asn Leu
        35                  40                  45
Asn Asp Lys Ala Leu Cys Phe Thr Lys Cys Arg Gln Ser Gly Ser Asp
    50                  55                  60
Ser Cys Asn Val Glu Asn Leu Gln Arg Tyr Trp Leu Asn Tyr Glu Ala
65                  70                  75                  80
His Leu Met Lys Glu Gly Leu Thr Gln Lys Val Asn Thr Pro Phe Leu
            85                  90                  95
Lys Ala Leu Val Gln Asn Leu Ser Thr Asn Thr Ala Glu Asp Phe Tyr
            100                 105                 110
Phe Ser Leu Glu Pro Ser Gln Val Pro Arg Gln Val Met Lys Asp Glu
        115                 120                 125
Asp Lys Pro Pro Asp Arg Val Arg Leu Pro Lys Ser Leu Phe Arg Ser
    130                 135                 140
Leu Pro Gly Asn Arg Ser Val Val Arg Leu Ala Val Thr Ile Leu Asp
145                 150                 155                 160
Ile Gly Pro Gly Thr Leu Phe Lys Gly Pro Arg Leu Gly Leu Gly Asp
            165                 170                 175
Gly Ser Gly Val Leu Asn Asn Arg Leu Val Gly Leu Ser Val Gly Gln
            180                 185                 190
Met His Val Thr Lys Leu Ala Glu Pro Leu Glu Ile Val Phe Ser His
    195                 200                 205
Gln Arg Pro Pro Pro Asn Met Thr Leu Thr Cys Val Phe Trp Asp Val
    210                 215                 220
Thr Lys Ala Leu Val Gly Gly Tyr Asp Ile Leu Ala Ile Tyr Glu Val
225                 230                 235                 240
Glu His Phe Gln Gln Glu Gln Cys Val Ala Val Ile Ser Val Cys Ser
            245                 250                 255
Arg Gly Gly Lys Gly Ser Ala Glu Cys Gly His Trp Gly Lys Gly Leu
            260                 265                 270
Thr Thr Glu His Ser Ser Pro Val Pro Ala Val Thr His Leu Ser Leu
    275                 280                 285
Ala Arg Ile Ala Glu Lys Gly Lys Ala Gly Cys Pro Ala Arg Ala Cys
    290                 295                 300
Arg Val His Ser Trp Val Leu Val Leu Ser Gly Lys Arg Glu Val Pro
305                 310                 315                 320
Glu Asn Phe Phe Ile Asp Pro Phe Thr Gly His Ser Tyr Ser Thr Gln
            325                 330                 335
Asp Glu His Phe Leu Gly Ile Glu Ser Leu Trp Asn His Lys Asn Tyr
            340                 345                 350
Trp Ile Asn Met Gln Asp Cys Trp Asn Cys Cys Lys Val Pro Arg Glu
    355                 360                 365
Gly Glu Leu Gly Asp Pro Glu Glu Arg Leu Ala His Leu Ser Trp Trp
    370                 375                 380
Leu Gly Leu Ser Val His Leu His Gly Gly Arg Ser Gln Ser Ala Ala
385                 390                 395                 400
Pro Glu Leu Pro Ser His His Pro Val Pro Ala Ala Leu Met Val Tyr
            405                 410                 415
Glu Pro Leu Pro Ala Thr Thr Gly Leu Asp Leu Xaa Pro Gly Xaa Pro
            420                 425                 430
```

```
Cys Glu Met Gly Val His Ala Pro Gly Asp Xaa Xaa Val Ser Ala Val
        435                 440                 445
Leu Asp Xaa Arg Arg Arg Gln Trp Asp Lys Arg Xaa Gly Xaa Cys Gly
        450                 455                 460
Lys Ser Gly Gln Gly Gly Xaa Gly Xaa Glu Leu Arg His Ala Pro Leu
465                 470                 475                 480
Val Val Glu Gln Ile Glu Ile Ser Pro Glu Gly Thr Asn Ile Leu Glu
                485                 490                 495
Ile Lys Glu Trp Tyr Gln Asn Arg Glu Asp Met Leu Glu Leu Lys His
                500                 505                 510
Ile Asn Lys Thr Thr Asp Leu Lys Thr Asp Tyr Phe Lys Pro Gly His
        515                 520                 525
Pro Gln Ala Leu Arg Val His Ser Tyr Lys Ser Met Gln Pro Glu Met
        530                 535                 540
Asp Arg Val Ile Glu Phe Tyr Glu Thr Ala Arg Val Asp Gly Leu Met
545                 550                 555                 560
Lys Arg Glu Glu Thr Pro Arg Thr Met Thr Glu Tyr Tyr Gln Gly Arg
                565                 570                 575
Pro Asp Phe Leu Ser Tyr Arg His Ala
        580                 585
```

```
<210> 303
<211> 457
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(457)
<223> Xaa = X or * as defined in Table 6


<400> 303
Gly Asp Gln Lys Val His Pro Phe Ser Thr Pro Ser Pro Gly Thr Pro
  1               5                  10                  15
Ala Phe His Ile Pro Thr Thr Phe Ser Pro Ala Ala Gly Pro Gly His
            20                  25                  30
His Leu Pro Met Asp Pro Gly Glu Gly Leu Ala Glu Gly Pro Gly Leu
        35                  40                  45
Pro Gly Ser Ser Gly Xaa Arg Pro Leu Xaa Val Pro Ser Arg Arg Ala
    50                  55                  60
Ser His Cys Pro Pro Gly Ala Thr Lys Ala Arg Gly Gly Arg Cys Arg
65                  70                  75                  80
Gly Pro Ala Ala Thr Thr Gly Xaa Ala Ala Cys Ala Gly Arg Thr Ala
                85                  90                  95
Ala Pro Gly Xaa Pro Gly Ala Ser Pro Pro Ala Ala Gln Ala Leu His
            100                 105                 110
His Ser Leu Gln Glu Pro Gly Glu His Arg Gly Arg Pro Gly Pro Ser
        115                 120                 125
Ala Ser Ala Pro Ser Ala Gly Thr Val Asp Gln Val Gly Gly Gly Ala
    130                 135                 140
Glu Arg Met Pro Thr Thr Pro Gly Pro Arg His Ala Val Gly Glu Cys
145                 150                 155                 160
Gly Pro Thr Cys Ser Ala Ser Leu Arg Gly Pro Leu Xaa Pro Leu Pro
                165                 170                 175
Asn Leu Ala Ala Pro Ala Gln Trp Gly Ser His Gln Leu Gln Gly Glu
            180                 185                 190
Glu Gln Ile Gln Val Pro Ser Cys Cys Phe Ala Pro Gly Ile Gln Arg
        195                 200                 205
Leu Leu Pro Arg Pro Gln Thr Gln Glu Pro Gly Phe Xaa Thr Gln Thr
    210                 215                 220
Pro Asp Pro Gly Leu Lys Pro Gln Asp Ser Lys Pro Arg Leu Pro Gly
```

```
225                      230   .                235                      240
Leu Gln Thr Gln Thr Pro Asp Pro Gly Pro Arg Thr Arg Ala Asp Gly
                245                      250                  255
Phe Pro Asp Gln Arg Gly Pro Val Gly Gln Gly Gln Trp Glu Gly Ala
            260                      265                  270
Pro Gly Gly His Thr Leu Gly Asn Ser Gly Gly Ser Cys Leu Ala Gly
        275                      280                  285
Pro Pro Trp Xaa Arg Ser Glu Gly His Glu Glu Cys Pro Ser Ser Cys
    290                      295                  300
Gln Ser Gln Phe Gly Glu Leu Arg Leu Trp Leu Pro Arg Gly Gly Trp
305                      310                  315                  320
Ala Glu Gly Val Ser Ala Gly Ser His Gly Pro Pro Trp Pro Ala Gly
                325                      330                  335
Pro Ala Pro Pro Gly Pro Gln Pro Leu Gly Trp Asp Ala Gly Pro His
            340                      345                  350
Phe Pro Glu Glu Ser Arg Thr Arg Pro Gly Pro Asp Pro Glu Pro Xaa
            355                      360                  365
Lys Asp His Gly Thr Val Leu Xaa Leu Thr Gln Arg Lys His Arg Asp
        370                      375                  380
Gly His Lys Glu Pro Arg Thr Lys Ile Gln Leu Pro Val Pro Gly Ala
385                      390                  395                  400
Glu Gly Gln Thr Cys Pro Pro Glu Pro Trp Ala Gly Ala His Arg Arg
                405                      410                  415
Asn Ala Asn Trp Gln Ala Gln Gly Ser Arg Arg Glu Arg Pro Ser Gly
            420                      425                  430
Phe Gln Thr Pro Arg Ser His Trp Val Pro Ser Ala Gly Arg Ser Gly
        435                      440                  445
Phe Leu Gly Pro Gln Phe Ser Cys Leu
    450                      455
```

```
        <210> 304
        <211> 42
        <212> PRT
        <213> Homo sapiens


        <400> 304
Met Ser Gly Arg Val Phe Arg Cys Gln Ala Leu Val Ala Tyr Thr Val
 1               5                   10                  15
Leu Ser Glu Leu Phe Thr Glu Ala Lys Glu Gln Arg Leu Ala Thr Asp
                20                  25                  30
Glu Gly Gln Lys Glu Phe Ser Ala Glu Ser
            35                  40
```

```
        <210> 305
        <211> 41
        <212> PRT
        <213> Homo sapiens


        <400> 305
Met Ser Gly Arg Val Phe Arg Cys Gln Ala Leu Val Ala Tyr Thr Val
 1               5                   10                  15
Leu Ser Glu Leu Phe Thr Glu Ala Lys Glu Gln Arg Leu Ala Thr Asp
                20                  25                  30
Glu Gly Gln Lys Glu Phe Ser Ala Glu
            35                  40
```

```
        <210> 306
        <211> 827
        <212> PRT
        <213> Homo sapiens


        <400> 306
Gly Lys Tyr Tyr Lys Leu Ser Ser Gly Thr Ala Pro Thr Cys Val Ser
 1               5                  10                  15
Leu Gly Trp Gly Leu Ala Arg Gly Asp Ser Ala Ala Pro Ala Leu Gly
            20                  25                  30
Ser Arg Thr Ser Ala Cys Ala Pro Cys Ser His Gly Thr Trp Lys Leu
        35                  40                  45
Ser Leu Glu Pro Ser Asp Arg Leu Ser Pro Cys Asp Arg Ser Ser Glu
    50                  55                  60
Glu Ala His Thr His Ala Pro His Arg Leu Leu Ala Leu Val Ala Ser
65                  70                  75                  80
Leu Pro Trp Ser Arg Leu Pro Leu Leu Ala Pro Gln Ser His Ser Glu
                85                  90                  95
Ala Glu Ala Thr Ser Gln Pro Thr Gly Val Glu Asn His His Gln Lys
            100                 105                 110
Thr Arg Tyr Val Lys Ala Gly Gly Pro Val Ile Cys Arg Ser Leu Pro
        115                 120                 125
Glu Ser Arg Gly Phe Leu Trp Ala Ser Glu Gly Arg Lys Cys Met Leu
    130                 135                 140
Ile Gly Ser Trp Ala Ala Met Gly Arg Leu Arg Lys Ser Thr Ile Ser
145                 150                 155                 160
Ser Arg Phe Gly Pro Gln Thr Leu Ala Gly Thr Gly Arg Pro Gln Ala
                165                 170                 175
Ile Pro Val Leu Lys Lys His Ser Asp Ala Val Leu Leu Gly Val Cys
            180                 185                 190
Phe Leu Lys Leu Leu His Gln His His Gln Glu Leu Gly Glu Asn Ala
        195                 200                 205
Asp Ser Gln Thr Leu Pro Gln Thr His Trp Glu Phe Ile Leu Ser Glu
    210                 215                 220
Asp Tyr Asn Lys Met Thr Pro Val Lys Asn Tyr Gln Val Leu Glu Val
225                 230                 235                 240
Leu Ala Arg Ala Met Arg Gln Glu Lys Gln Ile Lys Ser Ile Gln Leu
                245                 250                 255
Gly Lys Glu Glu Val Lys Leu Ser Val Phe Ala Asp Asp Met Ile Val
            260                 265                 270
Tyr Leu Glu Asn Pro Ile Val Ser Ala Gln Asn Leu Leu Lys Leu Ile
        275                 280                 285
Ser Asn Phe Ser Lys Val Ser Gly Tyr Lys Ile Asn Val Gln Lys Ser
    290                 295                 300
Gln Ala Phe Leu Tyr Thr Asn Asn Arg Gln Thr Glu Ser Gln Ile Ile
305                 310                 315                 320
Ser Glu Leu Pro Phe Thr Ile Pro Ser Lys Arg Ile Lys Tyr Leu Gly
                325                 330                 335
Ile Gln Leu Thr Arg Asp Val Lys Asp Leu Phe Lys Glu Asn Tyr Lys
            340                 345                 350
Pro Leu Leu Asn Glu Ile Lys Glu Asp Thr Asn Lys Trp Lys Asn Ile
        355                 360                 365
Pro Cys Ser Trp Val Gly Arg Ile Asn Ile Met Lys Met Ala Ile Leu
    370                 375                 380
Pro Arg Val Ile Tyr Ile Phe Asn Ala Ile Ser Ile Lys Leu Pro Met
385                 390                 395                 400
Thr Phe Phe Thr Glu Leu Glu Lys Thr Thr Leu Lys Phe Ile Trp Asn
                405                 410                 415
Gln Lys Arg Ala Arg Ile Ala Lys Thr Ile Leu Ser Gln Lys Asn Lys
            420                 425                 430
Ala Gly Gly Ile Thr Leu Pro Asp Phe Lys Leu Tyr Tyr Lys Ala Thr
        435                 440                 445
Val Thr Lys Thr Ala Trp Tyr Trp Tyr Gln Asn Arg Gly Val Asp Gln
```

```
        450                      455                     460
Trp Asn Arg Ile Glu Pro Ser Glu Ile Ile Pro His Ile His Asn His
465                     470                     475                 480
Leu Ile Phe Asp Lys Pro Asp Lys Asn Lys Lys Trp Gly Lys Asp Ser
                485                     490                     495
Leu Phe Thr Lys Trp Cys Trp Glu Asn Trp Leu Ala Ile Cys Arg Lys
                500                     505                     510
Leu Lys Leu Asp Pro Phe Leu Thr Pro Tyr Thr Lys Ile Asn Ser Thr
.               515                     520                     525
Trp Ile Lys Asp Leu Asn Val Arg Pro Lys Thr Ile Lys Thr Leu Glu
        530                     535                   540
Glu Asn Leu Gly Ile Thr Ile Gln Asp Ile Gly Met Gly Lys Asp Phe
545                     550                     555                 560
Met Ser Lys Thr Pro Lys Ala Met Ala Thr Lys Ala Lys Ile Asp Lys
                565                     570                     575
Trp Asp Leu Ile Lys Leu Lys Ser Phe Cys Thr Ala Lys Glu Thr Thr
                580                     585                     590
Ile Arg Val Asn Arg Gln Pro Thr Glu Trp Glu Lys Ile Phe Thr Ile
        595                     600                     605
Tyr Pro Ser Asp Lys Gly Leu Ile Pro Arg Ile Tyr Lys Glu Leu Lys
        610                     615                     620
Gln Asn Leu Gln Glu Lys Ile Lys Gln Pro His Gln Lys Val Gly Lys
625                     630                     635                 640
Gly Tyr Lys Gln Thr Phe Leu Lys Arg Arg His Leu Cys Ser Gln Gln
                645                     650                     655
Thr His Glu Lys Met Phe Ile Ile Thr Gly His Gln Arg Asn Ala Lys
                660                   ;   665                     670
Gln Asn His Asn Lys Ile His Leu Thr Pro Val Arg Met Ala Ile Ile
        675                     680                   685
Lys Lys Ser Gly Asn Asn Arg Asp Met Asp Glu Ala Gly Asn His His
        690                     695                   700
Ser Glu Gln Thr Ile Ala Arg Thr Glu Asn Gln Ala Pro Tyr Leu Leu
705                     710                     715                 720
Thr His Arg Trp Glu Leu Asn Asn Glu Asn Thr Trp Thr Gln Val Glu
                725                     730                     735
Glu His His Thr Leu Gly Pro Ile Val Gly Val Ile Cys Arg Lys Val
                740                     745                     750
Phe Pro Gly Asn Ser Gly Pro Ser Lys Pro Ser Gly Leu His Phe Ser
        755                     760                   765
Gln Pro Leu Pro Gln Val Thr Ser Val Val Ala Lys Ile Thr Ile Val
        770                     775                   780
Pro Trp Glu Met Lys Leu Ile Ala Met Gly Val Gln Asp Glu Leu Asn
785                     790                     795                 800
Ile Ala Phe His Lys Asn His Leu Leu Met Asn Asp Thr Thr Ile His
                805                     810                     815
Met Thr Pro Tyr Ile Gln Pro Ala Pro Lys Ser
                820                     825
```

```
        <210> 307
        <211> 135
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(135)
        <223> Xaa = X or * as defined in Table 6


        <400> 307
Thr Pro Leu Pro Val Cys His Phe Thr Cys Arg Lys Asn His Leu Lys
    1               5                   10                  15
```

```
Gly Met Glu Asn Leu Cys Leu His Lys Lys Cys Met Trp Met Ser Thr
            20                   ·25                   30
Val Ala Phe Ser Ile Ile Ala Lys Thr Trp Lys Gln Pro Arg Cys Pro
        35                   40                   45
Ser Ala Ala Pro Ser Trp Lys Gln Pro Thr His Leu Thr Thr Gly Asp
    50                   55                   60
Trp Ala Asn Gly Leu Gly Xaa Phe Ser Thr Arg Glu Tyr Val Thr Ala
65                   70                   75                   80
Xaa Glu Arg Thr Asn Gln Ser Lys Pro Asp Thr Thr Thr Trp Val Asn
                85                   90                   95
Leu Thr Asp Val Gln Leu Ser Asn Ser Ser Gln Ala Pro Arg Gly Val
            100                  105                  110
Ser Thr Thr Leu Gln Phe Pro Val Leu Gly Thr Val Asp Lys Ser Gly
        115                  120                  125
Val Thr Met Thr Phe Trp Val
    130                  135


        <210> 308
        <211> 313
        <212> PRT
        <213> Homo sapiens


        <400> 308
Met Gly Asn Lys Thr Tyr Gly Gly Gln Asn Gln Met Leu Ile Phe Ala
1                   5                   10                   15
Phe Thr Leu His Ser Leu Phe Leu Asn Ser Gly Asp Gly Arg Leu Ser
            20                   25                   30
Phe Glu Ser Ser Ser Gln Lys Pro Gly Gly Phe Arg Asn Ile Ala Ile
        35                   40                   45
Gln Thr Ser Pro Ser Leu Arg Lys His Phe Pro Val Phe Lys Arg Lys
    50                   55                   60
Arg Leu Thr Ala Ser Lys Ser Val Glu Glu Met Pro Thr Ala Ser Gln
65                   70                   75                   80
Ser Ala Ile His Val Asn Gly Asn Leu Ser Glu Gln Asp Ile Val Ser
                85                   90                   95
Ser Asp Leu Ala Tyr Leu Arg Leu Ala Gln His Leu Glu Asp Gly Pro
            100                  105                  110
Arg Arg Val Lys Val Ser His Ala Phe Leu Pro Arg Val Pro Lys Val
        115                  120                  125
Gln Ser Asn Gly Pro Val Ser Ile Cys Leu Glu Ala Gly Thr Trp Arg
    130                  135                  140
Ser Leu Glu Lys Ala Thr Ala Ala Ile Gln Val Pro Asp Asp Ile Tyr
145                  150                  155                  160
His Ser Pro Ser Trp Glu Ala Arg Glu Ser Ala Leu Ser Pro Asp Arg
            165                  170                  175
Ser Ala Glu His Asn Ser Leu Ser Arg Pro Ser Asp Pro Gly Leu Ser
            180                  185                  190
Leu Gln Pro Gln Leu Leu Pro Thr Leu Cys Leu Pro Phe His Val Leu
    195                  200                  205
Tyr Thr Arg Ser Pro Gln Ser Leu Gly His Gly Pro Ile Ala Val His
    210                  215                  220
Gly Leu Leu Gly Thr Met Leu Arg Ser Arg Arg Thr Trp Ser Phe Leu
225                  230                  235                  240
Tyr Pro Gly Phe Leu Pro Trp Cys Ser Gly Arg Ile Gly Ser Arg Val
            245                  250                  255
Gly Leu Glu Asn Glu Cys Lys Val Ser Leu Ser Gly Ser Ser Ser Gln
            260                  265                  270
Pro Met Gly Glu Pro Glu Gly Arg Trp Ser Ser Pro Glu Val Gly Pro
        275                  280                  285
Leu Ala Ser Pro Gly Ser Pro Leu Ile Ala Trp Ala Lys Leu Arg Phe
    290                  295                  300
```

Val Pro Pro Val Asp Asp Leu Pro Val
305   310

<210> 309
<211> 509
<212> PRT
<213> Homo sapiens

<400> 309
Met Asp Ser Gln Glu Val Glu Lys Tyr Pro Asn Thr Ser Val Ala Cys
1   5   10   15
Glu Glu Ile Pro Phe Ser Gly Ile His Val Ala Gly Gly Lys Ser Gly
                20   25   30
Ala Leu Glu His Gly Lys Asp Asp Leu Asp Glu Pro Ile Glu Asn Pro
            35   40   45
Leu Phe Cys Phe Ser Ser Phe Ser Asn Ala Leu Ala Ile Leu Leu Pro
        50   55   60
Lys Val Phe Leu Lys Asn Ile His Ile Leu Gln Phe Ile Tyr Arg Ser
65   70   75   80
Phe His Leu Leu Thr Met Ala Lys Ala Lys Phe Glu Gly Ala Glu Ser
                85   90   95
Val Glu Pro Val Ser Pro Ser Gln Pro Lys Arg Pro Ser Tyr Val Pro
            100   105   110
Leu Glu Glu Leu Trp Thr Arg Leu Thr Lys Gly Asn Ser Arg Pro Gln
        115   120   125
Gln Arg Asp Arg Glu Lys Gly Gly Trp Met Lys Gly Val Gln Gln Gly
    130   135   140
His Gln Gly Val Gly Lys Gln Glu Glu Gly Ser Glu Asn Ile Lys Glu
145   150   155   160
Lys Ala Gly Ile Val Val Cys Glu Val Pro Asn Asn Lys Leu Asp Lys
                165   170   175
Phe Met Gly Ile Leu Ser Trp Lys Asp Ser Lys His Ser Leu Asn Asn
                180   185   190
Glu Lys Ile Ile Leu Arg Gly Cys Ile Leu Arg Asn Thr Ser Trp Cys
        195   200   205
Phe Gly Met Val Ile Phe Ala Gly Pro Asp Thr Lys Leu Met Gln Asn
    210   215   220
Ser Gly Lys Thr Lys Phe Lys Arg Thr Ser Ile Asp Arg Leu Met Asn
225   230   235   240
Thr Leu Val Leu Trp Ile Met Leu Ile Ser Gln Pro Val Val Glu Phe
                245   250   255
Ile Met Arg Gly His Ser Tyr Phe Ile Asn Trp Asp Arg Lys Met Tyr
            260   265   270
Tyr Ser Arg Lys Ala Ile Pro Ala Val Ala Arg Thr Thr Thr Leu Asn
        275   280   285
Glu Glu Leu Gly Gln Ile Glu Tyr Ile Phe Ser Asp Lys Thr Gly Thr
    290   295   300
Leu Thr Gln Asn Ile Met Thr Phe Lys Arg Cys Ser Ile Asn Gly Arg
305   310   315   320
Ile Tyr Gly Glu Val His Asp Asp Leu Asp Gln Lys Thr Glu Ile Thr
                325   330   335
Gln Leu Ile His Arg Trp Leu Ala Arg Leu Lys Lys Lys Lys Arg Glu
            340   345   350
Lys Asn Gln Thr Asp Thr Ile Lys Asn Asp Lys Gly Asn Ile Thr Thr
        355   360   365
Asp Leu Ala Glu Thr Gln Thr Thr Ile Arg Glu Tyr Tyr Lys His Leu
    370   375   380
Tyr Thr Asn Lys Leu Glu Asn Leu Glu Glu Met Asp Lys Phe Leu Asp
385   390   395   400
Ala Tyr Thr Leu Ser Arg Leu Asn Gln Glu Glu Val Glu Ser Leu Ser
                405   410   415

204

```
Arg Pro Ile Thr Ser Ser Glu Ile Glu Ala Val Ile Asn Ser Leu Pro
        420                 425                 430
Thr Lys Lys Ser Pro Gly Pro Asp Arg Phe Thr Ala Glu Leu Tyr Gln
        435                 440                 445
Lys Tyr Lys Glu Glu Leu Glu Lys Glu Pro Val Asp Phe Ser Val Lys
        450                 455                 460
Ser Gln Ala Asp Arg Glu Phe Gln Phe Phe Asp His Asn Leu Met Glu
465                 470                 475                 480
Ser Ile Lys Met Gly Asp Pro Lys Val His Glu Phe Leu Arg Leu Leu
                485                 490                 495
Ala Leu Cys His Thr Val Met Ser Glu Glu Asn Ser Ala
        500                 505
```

```
        <210> 310
        <211> 70
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(70)
        <223> Xaa = X or * as defined in Table 6


        <400> 310
Asp Trp Thr Val Gly Phe Val Gly Asn Ser Asp Thr Glu Leu Pro Gly
1                   5                   10                  15
Ser Val Gly Arg Arg Ser Leu Trp Glu Ser Ser Tyr Ser Thr Arg Thr
            20                  25                  30
Arg Asn Gln Gly Arg Gln Ala Ile Gln Ile Gln His Ser Xaa Leu Arg
        35                  40                  45
Glu Val Glu Arg Lys Ser Gly Gln Lys Ala Thr Met Ser Ser Gly Gly
        50                  55                  60
Gly Tyr Cys Gln Pro Glu
65                  70
```

```
        <210> 311
        <211> 250
        <212> PRT
        <213> Homo sapiens


        <400> 311
Ala Ile Arg Gln Glu Lys Glu Ile Lys Gly Ile Gln Leu Gly Lys Glu
1                   5                   10                  15
Glu Val Lys Leu Ser Leu Phe Ala Asp Asp Met Ile Leu Tyr Leu Glu
            20                  25                  30
Asn Pro Ile Val Ser Ala Gln Asn Leu Leu Lys Leu Ile Ser Asn Phe
        35                  40                  45
Ser Lys Val Ser Gly Tyr Lys Ile Asn Val Gln Lys Ser Gln Ala Phe
        50                  55                  60
Leu Tyr Thr Asn Asn Arg Gln Thr Glu Ser Gln Ile Met Ser Glu Leu
65                  70                  75                  80
Pro Phe Thr Ile Ala Ser Lys Arg Ile Lys Tyr Leu Gly Ile Gln Leu
                85                  90                  95
Thr Arg Asp Val Lys Asp Leu Phe Lys Glu Asn Tyr Lys Leu Leu Leu
            100                 105                 110
Lys Glu Ile Lys Glu Asp Arg Asn Lys Trp Lys Asn Ile Pro Cys Ser
        115                 120                 125
Trp Val Gly Arg Ile Asn Met Val Lys Met Ala Ile Leu Pro Lys Val
```

```
        130                    135                    140
Ile Tyr Gly Phe Asn Ala Ile Pro Ile Lys Leu Pro Met Ile Phe Phe
145                    150                    155                    160
Thr Glu Leu Glu Lys Thr Thr Ser Lys Phe Ile Trp Asn Gln Lys Arg
                165                    170                    175
Ala His Ile Ala Lys Ser Ile Leu Ser Gln Lys Asn Lys Ala Gly Gly
                180                    185                    190
Ile Thr Pro Pro Asp Phe Lys Leu Tyr Tyr Lys Ala Thr Val Thr Lys
                195                    200                    205
Thr Ala Trp Thr Arg Lys Ile Tyr Ser Ala Lys Lys Arg Lys Val Lys
                210                    215                    220
Ile Ser Val Glu Pro Val Tyr Ser Gly Val Thr Leu Thr Thr Ala Ile
225                    230                    235                    240
Gln Leu Val Pro Leu Leu Cys Thr Ala Leu
                245                    250


        <210> 312
        <211> 297
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(297)
        <223> Xaa = X or * as defined in Table 6


        <400> 312
Met Asp Tyr Glu Lys Ala Asp Lys Arg Pro Thr Pro Trp Glu Ala Ala
 1               5                   10                  15
Ala Lys Ser Pro Leu Gly Leu Val Asp Asp Ala Phe Gln Pro Lys Asn
                20                  25                  30
Ile Gln Glu Ser Ile Val Ala Asn Val Val Ser Ala Ala Arg Arg Lys
            35                  40                  45
Val Leu Pro Gly Pro Pro Glu Asp Trp Asn Glu Arg Leu Ser Tyr Ile
        50                  55                  60
Pro Gln Thr Gln Lys Ala Tyr Met Gly Ser Cys Gly Arg Gln Glu Tyr
65                  70                  75                  80
Asn Val Thr Ala Asn Asn Asn Met Ser Thr Thr Ser Gln Tyr Gly Ser
                85                  90                  95
Gln Leu Pro Tyr Ala Tyr Tyr Arg Gln Ala Ser Arg Asn Asp Ser Ala
            100                 105                 110
Ile Met Ser Met Glu Thr Arg His Leu Tyr Thr Arg Gln Leu Tyr Cys
        115                 120                 125
Tyr Ser Phe Gly Asp Ser Gly Asn Phe Cys Glu Asn Thr Asn Gly Arg
        130                 135                 140
Pro Ala Ala Asp Ala Val Arg Gly Leu Thr Ile Leu Ser Leu Ser Thr
145                 150                 155                 160
Thr Ser Ile Pro Ser Ser Gly Ile Ser Glu Ala Leu Ile Ser Glu Asn
                165                 170                 175
Glu Asn Lys Asn Leu Glu His Leu Thr His Gly Gly Tyr Val Glu Ser
            180                 185                 190
Thr Thr Leu Gln Ile Arg Pro Ala Thr Lys Thr Gln Cys Thr Glu Phe
            195                 200                 205
Phe Leu Ala Pro Val Lys Thr Glu Val Pro Leu Ala Glu Asn Gln Arg
        210                 215                 220
Ser Gly Pro Asp Cys Ala Gly Ser Leu Lys Glu Glu Thr Gly Pro Ser
225                 230                 235                 240
Tyr Gln Arg Ala Pro Gln Met Pro Asp Ser Gln Arg Gly Arg Val Ala
            245                 250                 255
Glu Glu Leu Ile Leu Arg Glu Lys Val Glu Ala Ser Thr Gln Asn Asn
            260                 265                 270
```

```
Tyr Tyr Val Gly Glu Leu Thr Gly Val Thr Leu Gln Asn Gly Tyr Gly
        275                 280                 285
Glu Lys Pro Ile Leu Ala Thr Gln Xaa
        290                 295
```

```
        <210> 313
        <211> 325
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 313
Met Leu Lys Tyr Thr Gly Ala His Gln Glu Val Glu Leu Ser Ala Pro
1               5                   10                  15
Ile Val Thr Lys Met Ala Thr Gln Tyr Leu Arg Glu Asn Leu Phe Gly
            20                  25                  30
Arg Phe Asp Asn Asp Asn Phe Cys Leu Leu Asn Gly Asp Ala Val Ile
        35                  40                  45
Phe Arg Met Tyr Val Ser Trp Lys Leu Val Glu Lys Glu Arg Thr Glu
        50                  55                  60
Ile Met Leu Lys Tyr Thr Gly Ala His Gln Glu Thr Trp Leu Lys Asp
65                  70                  75                  80
Leu Glu Glu Ser Pro Leu Tyr Glu Ala Leu Ser Met Arg Gly Gln Asp
                85                  90                  95
Lys Glu Thr Leu Gly Leu Trp Ile Gln Leu Pro Trp Cys Pro Trp Gly
        100                 105                 110
Lys Ala Val Gln Met His Met Asn Pro Ser Ser Phe Gln Leu Asp Thr
        115                 120                 125
Lys Pro Gly Lys Gly Glu Leu Ala Gly Arg Leu Ile Ile Pro His Gln
        130                 135                 140
Glu Ala Ser Ile Leu Glu Leu Ser Leu Leu Leu Met Thr Cys Cys Val
145                 150                 155                 160
Glu Arg Glu Gly Lys Thr Ser Val Arg Val Ala Ala Val Gly Glu Cys
                165                 170                 175
Thr Ala Ser Glu Thr Pro Asn Gln Gly Ala Gly Arg Leu Ser Leu Trp
            180                 185                 190
Gln Gln Leu Thr Ser Lys Lys Glu Thr Ile Met Glu Lys Glu His Thr
        195                 200                 205
Asp Cys Val Ser Gln Thr Val Ala Leu Ile Ser Thr Cys Val Lys Glu
        210                 215                 220
Gly Gly Ser Arg Pro Ala Asp Lys Asp Leu Glu Glu Gly Gly Gly Leu
225                 230                 235                 240
Glu Ala Glu Ser Pro Lys Gln Ser Pro Asn Leu Cys Val Ile Leu Arg
                245                 250                 255
His Asn Leu Ala Ser Arg Pro Gly Gln Leu Ala Leu Val Thr Val Gly
            260                 265                 270
Thr Met Gln Gly Arg Pro Leu Ser His Ser Ser Glu Val Lys Gly Thr
        275                 280                 285
Thr Phe Val Thr His Ser Val Pro Ala Gly Lys Glu Lys Asp Glu Glu
        290                 295                 300
Arg Gly Ile Gly Asp Leu Glu His Ala Arg Asp Leu Arg Asn Ser Pro
305                 310                 315                 320
Thr Pro Leu Phe Tyr
                325
```

```
        <210> 314
        <211> 301
        <212> PRT
        <213> Homo sapiens
```

207

```
<400> 314
Met Ser Glu Leu Pro Phe Thr Ile Ala Ser Lys Arg Ile Lys Tyr Leu
1               5                   10                  15
Gly Ile Gln Leu Thr Arg Asp Val Lys Asp Phe Phe Lys Glu Asn Tyr
            20                  25                  30
Lys Pro Leu Leu Asn Glu Ile Lys Glu Glu Thr Asn Lys Trp Lys Asn
        35                  40                  45
Ile Pro Cys Ser Trp Val Gly Arg Ile Asn Ile Val Lys Met Ala Ile
        50                  55                  60
Leu Pro Gln Arg Leu Pro His Gly Phe Leu Pro Asn Met Lys Leu Glu
65              70                  75                      80
Val Val Asp Lys Arg Asn Pro Arg Leu Ile Arg Val Ala Thr Ile Val
                85                  90                  95
Asp Val Asp Asp Gln Arg Val Lys His Ser Met Thr Ala Ser Ser Gly
            100                 105                 110
Ser Gly Val Ser Ala Asp Leu Asn Thr Ala Ser Gln Pro Leu Trp Leu
        115                 120                 125
Leu Lys Thr Ala Leu Ala Val Ser Ser Ser Val Lys Val His Pro Pro
    130                 135                 140
Val Ser Gly Leu Ile Phe Ser Ser Ser Arg Thr Leu Leu Ser Phe Met
145                 150                 155                 160
Gly Ile Met Arg Glu Asp Leu Gly Phe Ser Arg Arg Gln Ile Leu His
            165                 170                 175
Phe Pro Met Ala Leu Ser Lys Ser Ala Gly Arg Arg Ser Lys Ile Gly
            180                 185                 190
Gln Leu Asp Ala Leu Ser Gln Asp Phe Gly Leu Arg Asp Arg Asp Ser
        195                 200                 205
Ser Lys Lys Gly Thr Gly Tyr Pro Asn Pro Glu Asn Phe Ser Trp Thr
    210                 215                 220
Glu Tyr Leu Glu Ala Thr Gln Thr Asn Ala Val Pro Ala Lys Val Phe
225                 230                 235                 240
Lys Met Asp Ser Asp Val Gly Glu Asn Arg Lys Ile Leu Arg Asp Glu
                245                 250                 255
Arg Pro Asn Tyr Ser Gln Tyr Thr Pro Phe Ser Arg Cys Asp Asn Ala
            260                 265                 270
Ser Tyr Lys Glu Asn Val Phe Leu Gln Lys Leu Glu Arg Asn Thr Pro
    275                 280                 285
Asp Ile Ala Glu Arg Phe Asp Cys Leu Leu Leu Thr Tyr
    290                 295                 300
```

```
<210> 315
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(80)
<223> Xaa = X or * as defined in Table 6
```

```
<400> 315
Met Met Ser Trp Ser Ser Ala Glu Lys Gly Pro Glu Gly His Arg Arg
1               5                   10                  15
Arg Glu Trp Pro Ser Gln Trp Glu Asp Glu Pro Xaa Asn Gln Asn Gly
            20                  25                  30
Glu Ser Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Lys Glu Thr Xaa
        35                  40                  45
Glu Glu Arg Arg Gly Glu Lys Arg Glu Lys Arg Glu Lys Lys Arg Arg
    50                  55                  60
Arg Glu Gly Arg Met Ser Ile Ser Phe Ala Arg Arg Tyr Ser Ile Leu
```

```
        <210> 316
        <211> 106
        <212> PRT
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)...(106)
        <223> Xaa = X or * as defined in Table 6


        <400> 316
Ser Gln Arg Thr Ala Gly Asn Pro Cys Leu His Pro Val Ser Leu Cys
 1               5                  10                  15
Gly Ser Ala Ser Trp Met Pro Met Ile Met Pro Gln Arg Trp Ser Ser
            20                  25                  30
Leu Cys Ser Ala Met Glu Lys Pro Ala Ser Pro Cys Leu Xaa Met Pro
            35                  40                  45
Pro Gln Ala Thr Cys Trp Cys Pro Ser Arg Leu Pro Met Ala Trp Ala
        50                  55                  60
Ser Gly His Xaa His Thr Ser Thr Gly His Ser Gln Leu Pro Ala Ile
65                  70                  75                  80
Pro Phe Asp Asn His Cys Gly Lys Arg Cys Arg Leu Gly Gly Lys Trp
                85                  90                  95
Arg Ala Pro Leu Gln His Pro Gln Trp Lys
                100                 105


        <210> 317
        <211> 89
        <212> PRT
        <213> Homo sapiens


        <400> 317
Arg Arg Pro Thr Arg Pro Gln Glu Glu Gly Gly Ser Glu Ser Ser Thr
 1               5                  10                  15
Met Thr Glu Leu Glu Thr Ala Met Gly Leu Ile Ile Asp Val Phe Ser
            20                  25                  30
Arg Tyr Ser Gly Ser Glu Gly Ser Thr Gln Thr Leu Thr Lys Gly Glu
            35                  40                  45
Leu Lys Val Leu Met Glu Lys Glu Leu Pro Gly Phe Leu Gln Leu Ser
        50                  55                  60
Gly Pro Gly Leu Gly His Gln His Thr Leu Leu Leu Leu Phe Arg Ser
65                  70                  75                  80
Ala Ser Trp Ser Arg Leu Val Pro Gln
                85


        <210> 318
        <211> 151
        <212> PRT
        <213> Homo sapiens


        <400> 318
```

```
Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser Tyr Val Asp Val Gln
 1               5                  10                  15
Arg Ala Cys Ala Gly Ile Arg Gly Ala Phe Glu Lys Pro Gln Gly Ala
            20              25                  30
Val Ala Arg Val His Ile Gly Gln Val Ile Met Ser Ile Cys Thr Lys
        35              40                  45
Leu Gln Asn Lys Glu His Val Ile Glu Ala Leu Cys Lys Ala Asn Phe
    50              55                  60
Lys Phe Pro Gly Arg Gln Asn Ile His Phe Ser Glu Lys Trp Asp Phe
65              70                  75                  80
Thr Lys Phe Ser Val Asp Glu Phe Glu Asp Met Met Ala Glu Lys Gln
            85                  90                  95
Leu Ile Pro Asp Asn Cys Gly Val Lys Tyr Thr Pro Asn Arg Asp Pro
            100                 105                 110
Pro Asp Lys Arg Asp Gly Val Ala Leu Gln His Gly Leu Leu Leu Trp
        115             120                 125
Gln Leu Leu Gln Asn Lys Ile Arg Leu His Gln Gly Arg Glu Lys Lys
    130             135                 140
Pro Pro Lys Lys Ala Arg Arg
145             150
```

```
<210> 319
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(124)
<223> Xaa = X or * as defined in Table 6


<400> 319
Met Ser Arg Arg Lys Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu
 1               5                  10                  15
Phe Ser Pro Arg Asp Arg Glu Glu Val Thr Thr Cys Phe Pro Cys Pro
            20                  25                  30
Pro Pro Thr Pro Pro Gly Leu Val Thr Ser Pro Pro Ala Pro Arg Ala
        35                  40                  45
Arg Leu Gly Gln Pro Cys Ser Ala Arg Asn Glu Asn Leu Leu Glu Ala
    50                  55                  60
Asp Tyr Asp Pro Pro Glu Pro Ile Val Leu Arg Asn Thr Thr Ala Thr
65                  70                  75                  80
His Thr His Ser His Ser Val Ser Pro Ser Leu Tyr Asn Ser Asp Ser
            85                  90                  95
Pro Gln Pro Leu Lys His Leu Gly Ala Val Ser Ala Ala Glu Thr Gly
            100             105                 110
Val Arg Gly Met Met Gly Met Tyr Leu Lys Pro Xaa
        115             120
```

```
<210> 320
<211> 1067
<212> PRT
<213> Homo sapiens


<400> 320
Met Cys Glu Leu Asp Ile Leu His Asp Ser Leu Tyr Gln Phe Cys Pro
 1               5                  10                  15
Glu Leu His Leu Lys Arg Leu Asn Ser Leu Thr Leu Ala Cys His Ala
```

```
                    20                          25                          30
Leu Leu Asp Cys Lys Thr Leu Thr Leu Thr Glu Leu Gly Arg Asn Leu
            35                          40                          45
Pro Thr Lys Ala Arg Thr Lys His Asn Ile Lys Arg Ile Asp Arg Leu
            50                          55                          60
Leu Gly Asn Arg His Leu His Lys Glu Arg Leu Ala Val Tyr Arg Trp
65                          70                          75                  80
His Ala Ser Phe Ile Cys Ser Gly Asn Thr Met Pro Ile Val Leu Val
                    85                          90                          95
Asp Trp Ser Asp Ile Arg Glu Gln Lys Arg Leu Met Val Leu Arg Ala
            100                         105                         110
Ser Val Ala Leu His Gly Arg Ser Val Thr Leu Tyr Glu Lys Ala Phe
            115                         120                         125
Pro Leu Ser Glu Gln Cys Ser Lys Lys Ala His Asp Gln Phe Leu Ala
            130                         135                         140
Asp Leu Ala Ser Ile Leu Pro Ser Asn Thr Thr Pro Leu Ile Val Ser
145                         150                         155                 160
Asp Ala Gly Phe Lys Val Pro Trp Tyr Lys Ser Val Glu Lys Leu Gly
                    165                         170                         175
Trp Tyr Trp Leu Ser Arg Val Arg Gly Lys Val Gln Tyr Ala Asp Leu
            180                         185                         190
Gly Ala Glu Asn Trp Lys Pro Ile Ser Asn Leu His Asp Met Ser Ser
            195                         200                         205
Ser His Ser Lys Thr Leu Gly Tyr Lys Arg Leu Thr Lys Ser Asn Pro
            210                         215                         220
Ile Ser Cys Gln Ile Leu Leu Tyr Lys Ser Arg Ser Lys Gly Arg Lys
225                         230                         235                 240
Asn Gln Arg Ser Thr Arg Thr His Cys His His Pro Ser Pro Lys Ile
                    245                         250                         255
Tyr Ser Ala Ser Ala Lys Glu Pro Trp Ile Leu Ala Thr Asn Leu Pro
            260                         265                         270
Val Glu Ile Arg Thr Pro Lys Gln Leu Val Asn Ile Tyr Ser Lys Arg
            275                         280                         285
Met Gln Ile Glu Glu Thr Phe Arg Asp Leu Lys Ser Pro Ala Tyr Gly
            290                         295                         300
Leu Gly Leu Arg His Ser Arg Thr Ser Ser Ser Glu Arg Phe Asp Ile
305                         310                         315                 320
Met Leu Leu Ile Ala Leu Met Leu Gln Leu Thr Cys Trp Leu Ala Gly
                    325                         330           '             335
Val His Ala Gln Lys Gln Gly Trp Asp Lys His Phe Gln Ala Asn Thr
            340                         345                         350
Val Arg Asn Arg Asn Leu Lys Ile Tyr Ser His Met Val Thr Leu Trp
            355                         360                         365
Gly Asn Tyr Glu Gly Ile Ser Gln Thr Gln Ala Phe Ala Lys Glu Asn
            370                         375                         380
Asn Gln Lys Ala Tyr Lys Glu Thr Tyr Gly Val Ser His Ile Thr Arg
385                         390                         395                 400
His Asp Met Leu Gln Ile Pro Lys Gln Gln Asn Glu Lys Tyr Gln
            405                         410                         415
Val Pro Gln Phe Asp Gln Ser Thr Ile Lys Asn Ile Glu Ser Ala Lys
            420                         425                         430
Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr
            435                         440                         445
Val Ala Glu Tyr Asn Gly Tyr His Val Val Phe Ala Leu Ala Gly Ser
            450                         455                         460
Pro Lys Asp Ala Asp Asp Thr Ser Ile Tyr Met Phe Tyr Gln Lys Val
465                         470                         475                 480
Gly Asp Asn Ser Ile Asp Ser Trp Lys Asn Ala Gly Arg Val Phe Lys
                    485                         490                         495
Asp Ser Asp Lys Phe Asp Ala Asn Asp Pro Ile Leu Lys Asp Gln Thr
            500                         505                         510
Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys Ile Arg
            515                         520                         525
Leu Phe Tyr Thr Asp Tyr Ser Gly Lys His Tyr Gly Lys Gln Ser Leu
```

```
          530                      535                      540
Thr Thr Ala Gln Lys Ala Tyr Arg Leu Glu Ile Val Ser Leu Glu Met
545                      550                      555                      560
Gln Lys Asn Gly Ala Ala Asp Ala Ala Pro Tyr Arg Gln Ile Glu Tyr
                    565                      570                      575
Trp Ala Leu Gly His Gly Asp Asp Ile Lys Lys Ala Val Ala Phe Trp
                580                      585                      590
Ser Ser Gly Trp Pro Val Gly Phe Ser Lys Met Glu Lys Ala Gly Lys
                595                      600                      605
Ile Leu Arg Ser Gln Val Lys Phe Pro Glu Tyr Met Glu Glu Ser Ser
        610                      615                      620
Cys Leu Gly Arg Gly Ser Leu Met Ser Leu Asn Asn Thr Ser Ser Ser
625                      630                      635                      640
Asn Gly Ser Phe Ile Phe Val Leu Pro Leu Lys Leu Leu Arg Val Gly
                    645                      650                      655
Asp Thr Tyr Asn Ser Ser Asp Gln Ser Arg Met Ala Trp Arg Leu Thr
                660                      665                      670
Ile Glu Phe Gly Gly Ser Glu Leu His Leu Gly Val Arg Glu Glu Ala
        675                      680                      685
Gly His Gln Lys Gly Leu Val His Glu Ser Gly Asn Pro Ala Arg Ser
    690                      695                      700
Ser Gly Ser Asp Pro Gln His Ala Arg His Arg Gln Pro Ser Ala Thr
705                      710                      715                      720
Arg Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu Pro Ala Pro
                    725                      730                      735
Leu Ser Leu Pro Val Pro Thr Ser Ala Ile Gln Val Arg Val Thr Ala
                740                      745                      750
Tyr Pro Leu Leu Ala Gln Cys Leu Gln Ala Ala Phe Pro Pro Leu Leu
        755                      760                      765
Gly Ser Gly Cys Gly Gln Glu Gly Thr Gly Ala Gly Gly Gly Gly Gly
    770                      775                      780
Ala Ala Gly Val Arg Glu Gln Leu Glu Asp Arg Arg Ala Ala Ala Glu
785                      790                      795                      800
Pro Gly Asp Leu Pro Gly Gly Lys Arg Val Arg Gly Arg Gly Ala Arg
                    805                      810                      815
Glu Gly Pro Gly Val Gly Ala Glu Gly Pro Pro Leu Glu Arg Asn Arg
                820                      825                      830
Pro Ser Ser Pro Leu Pro Trp Leu Ala Ala Pro Ala Ala Gly Ala Ser
        835                      840                      845
Gln Phe Ala Glu Ile Gln Gly Ala Gly Lys Gly Glu Met Arg Ala Lys
    850                      855                      860
Asp Ala Glu Arg Gly Arg Ala Lys Leu Arg Gly Glu Leu Ser Ser Ser
865                      870                      875                      880
Gly Arg Lys Ile Phe Asp Pro Asp Asp Leu Tyr Ser Gly Val Asn Phe
                    885                      890                      895
Ser Lys Val Leu Ser Thr Leu Leu Ala Val Asn Lys Ala Thr Glu Asp
                900                      905                      910
Gln Leu Ser Glu Arg Pro Cys Gly Arg Ser Ser Ser Leu Ser Ala Ala
        915                      920                      925
Asn Thr Ser Gln Thr Asn Pro Gln Gly Ala Val Ser Ser Thr Val Ser
    930                      935                      940
Gly Leu Gln Arg Gln Ser Lys Thr Val Glu Met Thr Glu Asn Gly Ser
945                      950                      955                      960
His Gln Leu Ile Val Lys Ala Arg Phe Asn Phe Lys Gln Thr Asn Glu
                    965                      970                      975
Asp Glu Leu Ser Val Cys Lys Gly Asp Ile Ile Tyr Val Thr Arg Val
                980                      985                      990
Glu Glu Gly Gly Trp Trp Glu Gly Thr Leu Asn Gly Arg Thr Gly Trp
            995                      1000                     1005
Phe Pro Ser Asn Tyr Val Arg Glu Ile Lys Ser Ser Glu Arg Pro Leu
    1010                     1015                     1020
Ser Pro Lys Ala Val Lys Gly Phe Glu Thr Ala Pro Leu Thr Lys Asn
1025                     1030                     1035                     1040
Tyr Tyr Thr Val Met Ser Arg Ser Leu Thr Ser Thr Val Leu Lys Asn
```

212

```
                    1045                      1050                        1055
        Ser Lys Val Ala Arg Ile His Ser Lys Pro Tyr
                         1060                    1065
```

```
        <210> 321
        <211> 191
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 321
Arg Ser Pro Thr Leu Ser Ser Pro Pro Pro Ala Ser Lys Ala Gln Ala
1                   5                   10                  15
Leu Ala Leu Arg Ser Glu Ala Gln Ala Gln Met Pro Arg Leu Pro Ala
             20                  25                  30
Pro Arg Val Arg Arg Ser Ser Ala Ala Ala Ser Ala Ala Ala Arg Ser
         35                  40                  45
Leu Ala Glu Thr Phe Ser Gly Lys Glu Cys Gln Trp Thr Asp Ala Cys
    50                  55                  60
Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr Thr Val Ala Asn
65                  70                  75                  80
Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly Gln Lys Cys Glu
             85                  90                  95
Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys Gln His Gly Gly
         100                 105                 110
Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln Cys Leu Gln Gly
    115                 120                 125
Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro Cys Ala Pro Ser
    130                 135                 140
Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly Asp Phe Thr Phe
145                 150                 155                 160
Glu Cys Asn Cys Leu Pro Glu Thr Val Arg Arg Gly Thr Glu Leu Trp
             165                 170                 175
Glu Arg Asp Arg Glu Val Trp Asn Gly Lys Glu Pro Asp Glu Asn
         180                 185                 190
```

```
        <210> 322
        <211> 71
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 322
Met Pro Gly Pro Ala Ala Ala Ser His Arg Ala Ser Thr Tyr Val Ser
1                   5                   10                  15
Thr Trp Ser Cys Pro Pro His His Ser Trp His Ala Trp Gln Cys Thr
             20                  25                  30
Val Ala Arg Pro His Leu Gln Thr Ser His Cys Cys Thr Ser Gly Leu
         35                  40                  45
Pro Leu Ala Asp Met Glu Ser Arg Leu Val Ala Ser Pro Ser Glu Trp
    50                  55                  60
Asn Lys Leu Thr Trp Ala Gln
65                  70
```

```
        <210> 323
        <211> 72
        <212> PRT
        <213> Homo sapiens
```

213

```
        <400> 323
Glu Ser Gln Ser Leu Glu Thr Gly Leu Arg Ala Leu Ile Trp Ser Thr
1               5                   10                  15
Arg Lys Pro Gly Gly Pro Val Leu Gly Gly Leu Val Leu Ile Lys Trp
            20                  25                  30
Ala Trp Ala Ser Arg Ser Pro Ala Ser Pro Ser Asp Pro Ser Pro Gly
        35                  40                  45
Pro Asn Leu Cys Cys Ser Pro Thr Ser Pro Ala Thr Lys Pro Arg Val
    50                  55                  60
Asp Gly Pro Phe Val Ile Arg Asn
65                  70
```

```
        <210> 324
        <211> 205
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 324
Met Asn Trp Val Leu Gln Lys Phe Ile Thr Ala Trp Lys Phe Met Gly
1               5                   10                  15
Tyr Arg Lys Ser Ser Asn Ser Ala Arg Gly Ser Thr Ile Lys Glu His
            20                  25                  30
Ile Glu Leu Asp Ala Gln Arg Pro Val Arg Arg Ser Gly Pro Ile Gln
        35                  40                  45
Ala Ser Gly Ala His Pro Lys Lys Gly Arg Gly Val Ser Cys Ser Val
    50                  55                  60
Glu Glu Pro Ser Asp Gln Gln Ser Pro Ser Pro Pro Ser Pro Leu Thr
65                  70                  75                  80
Phe Gln Pro Lys Asp Gly Glu Ile Asn Phe Ser Val Ile Gly Gln Tyr
                85                  90                  95
Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Gly Lys
            100                 105                 110
Ser Thr Leu Gly Met Ser Leu His Val Ser Ser Ser Val Phe Arg Arg
        115                 120                 125
Tyr Ile Leu Pro Gly Tyr Gln Pro Arg Gly His Thr Val Met Val Ser
    130                 135                 140
Gln Val Asn Ile Asp Phe Gln Thr Arg Glu Ala Thr Arg Lys Asn Leu
145                 150                 155                 160
Gln Glu Pro Ser Leu Thr Cys Phe Asp Gln Ala Gln Gly Lys Val His
                165                 170                 175
Ser Leu Met Glu Lys Asp Ser Tyr Pro Arg Phe Leu Arg Ser Lys Met
            180                 185                 190
Tyr Leu Asp Leu Leu Ser Gln Ser Gln Arg Arg Leu Ser
        195                 200                 205
```

```
        <210> 325
        <211> 222
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 325
Met Val Met Ser Phe Val Lys Pro Gly Val Lys Glu Lys Glu Gln Val
1               5                   10                  15
Lys Lys Arg Asp Gly Glu Phe Asn Ser Glu His Ala Glu Leu Asp Val
            20                  25                  30
Pro Ala Arg Asp Thr Lys Arg Lys Phe Trp Glu Pro Thr Arg Leu Ser
```

```
            35                      40                      45
Ser Thr Leu Arg Thr Ser Ser Asp Pro Leu Phe Ser Val Pro Ile Ser
    50                      55                      60
Ile Thr Met Val Cys Glu Pro Gly Ser Lys Ser Leu Gln Ser Cys Cys
 65                      70                      75                  80
Leu Thr Ala Gly Gly Ala Asn Val Trp Glu Lys Ser Thr Cys Arg Lys
                85                      90                      95
Lys Ser Arg Gln Leu Val Leu Arg Asn Val Lys Val Pro Gly Lys Ser
                100                     105                     110
Pro Cys Gly Glu Leu Leu Pro Ile Leu Lys Lys Asn Gln Leu Asn Ile
            115                     120                     125
Leu Leu Leu Gln Pro Val Asp Thr Glu Thr Leu Glu Gly Pro Pro Gly
        130                     135                     140
Leu Gly Leu Asp Ala Glu Gly Pro Glu Lys Arg His Ser Trp Ile Leu
    145                     150                     155                 160
Leu Pro Cys Pro Gly Ile Asp His Thr Ser Gly Leu Glu Val Met Ser
                165                     170                     175
Asp Leu Tyr His Arg Lys Gly Asn Ser Leu His Pro Gln Gly Lys Arg
                180                     185                     190
Thr Lys Asp Ala Arg Lys Glu Ser Phe Pro Gln Lys Met Gly Gln Phe
            195                     200                     205
Pro Leu Gln Ser Leu Ala Val Ile Tyr Pro Glu Ala Gly Thr
        210                     215                     220
```

```
        <210> 326
        <211> 680
        <212> PRT
        <213> Homo sapiens


        <400> 326
Met Glu Glu His Ser Met Leu Met Gly Arg Lys Asn Gln Tyr Arg Glu
 1               5                       10                      15
Asn Gly Arg Ile Ala Gln Glu Leu Glu Lys Thr Thr Leu Lys Phe Ile
                20                      25                      30
Trp Asn Gln Lys Arg Ala Cys Ile Thr Lys Ser Asn Leu Ser Gln Lys
        35                      40                      45
Asn Lys Ala Gly Gly Ile Thr Leu Pro Asp Phe Lys Leu Tyr Tyr Lys
    50                      55                      60
Ala Thr Val Thr Lys Thr Ala Trp Tyr Trp Tyr Gln Asn Arg Asp Ile
 65                      70                      75                  80
Asp Gln Trp Asn Arg Thr Glu Pro Ser Glu Ile Met Pro His Ile Tyr
                85                      90                      95
Asn Tyr Leu Ile Phe Asp Lys Pro Glu Lys Asn Lys Gln Trp Gly Lys
                100                     105                     110
Asp Ser Leu Phe Asn Lys Arg Phe Trp Glu Asn Trp Leu Ala Ile Phe
            115                     120                     125
Arg Lys Leu Lys Leu Asp Pro Phe Leu Thr Pro Tyr Thr Lys Ile Asn
        130                     135                     140
Ser Arg Trp Ile Lys Asp Leu His Val Arg Pro Lys Thr Ile Lys Thr
145                     150                     155                 160
Leu Glu Glu Asn Pro Gly Ile Thr Ile Gln Asp Thr Gly Met Gly Lys
                165                     170                     175
Asp Phe Thr Ser Lys Thr Pro Lys Ala Met Ala Thr Lys Ala Lys Ile
                180                     185                     190
Asp Lys Trp Asp Leu Ile Lys Leu Lys Ser Phe Cys Thr Ala Lys Glu
            195                     200                     205
Thr Thr Ile Arg Val Asn Arg Gln Pro Thr Lys Trp Glu Lys Ile Phe
        210                     215                     220
Ala Thr Tyr Ser Ser Asp Lys Gly Leu Thr Ser Arg Ile Tyr Asn Glu
225                     230                     235                 240
Leu Lys Gln Ile His Lys Lys Lys Thr Asn Asn Pro Ile Arg Lys Trp
```

215

```
                    245                        250                        255
Ala Lys Asp Met Asn Arg His Phe Ser Lys Glu Asp Ile Tyr Ala Ala
            260                        265                        270
Lys Lys His Met Lys Lys Cys Ser Pro Ser Leu Ala Ile Arg Glu Met
            275                        280                        285
Gln Ile Lys Thr Thr Met Arg Tyr His Leu Thr Ser Val Arg Met Ala
        290                        295                        300
Ile Ile Gln Lys Ser Gly Asn Asn Arg Val Leu Pro Leu Ala Pro Leu
305                        310                        315                        320
Ala Leu Ala Ala Leu Trp Met Asp Pro Val Met Pro Gly Met Asp Gly
                    325                        330                        335
Leu Leu Gly Asp Ser Glu Ser Phe Gln Gly Leu Ser Ala Thr Phe Phe
            340                        345                        350
Ala Ser Val Phe His Ser Ala Leu His Ile Asp Ser Ala Pro Gly Pro
            355                        360                        365
Cys Ile Gly Pro Gly Asp Ser Ser Ala Asp Ser Ser Pro Thr Phe Leu
    370                        375                        380
Pro Pro Glu Ala Lys Arg Lys Asn Tyr Leu Leu Leu Trp Arg Lys Asn
385                        390                        395                        400
Leu Lys Lys Phe Ser Asp Asp Pro Lys Arg Leu Ile Glu Gly Phe Pro
                    405                        410                        415
Lys Leu Ala Leu Thr Phe Arg Leu Ile Trp Lys Asp Ile Asn Val Leu
            420                        425                        430
Leu Gly Gln Ala Leu Leu Gln Glu Glu Arg Gln Thr Ile Cys Gly Ala
            435                        440                        445
Ala Ile His Cys Arg Asn Asp Leu His Leu Glu Asn Ala Asn Tyr Pro
        450                        455                        460
Gly Gly Ala Thr Ala Val Pro Gln Leu Asp Pro Asn Gln Asp Tyr Asn
465                        470                        475                        480
Ala Lys Ala Gly Ile Trp Ala Arg Asn His Arg Leu Leu Cys Leu Ile
                    485                        490                        495
Glu Thr Thr Thr Gln Gln Pro Thr Asn Ala His Ser Pro Gln Thr Gln
            500                        505                        510
Arg Gln Gln His Asp Thr Asp Lys Pro Gln Pro Asn Pro Pro Ala Lys
            515                        520                        525
Thr Thr Gly Val Pro Val Ser Phe Leu Ala Phe Leu Tyr Gln Tyr Leu
    530                        535                        540
Cys Gly His Ile Ser Ile Ser Trp Pro Val Val Ile Leu Lys Tyr Ala
545                        550                        555                        560
Ala Ser Val Tyr Gly Ile Ser Leu Ala Asp Arg Lys Arg Gln Tyr Asp
                    565                        570                        575
Arg Tyr Phe Arg Tyr Glu Arg Leu Arg Thr Ile Lys Pro Asn Phe Leu
            580                        585                        590
Pro Phe Gln Ile Phe Lys Ser Gly Ser Val Val Lys Leu Lys Ala Gly
        595                        600                        605
Phe Thr Ile Gly Lys Val His Asn Thr Glu Val Thr Ala Leu Lys Val
610                        615                        620
Ser Asp Thr Arg Arg Ala Gln His Leu Gln Thr Gly Cys Trp Ser Ala
625                        630                        635                        640
Val Val Thr His Pro Asn Asn Leu Glu Asn Val Val Arg His Pro Pro
                    645                        650                        655
Glu Ala Leu Ala Ala Ser Tyr Asn Lys Pro Phe Ile Cys Ser Leu Val
        660                        665                        670
Thr Leu Gln Gly Ala Phe Val Thr
    675                        680
```

```
<210> 327
<211> 371
<212> PRT
<213> Homo sapiens
```

<400> 327

```
Met Leu Met Val Tyr Pro Arg Thr Asn Lys Gln Asn Gln Lys Lys Lys
1               5                   10                  15
Trp Lys Val Glu Pro Pro Thr Pro Gln Glu Pro Gly Pro Ala Lys Val
            20                  25                  30
Ala Val Thr Thr Ser Ser Ser Ser Ser Ser Ile Pro Ser Ala Glu
        35                  40                  45
Lys Val Pro Thr Thr Lys Ser Thr Leu Trp Gln Glu Met Arg Thr
    50                  55                  60
Lys Asp Gln Pro Asp Gly Ser Ser Leu Ser Pro Ala Gln Ser Pro Ser
65                  70                  75                  80
Gln Ser Gln Pro Pro Ala Ala Ser Ser Leu Arg Glu Pro Gly Leu Glu
                85                  90                  95
Ser Lys Glu Glu Glu Ser Ala Met Ser Ser Asp Arg Met Asp Cys Gly
            100                 105                 110
Arg Ile Pro Ser Thr Pro Asn His Arg Arg Ser Gln Val Ile Glu Lys
        115                 120                 125
Phe Glu Ala Leu Asp Ile Glu Lys Ala Glu His Met Glu Thr Asn Ala
    130                 135                 140
Val Gly Pro Ser Pro Ser Ser Asp Thr Arg Gln Gly Arg Ser Glu Lys
145                 150                 155                 160
Arg Ala Phe Pro Ser Lys Gln Asp Phe Thr Asn Glu Ala Pro Pro Gln
                165                 170                 175
Ala Pro Leu Pro Asp Ala Ser Ala Ser Pro Val Ser Thr Pro Lys Ser
        180                 185                 190
Gln Val Thr Gly Gln Glu Gly Gln Asn Ile Ser Trp Asp Met Ala Val
        195                 200                 205
Val Leu Lys Ala Thr Gln Glu Ala Pro Ala Ala Ser Thr Leu Gly Ser
210                 215                 220
Tyr Ser Leu Pro Gly Thr Leu Ala Lys Ser Glu Ile Leu Glu Thr His
225                 230                 235                 240
Gly Thr Met Asn Phe Leu Asp Ser Ser Pro Gln Val Arg Tyr His Pro
                245                 250                 255
Arg Asn Leu Gly Thr Ala Cys Asn Gln Ala Gly Leu Asp Arg Tyr Tyr
                260                 265                 270
Pro Glu Gly Pro Leu Pro Arg Ser Gly Asp Asp Thr Val Leu Ser Pro
        275                 280                 285
Arg Pro Ala Trp Ser Lys Leu Ala Ala Thr Arg Ser Gln Arg Leu Asp
    290                 295                 300
Pro Arg Gln Arg Gly Ser Thr Glu Arg Glu Lys Gly Glu Ala His Asn
305                 310                 315                 320
Asp Pro Leu Ala Ala Ala Pro Ile Ser Ala Ala Gly Ser Arg Arg Gly
                325                 330                 335
Ala Leu Ala Ser Trp Leu Ala Ser Pro Thr Arg Ser Gln Asn Pro Ala
                340                 345                 350
Arg Pro Pro Thr Pro Asp Cys Arg Ala Pro Leu Thr Glu Ser Ala Arg
        355                 360                 365
Pro Thr Ser
370
```

<210> 328
<211> 117
<212> PRT
<213> Homo sapiens

<400> 328

```
Met Gly Lys Trp Asp Gly Gly Phe Asn Phe Met Val Phe Cys Val Leu
1               5                   10                  15
Glu Asn Thr Cys Ser Leu Asn Arg Ser Leu Leu Glu Asn Leu Ile Phe
            20                  25                  30
Ala Thr Leu Lys Ile Ser Trp Gly Gly Ala Gly Ile Lys Gly Trp Asn
```

```
            35                        40                        45
His Met Lys Ala Gln Leu Leu Thr Cys Val Val Phe Asp Ala Gly Phe
    50                        55                        60
Gln Leu Ser Pro Gln Gly Ser Leu Glu Gln Lys His Leu Ile Leu Tyr
65                        70                        75                80
Pro Glu Leu Thr Gly Pro Ile Glu Leu Asp Pro Ile Cys Tyr His His
                85                        90                        95
His Leu Ser Asn Leu Leu Ser Gln Thr Pro Lys Ala Ser Phe Glu Val
                100                       105                       110
Leu His Gln Asn His
            115
```

```
        <210> 329
        <211> 256
        <212> PRT
        <213> Homo sapiens


        <400> 329
Pro Ile Trp Ala Thr Arg Cys Tyr Gly Gly Trp Arg Gly Ser Leu Phe
1               5                        10                        15
Leu Glu Leu Pro Arg Cys Asp Gly Pro Leu Ser Arg Trp Gly Trp Ala
                20                        25                        30
Ala Pro Lys Met Ala Ala Ser Leu Leu Phe Ser Asp Gln Gly Phe Leu
        35                        40                        45
Ala Ser Trp Ile Pro Arg Asn Gly Thr Leu Gly His Ala Met Ser Gly
        50                        55                        60
Ile Ala Leu Leu Glu Ala Val Gly His Gly Arg Glu Leu Trp Asn Pro
65                        70                        75                80
Ala Thr Ser Ala Ala Ser Val Ile Ser Asn Thr Ser Ser Asp Ala Asn
                85                        90                        95
Gln Phe Pro Lys Leu Pro Leu Gly Glu Ile Ser Pro Asp Lys Glu Lys
                100                       105                       110
Ser Tyr Trp Ser Ser Asn Pro Thr Lys Asn Asn Pro Lys Glu Thr Thr
        115                       120                       125
Arg Val Ala Val Phe Ala Arg Ile Leu Asp Val Asn Asp Asn Ala Pro
        130                       135                       140
His Phe Ala Val Phe Tyr Asp Thr Phe Val Cys Glu Asn Ala Arg Pro
145                       150                       155                160
Gly Gln Arg Asp Ala Cys Gly Arg Leu Gly Asp Trp Asp Ser Glu Lys
                165                       170                       175
Gln Glu Gly Arg Lys Gly Phe Thr Ser Thr Asn Ser Val Ile Leu His
                180                       185                       190
Lys Lys Arg Thr Lys Arg Ser Val Leu Gly Gly Asp Lys Phe Trp Gln
        195                       200                       205
Lys Lys Ser Pro Glu Ser Pro Gln Gly Asp Phe Gln Asp Ser Arg Ser
        210                       215                       220
Leu Arg Ser Thr Val Lys Phe His Lys Ser Thr Arg Lys Leu Gln Gly
225                       230                       235                240
Glu Val Glu Lys Ser Ser Val Ala Arg Asn Tyr Gly Phe Asp Pro Leu
                245                       250                       255
```

```
        <210> 330
        <211> 96
        <212> PRT
        <213> Homo sapiens

        <220>
```

218

<210> misc_feature
<222> (1)...(96)
<223> Xaa = X or * as defined in Table 6

<400> 330
Gly Cys Leu Glu His Glu Ala Ser Ser Ala Tyr Glu Trp Leu Trp Ser
1   5   10   15
Leu Cys Ala Leu Leu Asp Met Tyr Thr Ala Gly Pro Thr Lys Thr Gln
            20   25   30
Thr Leu Gln Pro Met Gly Gln Pro Asn Leu Lys Gly Asp Gly Gly Phe
        35   40   45
Thr Arg Glu Ser Thr Gly Phe Met Gln Leu Pro Ala Asp Phe Ile Ser
    50   55   60
Ser Leu Ile Cys His Glu Thr Trp Val Pro Gly Lys Pro Ser Thr Ala
65   70   75   80
Met His Arg Gly Arg Tyr Trp Ala Glu Pro Ile Met Leu Pro Lys Xaa
                85   90   95

<210> 331
<211> 142
<212> PRT
<213> Homo sapiens

<400> 331
Met Ser Glu Lys Asn Thr Pro Leu Val Leu Ser Gly Glu Asn Gln Lys
1   5   10   15
Lys Gly Arg Glu Ile Gly Val Cys Arg Lys Gln Ser Gln Cys Asp His
            20   25   30
Gln Asp Asn Asn Ser His Thr Leu Arg Phe Ser Ser Tyr Ser Ser Ser
        35   40   45
Ser Gly Pro Val Thr Leu Val Ser Phe His Ser His Asn Tyr Pro Ser
    50   55   60
Lys Val Leu Leu Gln Gly Asn Leu Asp Thr Glu Thr Cys Thr Glu Arg
65   70   75   80
Arg Gln Arg Glu Ile Trp Thr Gln Arg His Glu Gly Lys Cys Gly His
                85   90   95
Arg Asp Met Tyr Arg Glu Lys Thr Lys Arg Lys Tyr Arg Glu Lys Ala
            100   105   110
Ile Tyr Lys Leu Arg Lys Gly Pro Glu Thr Asp Pro Ser Ser Gln Pro
        115   120   125
Ser Glu Arg Thr Asn Pro Ala Asn Thr Leu Ile Ser Asp Ser
    130   135   140

<210> 332
<211> 424
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(424)
<223> Xaa = X or * as defined in Table 6

<400> 332
Thr Ile Ser Trp Arg Gln Gly Arg Gly Gly Glu Ala Gly Arg Arg Leu

219

```
  1                   5                    10                   15
Trp His Thr Pro Pro Gln Val Lys His Leu Glu Pro Gly His Pro Glu
             20              25              30
Gln Gln Ala Arg Lys Ala Gln Ile Gln Gly Gln Pro Pro Ala Pro Gly
         35              40              45
Trp Asp Leu Thr Gln Gly Glu Gln Ala Gly Asn Ile His Gln His Cys
     50              55              60
Gly Gln Ser Arg Gly Xaa Gln Gln His Gln Lys Asp Pro Xaa Gly His
 65              70              75              80
Arg Phe Ala Glu Gly Met Gln Ser Leu Ser Lys Glu Leu Gln Ser Asp
             85              90              95
Xaa Thr Ser Arg Lys Gly Gly Phe Arg Val Pro Cys Ser His Asn Arg
         100             105             110
Glu Pro Pro Thr Arg Pro Gly Asp Pro Cys Asp Ser Pro Ala Gly Leu
     115             120              ·125
Gly Leu Gln Glu Cys Arg Ala Arg Tyr Arg Pro Gly Lys Pro Ser Ser
     130             135             140
Pro Pro Arg Gly Gln Ser Arg Ala Thr Gly Pro Val Arg Trp His Pro
145             150             155             160
Ser Pro Ser Arg Asn Xaa Gly Pro Pro Gly Ser Arg Pro Ala Pro Gly
             165             170             175
Thr Asp Pro Ala Pro Gly Arg Pro Pro Gly Arg Pro Leu Ala Ala Ser
         180             185             190
Gly Leu Leu Pro Asn Ser Pro Pro Ala Pro Gly Ser Pro Gln Gly Pro
     195             200             205
Pro Pro Pro Arg Gly Ser Asn Arg Pro Arg Phe Pro His Trp Leu Arg
     210             215             220
Arg Pro Ala Gly Arg Gly Ala Pro Cys Xaa Pro Gln Pro Arg Ser Pro
225             230             235             240
Gln Gln His Ile Pro Glu His Arg Thr Lys Pro Val Pro Ala Pro Glu
             245             250             255
Pro Pro Ser Gly Ser Arg Asn Thr Asp Pro Pro Gly Gln Pro Arg Ala
         260             265             270
Arg Gly Thr Trp Lys Ala Ser Pro Gly His Arg Ala Asp Ser Ala Ser
     275             280             285
Arg Arg Ala Ser Phe Leu Phe Arg Cys Leu Ala Asn Leu Gln Arg Ser
     290             295             300
Leu Lys Gln Met Arg Gly Lys Leu His Ser Gln Lys Ala Gln Phe Trp
305             310             315             320
Phe Ile Leu Asn Gly Phe Ile Gly Gly Val Ile Gly Arg Arg Met Thr
             325             330             335
Asp Cys Gln Ala Cys Glu Pro Arg Leu Arg Ser Ile Gln Cys Gln Leu
         340             345             350
Pro Glu Ser Tyr Thr Ser Leu Cys His Pro Ala Ala Leu Thr Gln Ser
     355             360             365
Gly Pro Lys Asn Val Leu Glu Arg Asp Gln Pro Ser Ala Cys Ser Leu
     370             375             380
Lys Thr Pro Ala Gln Thr Cys Leu Pro Gln Cys Ser Leu His Trp Thr
385             390             395             400
Leu Arg Asp Asp Gln Thr Gln Pro Leu Thr Ala Pro Ser Ser Thr Met
             405             410             415
Asn Gly Ala Tyr Arg Met Lys Cys
             420
```

```
        <210> 333
        <211> 49
        <212> PRT
        <213> Homo sapiens


        <400> 333
Pro Leu Val Val Cys Leu Leu Glu Phe Tyr Cys Thr His Leu Arg Asp
```

```
  1                5                   10                   15
Gly Leu Asn Ser Val Gln Leu Ala Tyr Arg Gly Cys Arg Pro Thr Glu
            20                  25                  30
Ala Thr Phe Thr Pro Ala Arg Arg Pro Trp Gln Ala Arg Ala Pro Cys
        35                  40                  45
Arg
```

```
        <210> 334
        <211> 30
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 334
Met Ala Glu Tyr Asp Leu Thr Thr Arg Ile Ala His Phe Leu Asp Arg
  1                5                   10                   15
His Leu Val Phe Pro Leu Leu Glu Phe Leu Ser Val Lys Glu
            20                  25                  30
```

```
        <210> 335
        <211> 123
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 335
Arg Gly Ala Arg Ile Arg Tyr Ala Val Cys Val Cys Val Cys Val Cys
  1                5                   10                   15
Val Tyr Pro Cys Val His Val Cys Thr Cys Val Arg Met Cys Leu Cys
            20                  25                  30
Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Gly Gly Cys Lys
        35                  40                  45
Cys Thr Cys Gly Pro Thr Glu Gly Gly Glu Lys Ala Trp Leu Phe Thr
    50                  55                  60
Ser Ile Gln Glu Gly Arg Arg Cys Gly Trp Ser Ser Ser Leu Arg Gly
65                  70                  75                  80
Ser Ala Ala Gly Arg Asp Leu Tyr Ser Ala Arg Leu Phe Ala His Arg
                85                  90                  95
Leu Leu Leu Leu Glu Gly Arg Pro Trp Gln Asp Ala Gly Ala Pro Ser
            100                 105                 110
Ala Ala Arg Ile Ser Arg Ser Glu Pro Trp Ser
            115                 120
```

INTERNATIONAL SEARCH REPORT

	International application No.
	PCT/US01/10472

A. CLASSIFICATION OF SUBJECT MATTER
IPC(7)   : C07H 21/04; C12N 1/20, 5/02, 15/00, 15/12; C12P 21/06; C12Q 1/68
US CL   : 435/6, 69.1, 252.33, 320.1, 325; 536/23.1, 23.5
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
    U.S. : 435/6, 69.1, 252.33, 320.1, 325; 536/23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GenBank, Accession No. L29164, 16 May 1995 (16.06.95), see entire entry.	2, 19
---		-----------
A		1, 3-9

☐ Further documents are listed in the continuation of Box C.	☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier application or patent published on or after the international filing date	"X"	document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
03 August 2001 (03.08.2001)	**3 0 AUG 2001**

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Marianne P. Allen
Facsimile No. (703)305-3230	Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/10472

Box I   Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest   ☐   The additional search fees were accompanied by the applicant's protest.
                        ☐   No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING
This application contains the following inventions or groups of inventions which are not so linked as to form a single general
inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must
be paid.

Group I, claims 1-9 and 19 drawn to polynucleotides.

Group II, claims 10-11 and 20, drawn to polypeptides.

Group III, claim 12, drawn to antibodies.

Group IV, claims 13-15, drawn to methods of detection using polynucleotides.

Group V, claim 16, drawn to methods of detection using polypeptides.

Group VI, claims 17-18, drawn to methods of identifying compounds that bind to a polypeptide.

Group VII, claim 21, drawn to a polypeptide array.

Group VIII, claims 22-26, drawn to a polynucleotide array.

Group IX, claim 27, drawn to a method of treatment using a polypeptide.

Group X, claim 28, drawn to a method of treatment using an antibody.

Group XI, claim 29, drawn to a method of detecting bone marrow cells by means of polynucleotides.

Group XII, claim 30, drawn to a method of detecting bone marrow cells by means of polypeptides.

The inventions listed as Groups I-XII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT
Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

For each of the above named groups, each SEQ ID NO. recited in the claims is considered to be a different inventive concept. If no
additional fees are paid and in the absence of a request to search a specific sequence, Group 1 will be examined with respect to SEQ
ID NO: 1. Each SEQ ID NO. has a different structure and does not share an obvious special technical feature with any other SEQ ID
NO. With respect to Groups VI and VIII, each different subset of polypeptides or polynucleotides on the array is considered to be a
different inventive concept. The inventions listed as Groups I-XII do not relate to a single inventive concept because the
compositions of Groups I, II, III, VII, and VIII differ structurally and functionally and do not share any obvious special technical
feature. The methods of Groups IV, V, IX, X, XI, and XII each have different starting materials, method steps, and/or goals. For
purposes of calculating the number of inventions, each group embraces at least 168 SEQ ID NOS. (directly or by dependency), and as
such, 12 groups multiplied by 168 SEQ ID NOS. gives 2016 inventions.